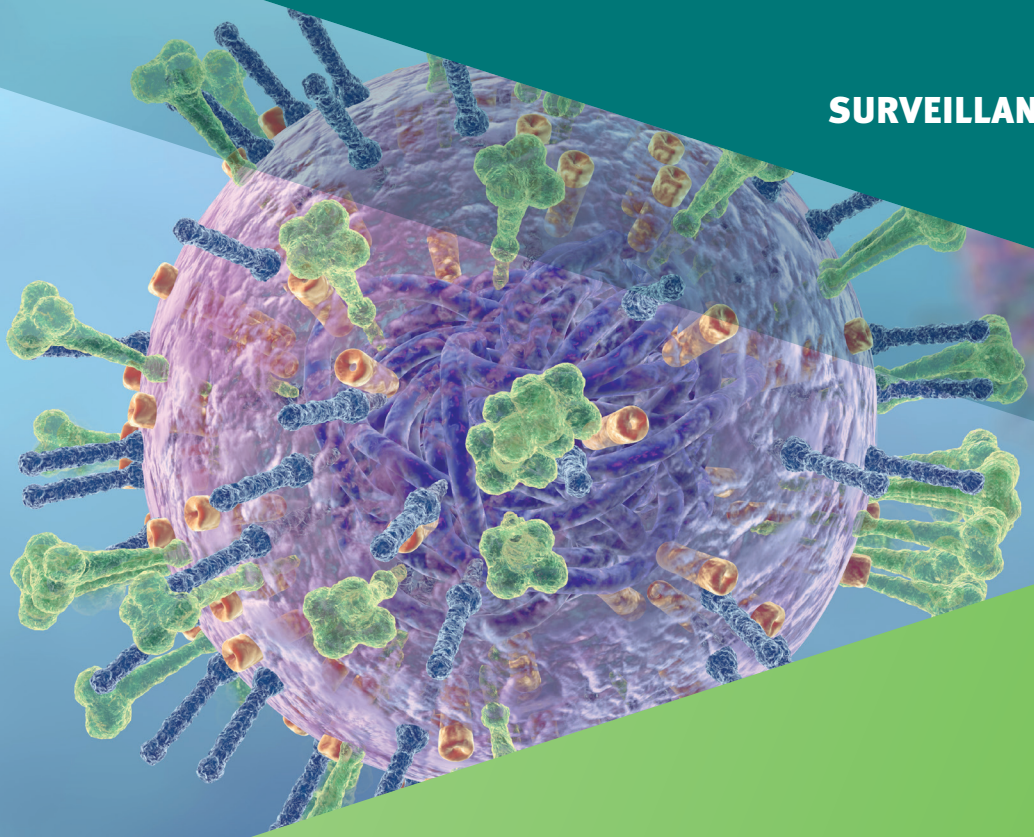
SURVEILLANCE & MONITORING



Influenza virus characteristics, week 40 2025 to week 33 2026, EU/EEA

ECDC SURVEILLANCE & MONITORING

Influenza virus characteristics, week 40 2025 to week 33 2026, EU/EEA



This report was produced by the European Centre for Disease Prevention and Control on behalf of the European Respiratory Virus Network (ERVI-Net) and its subnetwork the European Reference Laboratory Network for Human Influenza (ERLI-Net).

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Disclaimer
The data presented in this report were extracted on 20 August 2026 from the TESSy database. Any error in the database on 20 August 2026 will have affected the analysis. All countries with unclear reports have been contacted to correct the data in between data extractions and retrospectively for future reports.

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Abbreviations

A(H1)pdm09	A(H1N1) subtype of influenza A viruses
A(H1N1)pdm09	A(H1N1) subtype of influenza A viruses
A(H3)	A(H3N2) subtype of influenza A viruses
A(H3N2)	A(H3N2) subtype of influenza A viruses
AAHRI	Amino acid mutations associated with highly reduced inhibition
AANI	Amino acid mutations associated with normal inhibition
AANS	Amino acid mutations associated with normal susceptibility
AARI	Amino acid mutations associated with reduced inhibition
AARS	Amino acid mutations associated with reduced susceptibility
AAINP	Amino acid mutations interpretation not possible
B(Vic), B/Victoria	B/Victoria/2/87-lineage of influenza B viruses
ERLI-Net	European Reference Laboratory Network for Human Influenza
ERVI-Net	European Respiratory Viruses Network
EU/EEA	European Union and European Economic Area
H and HA	Haemagglutinin
HI	Haemagglutination inhibition
HRI	Highly reduced inhibition
N and NA	Neuraminidase
NAI	Neuraminidase Inhibition Assay
NAAT	Nucleic Acid Amplification Tests
NH	Northern hemisphere
NI	Normal inhibition
NRL	National Reference Laboratory
NS	Normal susceptibility
RI	Reduced inhibition
RS	Reduced susceptibility
SH	Southern hemisphere
VCM	Vaccine composition meeting
VE	Vaccine effectiveness
WHO	World Health Organization
WHO CC	World Health Organization Collaborating Centre

Executive summary

This report summarises influenza virological surveillance data from all 30 European Union and European Economic Area (EU/EEA) countries from week 40 2025 to week 33 2026, as reported by National Reference Laboratories (NRLs) to The European Surveillance System (TESSy) at the European Centre for Disease Prevention and Control.

Detections

Within the reporting period, 256 967 influenza virus detections (sentinel and non-sentinel combined) were reported, of which 249 514 (97.1 %) were type A and 3 292 (1.3 %) were type B viruses; another 4 161 viruses were reported untyped.

Of the 56 946 subtyped influenza A viruses (23 % of type A viruses), 20 072 (35 %) were A(H1)pdm09 and 36 874 (65 %) were A(H3). Of the 3 292 reported influenza type B viruses, the lineage for 372 (11 %) was determined as all falling into the B/Victoria/2/87-lineage (B/Victoria).

A(H1N1)pdm09

For A(H1N1)pdm09 viruses, 25 countries reported 6 636 haemagglutinin (HA) sequences. Of all A(H1N1)pdm09 viruses, the majority belonged to clade 5a.2a.1, newly emerged subclade D.3.1.1 (6 270, 95 %), defined by HA substitutions R113K, A139D, E283K and K302E and which was not represented by any reporting category or reference strain defined for this season. Within the genetic diversification of 5a.2a.1 clade, 340 (5 %) viruses belonged to subclade D.3.1, carrying HA substitutions T216A, T120A, I372V, I460T, V520A and was represented by A/Missouri/11/2025 egg- and cell-based vaccine strains for northern hemisphere 2026-2027 influenza season.

Among the 838 antigenically characterised A(H1)pdm09 viruses, the main reported categories were A/Missouri/11/2025-like, clade 5a.2a.1(D.3.1) and A/Victoria/4897/2022-like, clade 5a.2a.1(D), representing 44.2 % and 51.1 %, respectively.

In total, 6 612 A(H1N1)pdm09 viruses were assessed for antiviral susceptibility to oseltamivir and/or zanamivir and/or baloxavir marboxil by 25 countries. Phenotypically assessed reduced and highly reduced inhibition by Oseltamivir was observed for ten (2.3 %) and three (0.7 %) of the 437 tested A(H1N1)pdm09 viruses. Genetic substitutions associated with reduced and highly reduced inhibition by Oseltamivir were observed for 147 (2.4 %, associated with neuraminidase (NA) gene substitutions I223V and S247N mainly, or NA_I223M/T or NA_S247R) and 15 (0.2 %, associated with NA_H275Y or NA_N295S) of the 6 088 assessed viruses, respectively. For Zanamivir, substitutions associated with reduced and highly reduced inhibition were observed for one (<0.1 %, associated with NA_S247R) and one (<0.1%, associated with NA_Q136K) of the 6 089 assessed viruses, respectively. Out of the 4 020 assessed A(H1N1)pdm09 viruses for baloxavir marboxil, substitutions associated with reduced susceptibility were observed for four (0.1 %, associated with polymerase acidic (PA) protein gene substitutions E23G or PA_A37T or PA_E199G/K) viruses.

A(H3N2)

For A(H3N2) viruses, 25 countries reported 9 538 HA sequences. All A(H3) HA sequences fell into clade 2a.3a.1 and there to seven different subclades. Most viruses (8 808, 92%) fell into newly emerged subclade K (former J.2.4.1) characterised by K2N, S144N (a potential addition of an N-glycosylation site), N158D, I160K, Q173R, T328A and S378N and represented by A/Norway/8765/2025. The remaining 719 A(H3N2) viruses belonged to subclades J.2 (83, 0.9%; which is the NH 2025-26 season vaccine strain represented by A/Croatia/10136RV/2023), J.2.2 (47, 0.5%), J.2.3 (235, 2.5%), J.2.4 (47, 0.5%) and J.2.4.2 (307, 3.2%).

Among the 1 137 antigenically characterised A(H3) viruses, the main reported categories were A/Croatia/10136RV/2023-like, subclade J.2, A/Singapore/GP20238/2024-like, subclade J.2.4 and A/Norway/8765/2025-like, subclade K, representing 43.3 %, 34.7 % and 10.6 %, respectively.

In total, 9 441 A(H3N2) viruses were assessed for antiviral susceptibility to oseltamivir and/or zanamivir and/or baloxavir marboxil by 25 countries. Phenotypically assessed reduced inhibition to Oseltamivir was observed for one (0.2%) of the 505 tested A(H3N2), and reduced inhibition to Zanamivir was observed for one (0.2%) of 491 tested A(H3N2) viruses. Genetic substitutions associated with reduced and highly reduced inhibition by Oseltamivir were observed for 19 (0.2%, associated with NA_S331R mainly or NA_K249E or NA_N329R) and three (<0.1%, associated with NA_E119V or NA_del245-248/247-250), respectively, of the 8 869 viruses that could be assessed. Reduced inhibition by Zanamivir was observed for 17 (0.2%, associated with NA_S331R mainly or NA_del245-248/247-250) among the 8 883 viruses that could be assessed. Out of the 5 397 assessed A(H3N2) viruses, substitutions associated with reduced susceptibility for baloxavir marboxil were observed for seven (0.1%, associated with PA_I38L) A(H3N2) viruses.

B/Victoria

For B/Victoria viruses, 14 countries reported 318 HA sequences. The majority (288, 91%) of the viruses fell in the branch of subclade C.5 defined by D197E, compared with NH 2025-26 vaccine virus B/Austria/1359417/2021_Egg. In that clade, the B/Victoria viruses fell into subclades C.5.6 (126, 40%), C.5.6.1 (89, 28%), C.5.1 (54, 17%) and C.5.7 (18, 6%). Twenty-eight (9%) viruses represented the subclade C.3, where half of them belonged to subclade C.3.1 and half to C.3.3.

The 21 antigenically characterised B/Victoria viruses were all reported as B/Austria/1359417/2021-like, subclade C.

None of the 298 genotypically and 14 phenotypically tested B/Victoria viruses showed reduced susceptibility to neuraminidase inhibitors or baloxavir marboxil (when 250 viruses were tested for baloxavir).

Introduction

Influenza viruses frequently undergo genetic and antigenic changes and therefore, the virological surveillance objectives of European Centre for Disease Prevention and Control (ECDC) are [2] to:

- Identify emerging genetic lineages–clade, subclade, variant;
- Determine the susceptibility of circulating viruses to available antiviral drugs;
- Assess the evolution of viruses compared to previous seasons, including their match with immunisation products;
- Determine if circulating viruses are detected by available diagnostics;
- Assess if an emerging virus/lineage is more transmissible or virulent.

To fulfill the surveillance objectives, EU/EEA Member States diagnostic and public health laboratories characterise circulating influenza viruses and submit virus detection and characterisation data to ECDC and the World Health Organization (WHO) on a weekly basis.

This report summarises influenza virological surveillance data from all 30 European Union and European Economic Area (EU/EEA) countries from week 40 2025 to week 33 2026, as reported by National Reference Laboratories (NRLs) to The European Surveillance System (TESSy) at the European Centre for Disease Prevention and Control.

Purpose

The purpose of this report is to:

- summarise the reported influenza virus detections and antigenic and genetic data provided to TESSy by ERLI-Net laboratories in the EU/EEA during the 2025–26 influenza season (from week 40 2025 to week 33 2026);
- monitor the diversity and circulation of viruses, their geographical occurrence and frequency;
- provide feedback to laboratories through analysing their antigenic and genetic characterisation results in the regional context;
- monitor, maintain and enhance the quality of the characterisation data in TESSy through regular close review and analysis.

Surveillance system

National Reference Laboratories (NRLs) in 30 EU/EEA countries participate in the European Reference Laboratory Network for Human Influenza (ERLI-Net), coordinated by ECDC [5]. This laboratory network is responsible for the virological surveillance of influenza in the EU/EEA and is part of the European Respiratory Viruses Network (ERVI-Net) and GISRS, as the laboratories are also National Influenza Centres [6-8].

NRLs provide information on circulating influenza viruses by testing clinical specimens obtained from surveillance systems in their countries (outpatient and inpatient healthcare settings) for the presence of influenza virus by type (A and B) and subtype (A(H1)pdm09 or A(H1N1)pdm09 and A(H3) or A(H3N2)) or lineage (B/Victoria), as well as by analysing data from diagnostic testing for influenza in other subnational laboratories.

NRLs also conduct preliminary antigenic characterisation of viruses, using strain-specific post-infection ferret antisera raised against vaccine viruses and reference viruses raised in-house or obtained from the WHO Collaborating Centres (WHO CCs) within GISRS, and genetic characterisation through sequencing.

Susceptibility to neuraminidase inhibitor (NAI) antiviral agents and the cap-dependent endonuclease inhibitor baloxavir marboxil – for which reduced susceptibility markers are in the polymerase acidic (PA) protein genome segment – are also assessed by phenotypic and/or genotypic tests. Influenza reference laboratories are encouraged to submit their characterisation results to The European Surveillance System (TESSy), managed by ECDC.

Data sources and methods

Before this analysis was conducted, we performed initial data cleaning and provided feedback to the participating NRLs. We contacted the individual laboratories by email and asked them to update and clean their weekly virus detection and characterisation data in TESSy by 20 August 2026. The data for week 40 2025 to week 33 2026 were then downloaded from TESSy database. A few countries expressed interest in participating but could not perform data analysis to extract the genetic information requested in INFLANTIVIR in time for the end-of-season report, and ECDC provided support by performing the data analysis on their behalf: sequences of the viruses reported to ECDC by the NRLs were downloaded from GISAID using the provided accession numbers; clade assignment was performed using NextClade; identification and interpretation of substitutions known to confer reduced susceptibility to antivirals were performed using an internally developed R script on an alignment built with MAFFT. All characterization data were then included and summarised in this report.

Data sources

EU/EEA countries regularly report influenza surveillance data to TESSy. All 30 countries have NRLs that are also WHO National Influenza Centres. The laboratories receive clinical specimens and data from sentinel and non-sentinel surveillance sources for virological analysis. They report epidemiological and virological influenza surveillance data to ECDC and the WHO Regional Office for Europe (WHO/Europe) from primary care sentinel sites and other sources (e.g. hospitals, non-sentinel primary care, outbreak investigations), reported as non-sentinel data. A detailed overview of country-specific surveillance systems can be found on the WHO website [9].

Detection methods

The detection of influenza A and B viruses, subtyping of influenza A(H1N1)pdm09 and A(H3N2) viruses, and in some instances, type B lineage determination was performed with Nucleic Acid Amplification Tests (NAAT) or sequencing. Weekly detection data by country were reported to TESSy in aggregate format through INFLVIRWAGGR and RESPIAGGR record types until week 20 2026; from week 21 2026 onwards, reporting was moved to the EpiPulse Cases platform through RESPIAGGR, RESPISEVERE and RESPICASE subject codes.

Virus isolation and antigenic characterisation

Laboratories cultured influenza viruses from a subset of influenza-positive clinical specimens, in MDCK, MDCK-SIAT or other cell lines [10 ,11]. Virus recovery was commonly assessed by agglutination of red blood cells (RBCs), most commonly from turkeys, guinea pigs or humans.

A haemagglutination inhibition (HI) assay was used for antigenic characterisation of recovered influenza viruses using post-infection ferret antisera raised against vaccine/reference influenza strains (supplied by WHO CC London or generated in-house by the laboratories) [11] to inhibit virus-induced agglutination of RBCs. A virus isolate was considered antigenically similar to a reference virus if the HI titre with the respective post-infection ferret antiserum differed by no more than four-fold (usually a decrease), in a two-fold dilution series, from the HI titre of the antiserum with the reference virus itself. To consider an isolate antigenically different from a reference virus, the HI titre had to show a decrease of eight-fold or more.

For antigenic characterisation of A(H3N2) viruses, some laboratories conducted HI assays in the presence of oseltamivir, to prevent haemagglutination by the N2 neuraminidase, and/or performed virus neutralisation assays. Antigenic characterisations are reported to TESSy under the different representative influenza virus categories in strain-based format. In addition, 'not attributed to category' was available for each subtype and lineage to accommodate viruses that either did not match one of the pre-set major antigenic groups or did not yield a conclusive HI assay result. Viruses that did not match reporting categories were included in total counts of characterised viruses, but were explained further in the text upon consultation with the reporting country.

Genetic characterisation

Laboratories also conducted genetic characterisation of viruses through sequencing, often directly on clinical specimens. Antigenic group and genetic clade category reports are presented in Annex 1. To report a virus as belonging to a specific genetic group, the phylogenetic and amino acid sequence analyses must meet the following criteria:

- in phylogenetic analysis of the HA gene, the virus should cluster within the clade represented by the indicated vaccine/reference strain; and
- it should not contain many nor critical amino acid substitutions when compared with viruses recognised as belonging to the specific group with which it associates.

WHO CC London provided the list of reference viruses to be used for the purpose of genetic analysis in November 2025, together with reporting categories for influenza virus characterisation related to the HA gene (genetic) and the encoded glycoprotein product (antigenic) (ECDC and WHO/Europe, 'TESSy technical note - Influenza virus characterization guidelines for the northern hemisphere influenza season 2025-2026, November 2025', available upon request).

GISAID accession numbers were also reported; sequences were obtained either through sequencing at the influenza reference laboratories and/or at the WHO CCs. Weekly virus characterisation data were reported to TESSy in strain-based format by date of sampling (or in some cases by date of onset if date of sampling was not available). Viruses that were reported as 'subgroup not listed' or which did not match reporting categories were included in total counts of characterised viruses but were explained further in the text upon phylogenetic analysis if sequence was available, or upon consultation with the reporting country.

Antiviral drug susceptibility testing

Data on susceptibility to NAI antiviral agents were produced by the laboratories using genotypic (limited SNP detection by RT-PCR or pyrosequencing, or partial or full NA gene sequence analysis) and/or phenotypic analysis (drug-specific IC50 determination), and results were reported to TESSy. Antiviral susceptibility testing data are included in Annex 2.

For genotypic analysis, susceptibility was determined by the reported amino acid substitutions associated with reduced/highly reduced inhibition (RI/HRI) by NAIs oseltamivir or zanamivir [12]. Phenotypic susceptibility was assessed by determining IC50 values representing the concentration of oseltamivir or zanamivir needed to inhibit viral neuraminidase activity by 50%.

For influenza A viruses, inhibition was classified as normal inhibition (NI) if a reported value was a <10-fold increase above the median IC50 value after removal of obvious outliers. Reduced inhibition (RI) required a 10 to 100-fold increase above the median IC50 and highly reduced inhibition (HRI) >100-fold above the median IC50.

For influenza B viruses, the corresponding values were: <5-fold increase above median (NI); 5 to 50-fold increase above median (RI) and >50-fold increase above median (HRI) [12].

Median values and fold-changes were calculated by virus (sub)type, antiviral drug and IC50 assay method by season if more than 20 values were available; otherwise, data from the previous season was included to have enough values to calculate a trustworthy median.

The submitting laboratories reported their own interpretation of phenotypic assessments as NI, RI or HRI to TESSy, and the same with the prefix 'AA' for genotypic assessments. Reported values for interpretation of baloxavir marboxil susceptibility are described below. If no assessment was done, 'not applicable' (NA) was reported, and if genotypic interpretation was not possible that was reported separately as 'amino acid interpretation not possible' (AAINP). These assessments of the submitting laboratories were used for the calculations in this report.

Baloxavir marboxil susceptibility data have been reported based on the amino acid substitutions present in the polymerase acidic protein (PA). The PA amino acid substitutions that have been detected in viruses from respiratory specimens and associated with reduced susceptibility are listed in the WHO 2026 guidance [13]. The WHO table includes all the studied amino acid positions for all virus subtypes and their observed values so far, not only those that are considered reduced susceptible (i.e. 'amino acid mutations associated with reduced susceptibility' (AARS)).

Susceptibility to baloxavir is determined using cell culture-based assays, and the effective concentration 50% (EC_{50}) value can vary depending on the assay methodology [13]. For virologic surveillance purposes, a provisional criterion has been introduced: a greater than three-fold increase in the EC_{50} value of the test virus compared to the EC_{50} value of a PA sequence-matched control virus is reported as reduced baloxavir susceptibility [13]. For reporting purposes, amino acid substitutions associated with EC_{50} fold-change of up to three-fold change in phenotypic assays are considered normal ('amino acid mutations associated with normal susceptibility' (AANS)), while those associated with a value greater than three-fold are considered reduced susceptible (AARS) [13]. When there is no amino acid

substitution in PA previously associated with reduced susceptibility, the virus is reported as AANS, and when interpretation is not possible, it is reported as 'Genotypic interpretation not possible' (AAINP).

All virus characterisation data were reported in strain-based format through INFLANTIVIR TESSy record type. If a virus was reported with a 'not applicable' result in TESSy, these data were excluded from the analysis.

Phylogenetic analysis

A phylogenetic analysis was performed on human influenza HA sequences retrieved from the GISAID EpiFlu database (accessed 1 September 2026 for the period 30 September 2025 to 23 August 2026), including only sequences where the isolate could be linked to a record in the TESSy INFLANTIVIR database for the 2025–26 season (extracted 20 August 2026). Phylogenetic analysis data are presented in the Results section below and in Annex 3.

Linkage was made primarily by the provided accession (either HA accession or Isolate ID) number and, if not successful, by matching NationalRecordId in TESSy with Isolate name in GISAID.

The Nextstrain [14] build for seasonal influenza viruses (https://github.com/nextstrain/seasonal-flu) was used to create a phylogenetic tree, assign clade and subclade, and detect amino acid substitutions of HA1. The custom reference strains A/Victoria/2570/2019 (EPI_ISL_417210|EPI1718610) for A(H1N1pdm09) and A/Darwin/9/2021 (EPI_ISL_3801278|EPI1888006) for A(H3N2) were used, and default B/Brisbane/60/2008 (GenBank: KX058884.1) for B/Victoria. The resulting tree was manually inspected and misclassified strains were corrected. This occurred for a very small subset of sequences.

Trees were rooted by inferred ancestral sequences (default mode). Sequences of reference strains (Annex 3, Table 10A) were always included. No filters were applied, except when generating subsampled trees by setting subsample-max-sequences to 100. The clock_filter_iqd variable was set to 0. The resulting tree file was converted to nexus format using an in-house script where branches were annotated with their amino-acid substitutions and nodes were coloured according to month of collection. The nexus tree was further edited in FigTree and Inkscape.

Results

Weekly aggregate reports of detections

From week 40 2025 to week 33 2026, 256 967 influenza virus detections were reported from sentinel and non-sentinel surveillance sources in 30 countries in the EU/EEA, including 249 514 (97.1 %) as type A influenza viruses and 3 292 (1.3 %) as type B influenza viruses. The type was not reported for the 4 161 remaining viruses (Table 1, Figure 1-2). Out of the 56 946 type A viruses with a defined subtype (22.8 % of type A viruses), 20 072 (35.2 %) were A(H1)pdm09 and 36 874 (64.8 %) were A(H3).

For A(H1)pdm09, the neuraminidase subtype N1 was determined for 2 196 of the 4 070 sentinel detections (54 %) and 6 489 of the 16 002 non-sentinel detections (40.6 %). For A(H3), the neuraminidase subtype N2 was determined for 3 864 of the 10 365 sentinel detections (37.3 %) and 6 261 of the 26 509 non-sentinel detections (23.6 %). Out of the 372 type B viruses with a defined lineage (11.3 % of type B viruses), 372 (100 %) were assigned to the Victoria lineage.

Table 1. Number and proportion of detected influenza viruses, by type and subtype, reported to TESSy, EU/EEA, week 40 2025 to week 33 2026

Type	Subtype	Sentinel		Non-sentinel		Total	
		N	%	N	%	N	%
A	A(H1)pdm09	4 070	22.6	16 002	6.7	20 072	7.8
	A(H3)	10 365	57.5	26 509	11.1	36 874	14.4
	A unsubtyped	2 988	16.6	189 580	79.3	192 568	74.9
B	B(Vic)	37	0.2	335	0.1	372	0.2
	B(Yam)	0	0.0	0	0.0	0	0.0
	B lineage not determined	82	0.5	2 838	1.2	2 920	1.1
Untyped	Untyped	480	2.7	3 681	1.5	4 161	1.6
Total	**–**	**18 022**	**100.0**	**238 945**	**100.0**	**256 967**	**100.0**

Figure 1. Number and proportion of influenza virus cumulative detections in sentinel and non-sentinel surveillance systems by subtype, EU/EEA, week 40 2025 to week 33 2026 (N = 256 967)

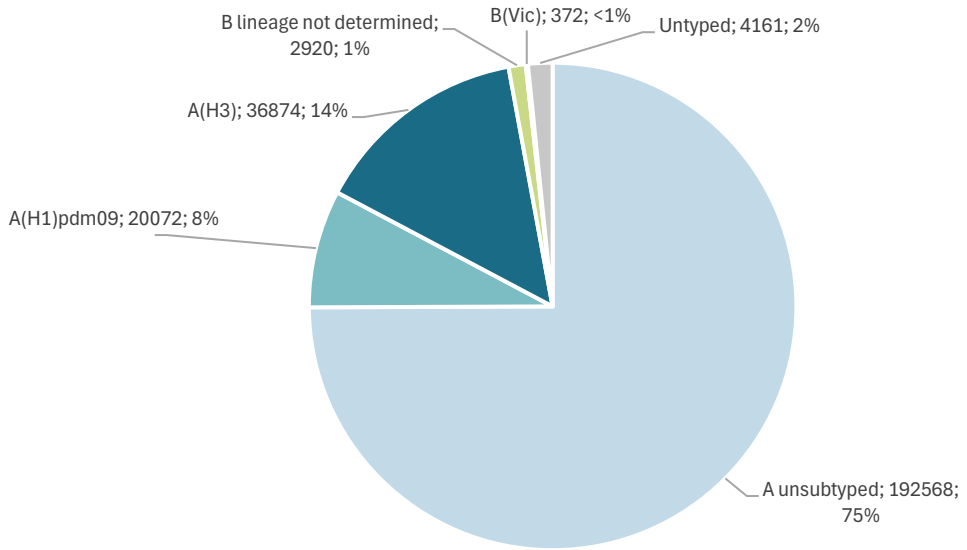
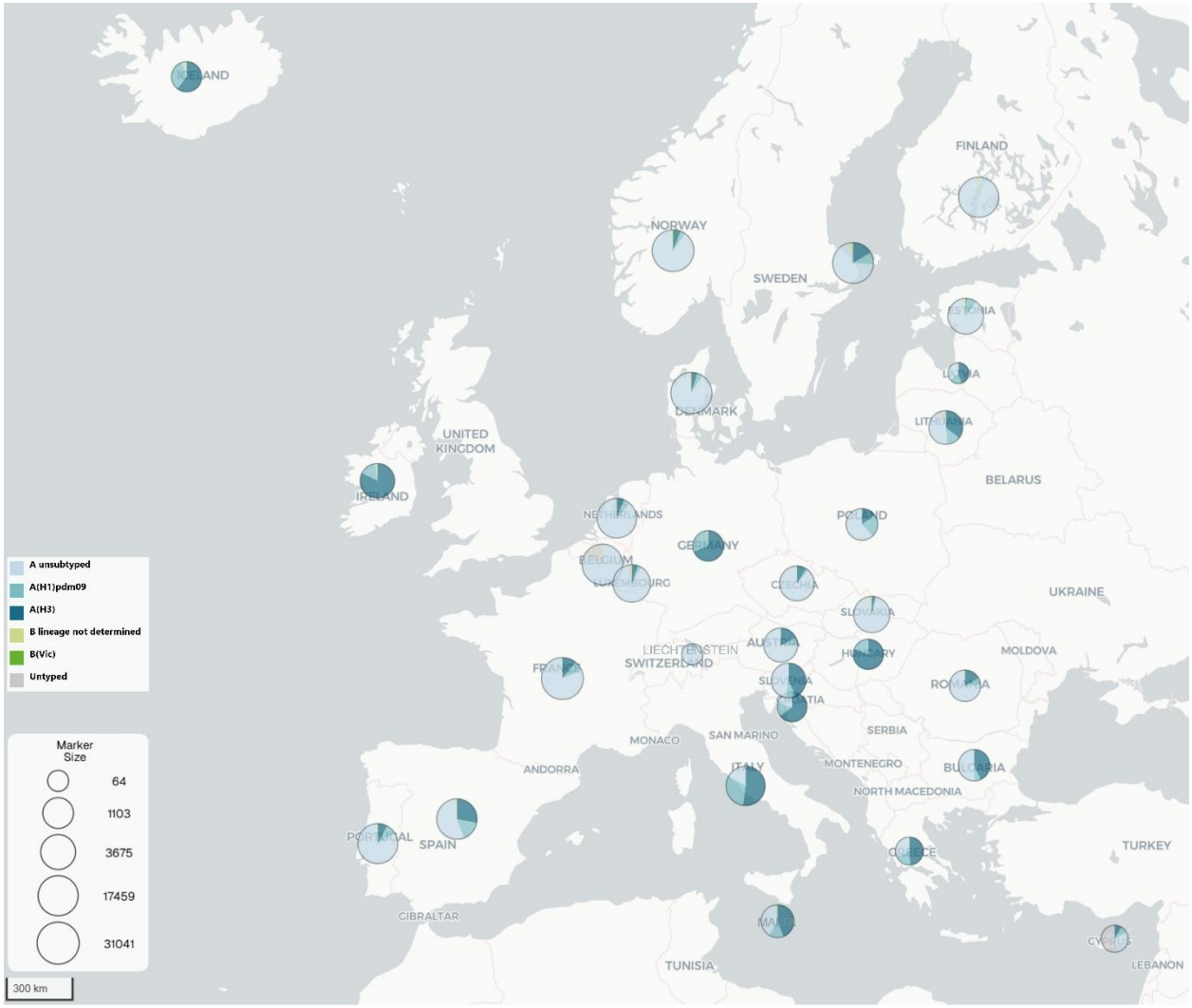


Figure 2. Proportions of influenza types and subtypes, sentinel and non-sentinel surveillance systems, EU/EEA, week 40 2025 to week 33 2026



An interactive map is available at: Map 1 (microreact.org).

Sentinel detections

Among the 18 022 virus detections reported in the sentinel surveillance systems between week 40 2025 and week 33 2026, 17 423 (96.7 %) were type A and 119 (0.7 %) were type B. The type was not reported for the 480 remaining viruses (Table 2, Figure 3). Out of the 14 435 type A viruses with a defined subtype (82.9 % of type A viruses), 4 070 (28.2 %) were A(H1)pdm09 and 10 365 (71.8 %) were A(H3). Out of the 37 type B viruses with a defined lineage (31.1 % of type B viruses), all were assigned to the Victoria lineage.

Figure 3. Number and proportion of influenza virus cumulative detections in sentinel surveillance systems by subtype, EU/EEA, week 40 2025 to week 33 2026 (N = 18 022)

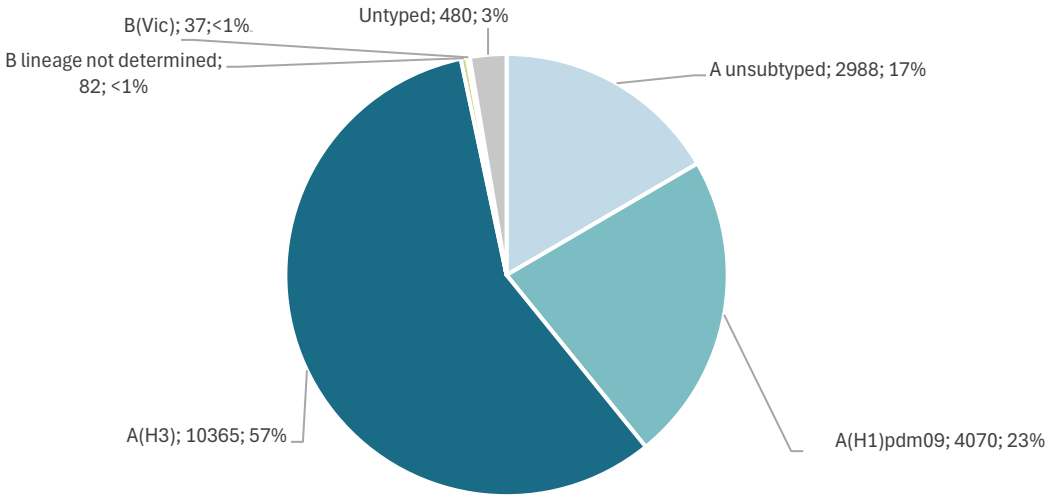
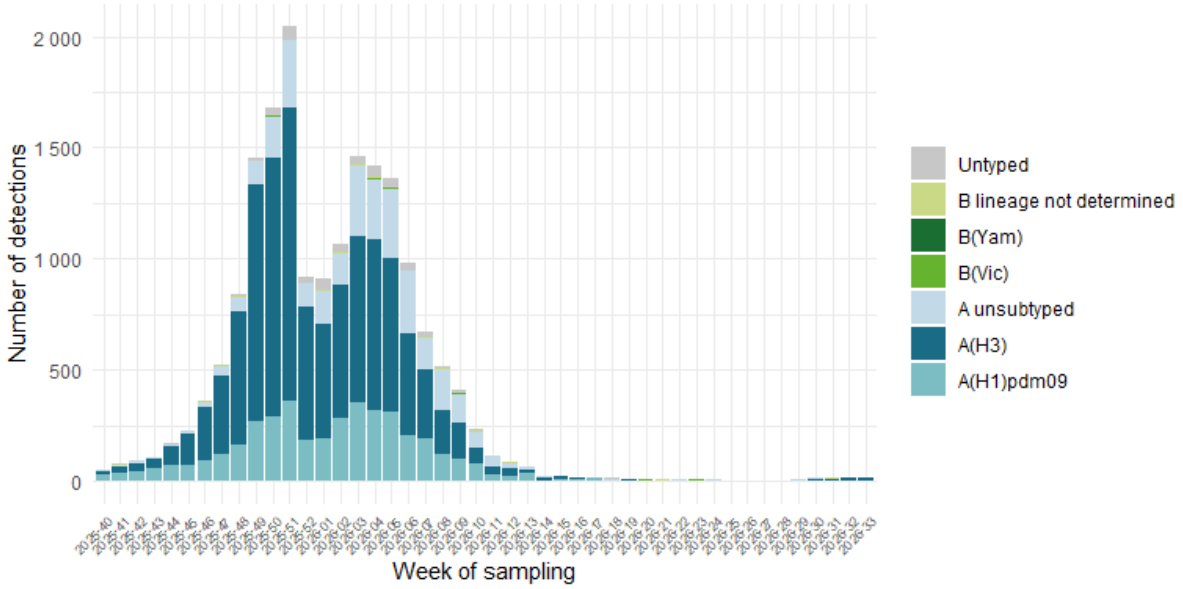


Figure 4. Distribution of detected influenza viruses in sentinel surveillance by week, subtype and lineage, EU/EEA, week 40 2025 to week 33 2026



Non-sentinel detections

Among the 238 945 virus detections reported in the non-sentinel surveillance systems between week 40 2025 and week 33 2026, 232 091 (97.1 %) were type A and 3 173 (1.3 %) were type B. The type was not reported for the 3 681 remaining viruses (Table 1, Figure 5). Out of the 42 511 type A viruses with a defined subtype (18.3 % of type A viruses), 16 002 (37.6 %) were A(H1)pdm09 and 26 509 (62.4 %) were A(H3). Out of the 335 type B viruses with a defined lineage (10.6 % of type B viruses), all were assigned to the Victoria lineage.

Figure 5. Number and proportion of influenza virus cumulative detections in non-sentinel surveillance systems by subtype, EU/EEA, week 40 2025 to week 33 2026 (N= 238 945)

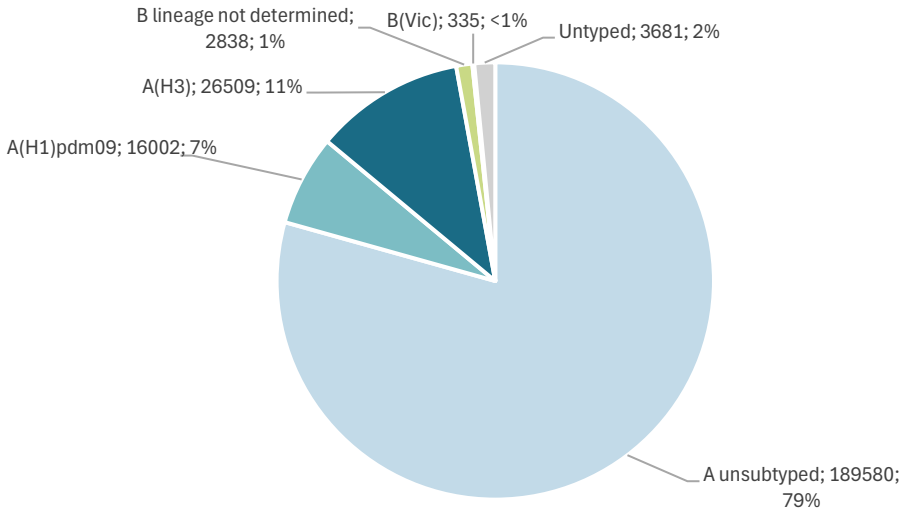


Figure 6. Distribution of detected viruses in non-sentinel surveillance by week, subtype and lineage, EU/EEA, week 40 2025 to week 33 2026

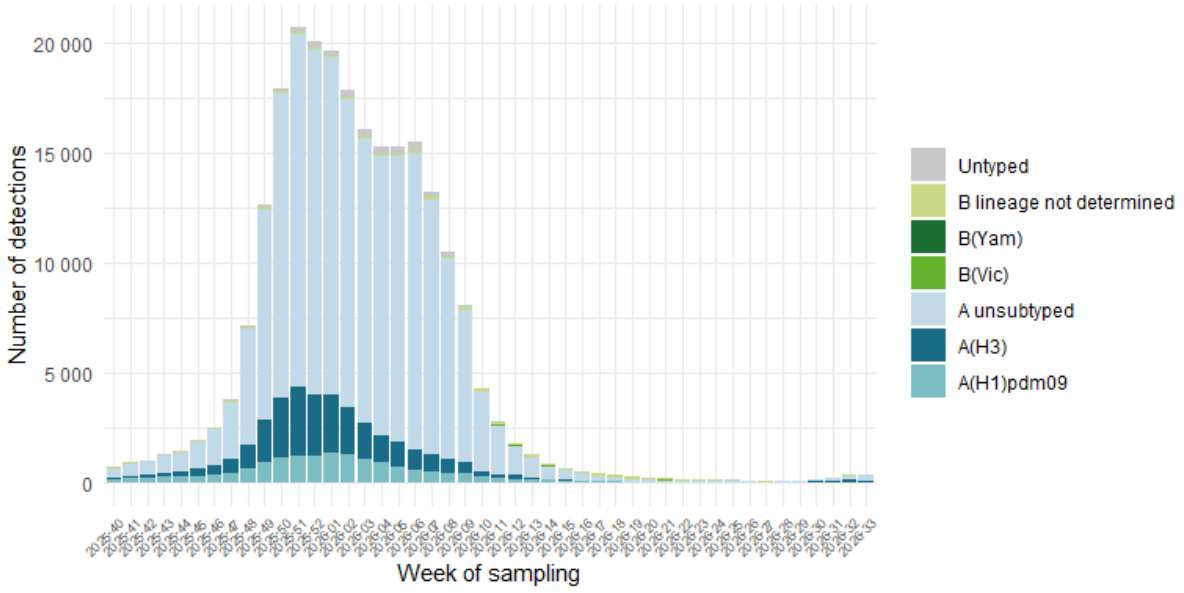
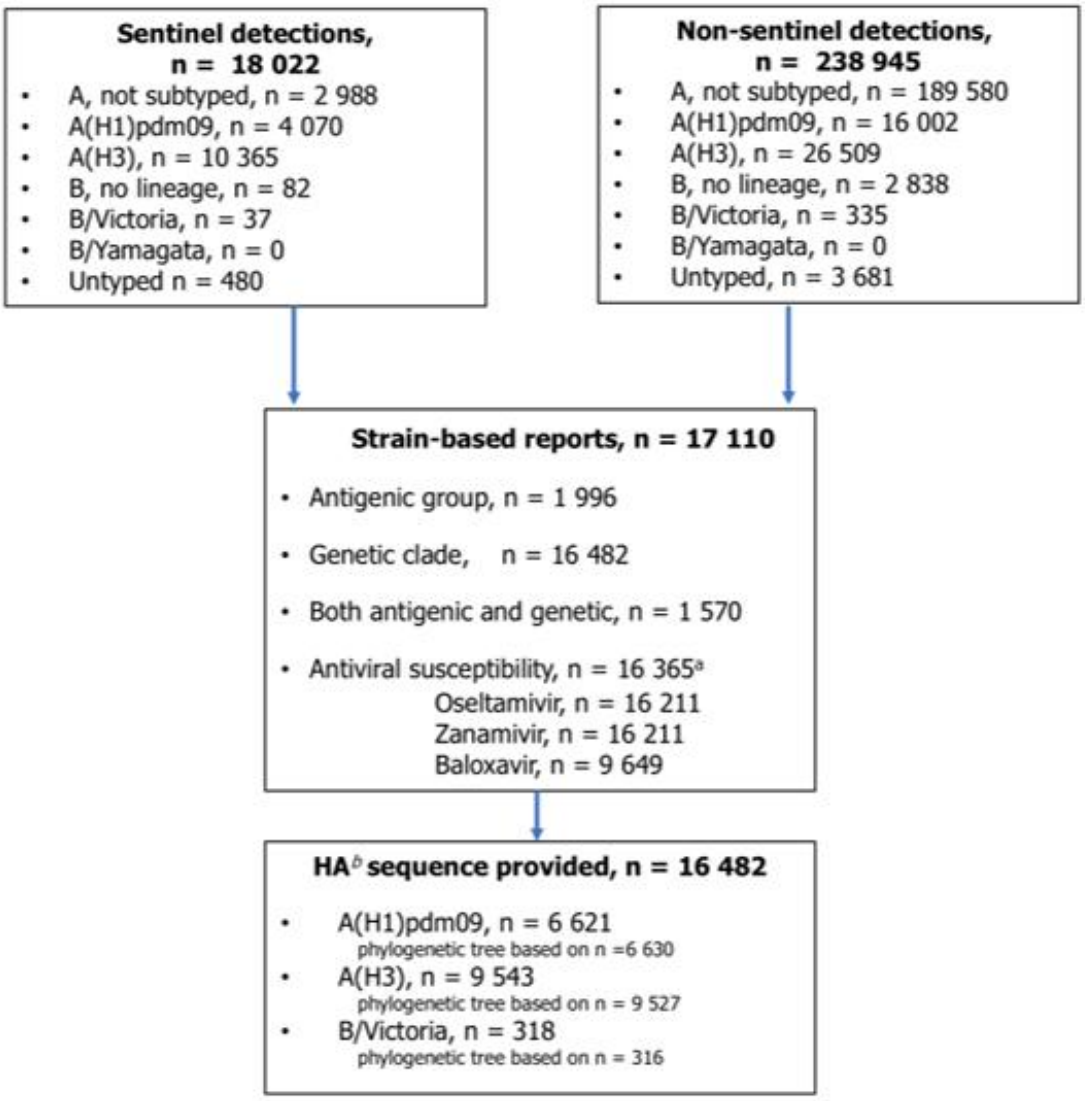


Figure 7. Flowchart of the specimens used in the analysis of this report, reported by country/territory surveillance systems, EU/EEA, week 40 2025 to week 33 2026



[a]Number of viruses assessed genotypically and/or phenotypically for susceptibility to at least one drug.
[b]HA: haemagglutinin.

Virus characterisation

Using the INFLANTIVIR record type in TESSy, countries were invited to report strain-based characterisation of influenza viruses detected and/or isolated during the season.

Overview of the reported data

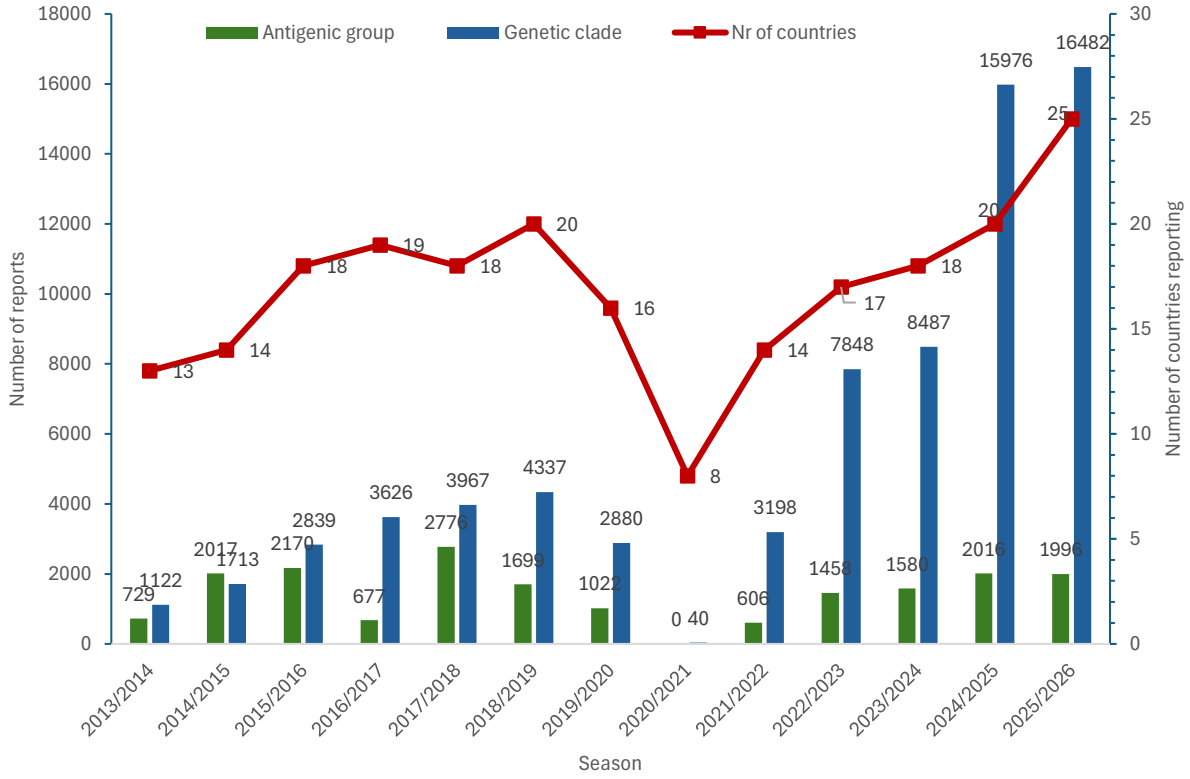
From week 40 2025 to week 33 2026, 17 110 influenza strain-based reports from sentinel (5 263, 30.8 %) and non-sentinel (11 576, 67.7 %) surveillance sources were submitted by 25 countries in the EU/EEA (Table 2).

Table 2. Number of reported viruses with virus characterisation data, EU/EEA, weeks 40 2025 through 33 2026

Type	Subtype	Surveillance system			Total
		Sentinel	Non-sentinel	Unknown	
A	A(H1)pdm09	1 743	5 000	89	6 832
	A(H3)	3 476	6 301	181	9 958
B	B(Vic)	44	275	1	320
Total	–	5 263	11 576	271	17 110

Those data included 1 996 antigenic and 16 482 genetic reports. Previous season results in comparison to this season are depicted in Figure 8.

Figure 8. Number of antigenic and genetic reports as well as number of reporting countries by season, EU/EEA, weeks 40 2013 to week 33 2026



Out of the 16 790 type A influenza viruses, 6 832 (40.7 %) were reported as subtype A(H1N1)pdm09 or A(H1)pdm09 and 9 958 (59.3 %) as subtype A(H3N2) or A(H3). Of the 320 type B influenza viruses, virus characterisation data were reported only for viruses assigned to the Victoria lineage.

The neuraminidase subtype was determined for 6 831 (almost 100 %) of the 6 832 influenza A(H1)pdm09 viruses, and 9 903 (99.4 %) of the 9 958 influenza A(H3) viruses. The remainder of the type A viruses were reported without N-subtype, and therefore we are using A(H1)pdm09 and A(H3) nomenclature for all type A viruses throughout the characterisation parts of this report.

Age was provided for 14 083 cases, 4 930 (35 %) from sentinel and 8 948 (63.5 %) from non-sentinel surveillance systems (Table 3). The majority of the virus charactersation data were reported for 15-65 years old for A(H3) and B/Victoria, while the majority of A(H1)pdm09 virus characterisation data were reported for persons 65 years and older (Table 3). Further details on age, outcomes and vaccination status are available in Annex 4.

Table 3. Number of reported viruses by age group, EU/EEA, weeks 40 2013 to week 33 2026

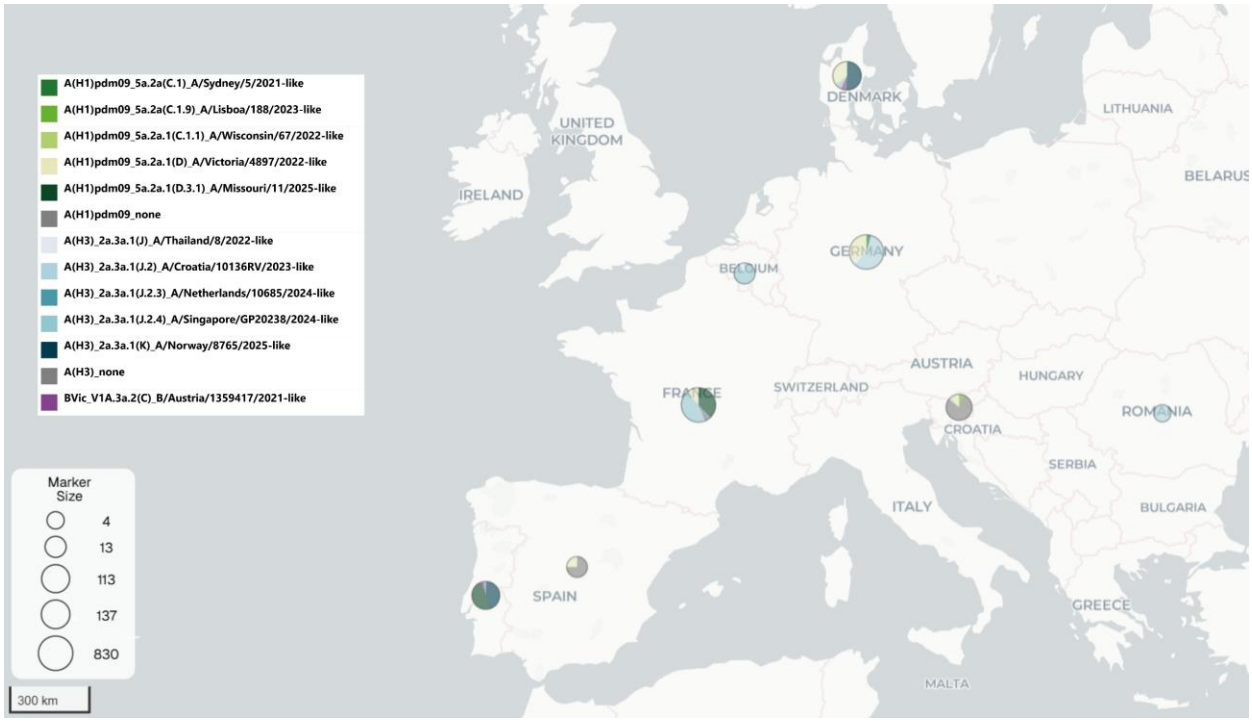
		Surveillance system							
		Sentinel		Non Sentinel		Unknown		Total	
Subtype	Age group	nb	%	nb	%	nb	%	nb	%
A(H1)pdm09	<5y	201	12.4	282	7.0	4	5.3	487	8.5
	[5y,15y)	194	11.9	206	5.1	8	10.7	408	7.1
	[15y,65y)	742	45.6	1 419	35.3	31	41.3	2 192	38.3
	>=65y	490	30.1	2 117	52.6	32	42.7	2 639	46.1
	Total	1 627	100	4 024	100	75	100	5 726	100
A(H3)	<5y	488	14.9	559	11.8	9	7.0	1 056	13.0
	[5y,15y)	788	24.1	605	12.8	46	35.7	1 439	17.7
	[15y,65y)	1 369	41.9	1 724	36.4	52	40.3	3 145	38.7
	>=65y	624	19.1	1 849	39.0	22	17.1	2 495	30.7
	Total	3 269	100	4 737	100	129	100	8 135	100
B(Vic)	<5y	2	5.9	13	7.0	0	0.0	15	6.8
	[5y,15y)	10	29.4	27	14.4	0	0.0	37	16.7
	[15y,65y)	21	61.8	136	72.7	0	0.0	157	70.7
	>=65y	1	2.9	11	5.9	1	100	13	5.9
	Total	34	100	187	100	1	100	222	100

Antigenic or genetic characterisation was reported to TESSy by 25 countries during the reporting period (Table 4). Both genetic and antigenic characterisation data were reported by 8 countries (Belgium, Denmark, France, Germany, Portugal, Romania, Slovenia and Spain), and the remaining 17 countries (Austria, Croatia, Czechia, Estonia, Finland, Greece, Hungary, Ireland, Italy, Lithuania, Luxembourg, Malta, Netherlands, Norway, Poland, Slovakia and Sweden) provided only genetic data.

Table 4. Number of viruses characterised antigenically (AG) and genetically (GEN), as reported to TESSy by country (n=25) and week of sampling, EU/EEA, week 40 2025 to week 10 2025 and weeks 11 to 33 2026

| | | 2025 | | | | | | | | | | | | | 2026 | | | | | | | | | | | | |

Figure 9. Proportions of antigenic categories reported by countries, EU/EEA, week 40 2025 to week 33 2026



An interactive map is available at: Map 2. Antigenic categories.

Figure 10. Proportions of genetic groups reported by countries, EU/EEA, week 40 2025 to week 33 2026



An interactive map is available at: Map 3. Genetic groups.

A(H1N1)pdm09 viruses

Antigenic characterisation

From week 40 2025 to week 33 2026, with latest data reported for week 32 2026, six countries reported antigenic characterisation to TESSy for 838 A(H1N1)pdm09 influenza viruses. The countries that contributed were: France (408, 48.7 %), Germany (310, 37 %), Portugal (55, 6.6 %), Denmark (51, 6.1 %), Slovenia (11, 1.3 %) and Spain (3, 0.4 %).

Countries were asked to report antigenic characterisation results in TESSy according to the predefined categories described in Table 5.

Table 5. Predefined antigenic reporting categories for A(H1)pdm09 viruses.

TESSy category	Virus of reference	Clade name	Subclade name
agAH1/Sydney/5/2021	A/Sydney/5/2021-like	6B.1A.5a.2a	5a.2a(C.1)
agAH1/Lisboa/188/2023	A/Lisboa/188/2023-like	6B.1A.5a.2a	5a.2a(C.1.9)
agAH1/Wisconsin/67/2022	A/Wisconsin/67/2022-like	6B.1A.5a.2a.1	5a.2a.1(C.1.1)
agAH1/Victoria/4897/2022[a]	A/Victoria/4897/2022-like[a]	6B.1A.5a.2a.1	5a.2a.1(D)
agAH1/Missouri/11/2025[b]	A/Missouri/11/2025-like[b]	6B.1A.5a.2a.1	5a.2a.1(D.3.1)
agAH1NOCAT	none	none	none

[a] *WHO recommended vaccine virus from the 2025–2026 northern hemisphere influenza season.*
[b] *WHO recommended vaccine virus for the 2026 southern hemisphere influenza season.*

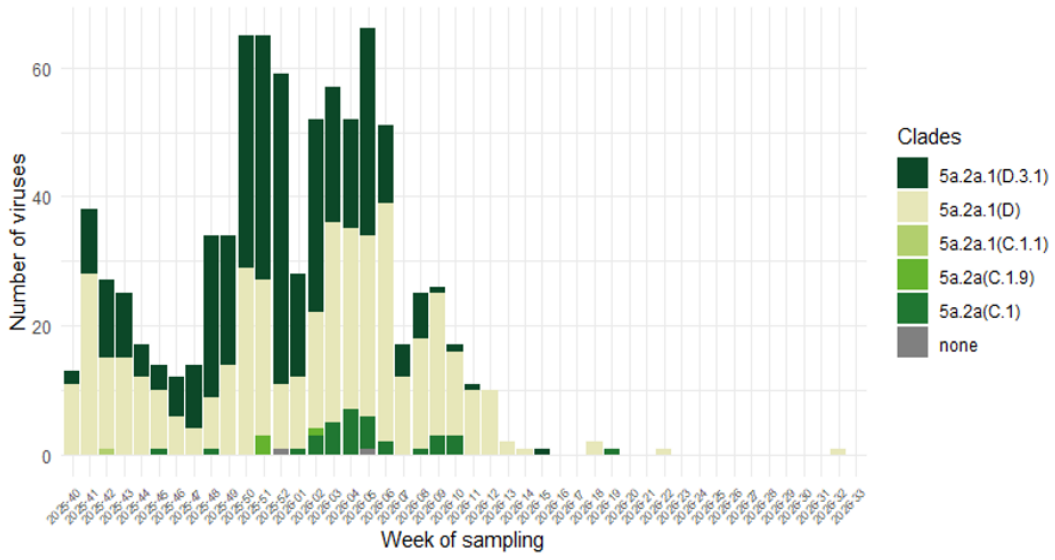
Among the 838 characterised A(H1)pdm09 viruses, the main reported categories were A/Missouri/11/2025-like, clade 5a.2a.1(D.3.1) and A/Victoria/4897/2022-like, clade 5a.2a.1(D), representing 44.2 % and 51.1 %, respectively (Table 6).

Table 6. Number of viruses by A(H1)pdm09 antigenic reporting categories, EU/EEA, week 40 2025 to week 33 2026

Subclade	Virus_of_reference	nb	percent
5a.2a(C.1)	A/Sydney/5/2021-like	33	3.9
5a.2a(C.1.9)	A/Lisboa/188/2023-like	4	0.5
5a.2a.1(C.1.1)	A/Wisconsin/67/2022-like	1	0.1
5a.2a.1(D)	A/Victoria/4897/2022-like[a]	428	51.1
5a.2a.1(D.3.1)	A/Missouri/11/2025-like[b]	370	44.2
none	none	2	0.2

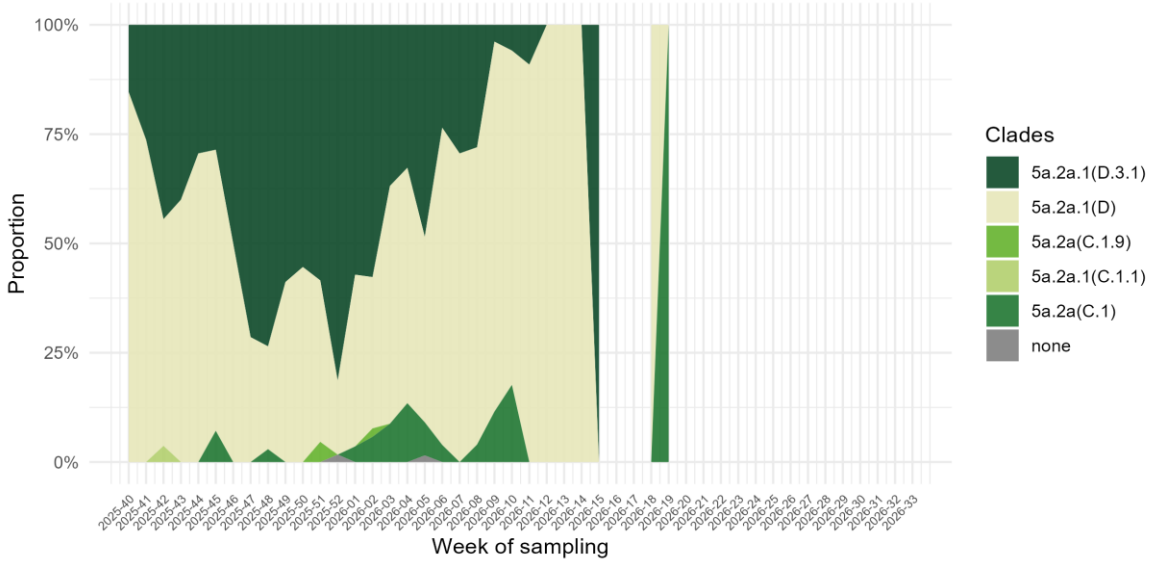
[a] *WHO recommended vaccine virus from the 2025–2026 northern hemisphere influenza season.*
[b] *WHO recommended vaccine virus for the 2026 southern hemisphere influenza season.*

Figure 11. A(H1)pdm09 clade weekly distribution based on antigenic characterisation, EU/EEA, week 40 2025 to week 33 2026



In the legend, the short clade name is given with the subclade in brackets.

Figure 12. A(H1)pdm09 clade weekly proportion based on antigenic characterisation, EU/EEA, week 40 2025 to week 33 2026



In the legend, the short clade name is given with the subclade in brackets.

Genetic characterisation

From week 40 2025 to week 33 2026, with latest data reported for week 32 2026, 25 countries reported genetic characterisation to TESSy for 6 621 A(H1N1)pdm09 influenza viruses. The countries that contributed were: Spain (2 334, 35.3 %), France (1 608, 24.3 %), Netherlands (687, 10.4 %), Portugal (382, 5.8 %), Denmark (358, 5.4 %), Norway (286, 4.3 %), Germany (227, 3.4 %), Belgium (97, 1.5 %), Finland (97, 1.5 %), Sweden (88, 1.3 %), Ireland (72, 1.1 %), Luxembourg (70, 1.1 %), Austria (60, 0.9 %), Slovakia (58, 0.9 %), Estonia (48, 0.7 %), Romania (32, 0.5 %), Italy (30, 0.5 %), Czechia (19, 0.3 %), Lithuania (17, 0.3 %), Malta (17, 0.3 %), Croatia (12, 0.2 %), Slovenia (11, 0.2 %), Hungary (6, 0.1 %), Greece (3, <0.1 %) and Poland (2, <0.1 %).

Countries were asked to report genetic characterisation results in TESSy according to the predefined categories described in Table 7.

Table 7. Predefined genetic reporting categories for A(H1)pdm09 viruses

TESSy category	Virus of reference	Clade name	Subclade name
genAH1/Netherlands/10468/2023	A/Netherlands/10468/2023	6B.1A.5a.2a	5a.2a(C.1)
genAH1/Lisboa/188/2023	A/Lisboa/188/2023	6B.1A.5a.2a	5a.2a(C.1.9)
genAH1/Hungary/286/2024	A/Hungary/286/2024	6B.1A.5a.2a	5a.2a(C.1.9.3)
genAH1/Victoria/4897/2022	A/Victoria/4897/2022 [a]	6B.1A.5a.2a.1	5a.2a.1(D)
genAH1/Missouri/11/2025	A/Missouri/11/2025 [b]	6B.1A.5a.2a.1	5a.2a.1(D.3.1)
genAH1NOClade	none	none	none
genAH1SubgroupNotListed	other	other	other

[a] *WHO recommended vaccine virus from the 2025–2026 northern hemisphere influenza season.*
[b] *WHO recommended vaccine virus for the 2026 southern hemisphere influenza season.*

Among the 6 621 characterised A(H1)pdm09 viruses, the main reported categories were A/Missouri/11/2025, clade 5a.2a.1(D.3.1), other clades not among the reporting categories, and A/Victoria/4897/2022, clade 5a.2a.1(D), representing 92.3 %, 6.1 % and 1.3 %, respectively (Table 8).

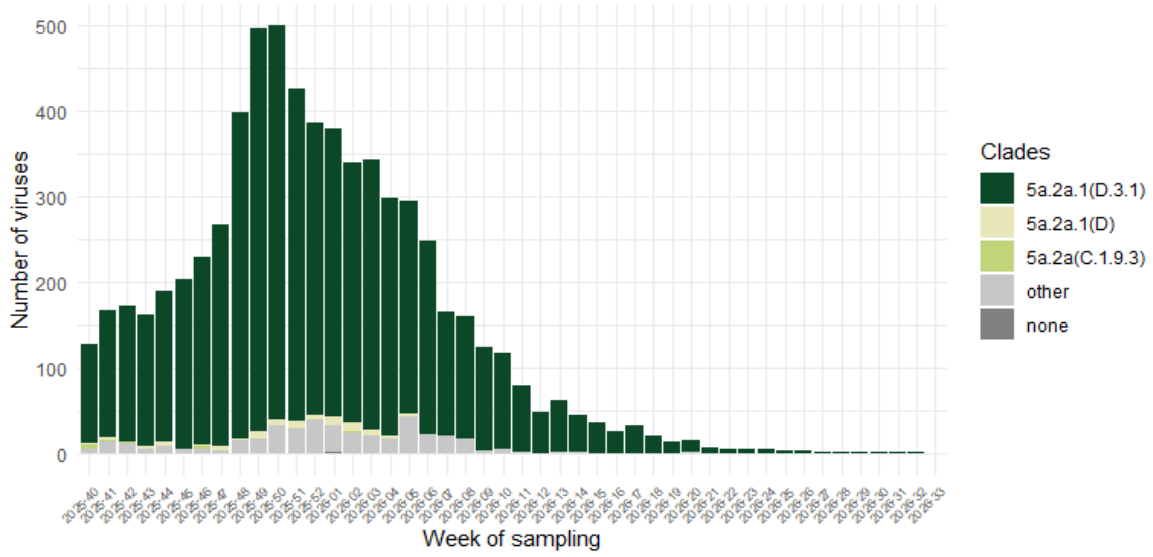
In INFLANTIVIR, countries have the possibility to add comments and to report a list of substitutions in the HA protein that can be of interest. Using this reported additional data, further classification was possible. Clade 5a.2a.1(D.3.1.1) characterised by R113K, A139D, E283K, and K302E in HA, not included in the reporting categories for the 2025-2026 season, could be identified for 3 099 among the reported parental clade 5a.2a.1(D.3.1) (50.7 %), 52 among the reported clade 5a.2a.1(D) (60.5 %), and 363 among those reported as 'other' clade (89.9 %). Clades 5a.2a.1(D.3.1.1) and 5a.2a.1(D.3.1) thus represented 53.1 % and 45.5 % of the reported genetic groups, respectively, all the other reporting categories amounting for less than 1 % each.

Table 8. Number of viruses by A(H1)pdm09 genetic reporting categories, EU/EEA, week 40 2025 to week 33 2026

Subclade	Virus_of_reference	nb	percent
5a.2a(C.1.9.3)	A/Hungary/286/2024	19	0.3
5a.2a.1(D)	A/Victoria/4897/2022[a]	86	1.3
5a.2a.1(D.3.1)	A/Missouri/11/2025[b]	6 111	92.3
none	none	1	0.0
other	other	404	6.1

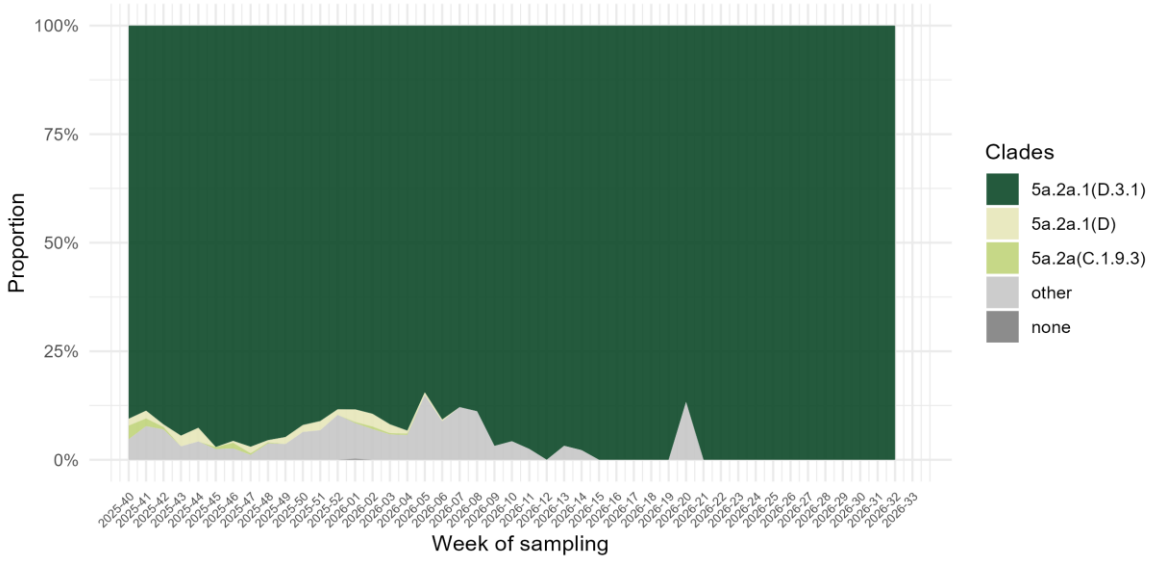
[a] *WHO recommended vaccine virus from the 2025–2026 northern hemisphere influenza season.*
[b] *WHO recommended vaccine virus for the 2026 southern hemisphere influenza season.*

Figure 13. A(H1)pdm09 clade weekly distribution based on genetic characterisation, EU/EEA, week 40 2025 to week 33 2026



In the legend, the short clade name is given with the subclade in brackets.

Figure 14. A(H1)pdm09 clade weekly proportion based on genetic characterisation, EU/EEA, week 40 2025 to week 33 2026



In the legend, the short clade name is given with the subclade in brackets.

Phylogenetic analysis

From week 40 2025 to week 33 2026, a total of 6 636 A(H1)pdm09 HA sequences from 25 countries were reported, retrieved and included in the analyses (Figure 15). Countries that reported HA sequences are shown in Annex 3, Table 7A. There were six sequences that failed Nextstrain's quality control and were excluded from the phylogenetic tree (please see subsampled tree in Figure 15 and full tree svg files at h1n1pdm_2026_2026-09-03_2057.svg).

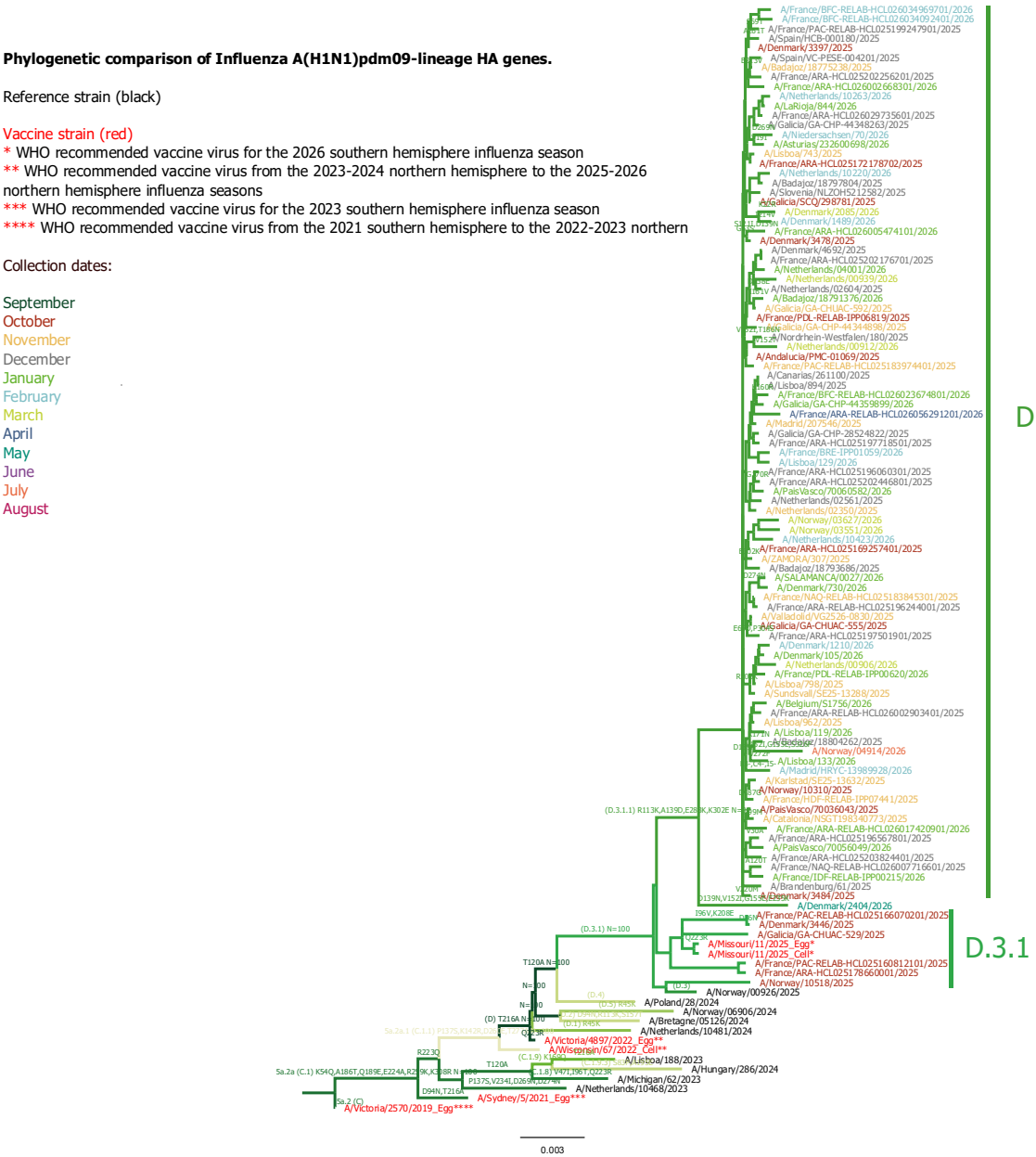
All A(H1N1)pdm09 viruses fell into the branch of clade 5a.2a. Of the 6 626 viruses within clade 5a.2a, 6 607 (99.7 %) were further characterised into clade 5a.2a.1 subclade D that has the additional P137S, K142R, T216A, D260E, T277A amino acid substitution and is represented by A/Victoria/4897/2022_Egg, the NH 2025-26 vaccine strain for egg-based vaccines.

Of all A(H1N1)pdm09 viruses, the majority belonged to clade 5a.2a.1, subclade D.3.1.1 (6 270, 95 %), defined by R113K, A139D, E283K and K302E and which was not represented by any reference strain defined for this season. Within the genetic diversification of D.3.1.1 viruses, we detected 60 viruses with substitutions in position G155E (this substitution alone, n=20), of which some were in combination with other substitutions: D139N+G155E (n=16), Q54H+D139N+G155E (n=3), D139N+V152I+G155E (n=11) and D139N+V152I+G155E+E235K (n=10). These viruses were dispersed across the phylogenetic tree and did not form any single branch and are therefore not depicted separately in Figure 15.

Within the genetic diversification of 5a.2a.1 clade, 340 (5.1 %) viruses belonged to subclade D.3.1, carrying substitutions T120A, I372V, I460T, V520A and was represented by A/Missouri/11/2025 egg- and cell-based vaccine strains for northern hemisphere 2026-2027 influenza season, and A/Norway/00926/2025.

A comparison of reported versus assigned clade and subclade were made by grouping the assigned ones to the corresponding reporting categories. The clade and sub-clade assignments from the phylogenetic results for A(H1)pdm09 aligned well with the categories of genetic clades that the countries had reported. The clade, as well as subclade, matched for 6 207 (94 %) of 6 630 viruses.

Figure 15. Phylogenetic comparison of 100 sub-sampled influenza A(H1N1)pdm09 HA genes



The vaccine strains are given in red, reference strains in black and sequences reported to TESSy are coloured according to the virus collection date, by month. Please see subsampled and full tree svg files here:).

Match between antigenic and genetic characterisations

In the INFLANTIVIR dataset, it is possible to compare antigenic and genetic categorical reports for the individual virus reports. This is done to analyse how the genetic (sub)clades translate to antigenic categories and match with the vaccine strains.

Of the 701 A(H1N1)pdm09 viruses that had both genetic and antigenic data reported, more than half (366, 52.2 %) were reported antigenically as 5a.2a.1 subclade D.3.1 agAH1/Missouri/11/2025-like, the upcoming NH 2026-27 vaccine strain (Annex 1, Table 4A), which is antigenically distinct from the current season vaccine strain A/Victoria/4897/2022-like viruses. Of these, the majority (241, 65.9 %) were reported as homologous genetic subgroup 5a.2a.1 subclade D.3.1 represented by A/Missouri/11/2025. Among the remaining viruses, one was reported similar to A/Hungary/286/2024, subclade 5a.2a (C.1.9.3) and 124 (33.9 %) were reported as not assigned to any genetic group. However, 117 out of the 124 could be genetically assigned to subclade 5a.2a.1(D.3.1.1) based on additional information provided by the countries as comment or in the list of HA substitutions and could have been genetically reported as A/Missouri/11/2025, subclade 5a.2a.1(D.3.1).

Another large group of A(H1N1)pdm09 viruses (306, 43.7 %) were antigenically assigned as 5a.2a.1(D) A/Victoria/4897/2022-like, the current NH 2025-26 egg-based vaccine strain. Most (279, 91.2 %) were genetically assigned as 5a.2a.1(D.3.1) represented by A/Missouri/11/2025, which is the upcoming NH 2026-27 vaccine strain. Among the remaining viruses, one was reported similar to A/Hungary/286/2024, subclade 5a.2a (C.1.9.3) and 26 (8.5 %) were reported as not assigned to any genetic group. Out of these 26, 23 could be genetically assigned to subclade 5a.2a.1(D.3.1.1) based on additional information provided by the countries as comment or in the list of HA substitutions.

Two A(H1N1)pdm09 viruses were reported both antigenically and genetically distinct from existing reporting categories. Based on additional information provided by the countries as comment or in the list of HA substitutions, both were found to genetically belong to subclade 5a.2a.1(D.3.1.1).

Further details on the reported categories are presented in Annex 1, Table 4A.

Antiviral susceptibility

From week 40 2025 to week 33 2026, with latest data reported for week 32 2026, 6 612 A(H1N1)pdm09 influenza viruses were assessed genotypically and/or phenotypically for resistance to at least one drug (oseltamivir, zanamivir or baloxavir marboxil) by 25 countries. The countries that contributed were: Spain (2 267, 34.3 %), France (1 608, 24.3 %), Netherlands (687, 10.4 %), Portugal (383, 5.8 %), Denmark (358, 5.4 %), Norway (286, 4.3 %), Germany (250, 3.8 %), Finland (98, 1.5 %), Belgium (97, 1.5 %), Sweden (89, 1.3 %), Ireland (70, 1.1 %), Luxembourg (70, 1.1 %), Austria (63, 1 %), Poland (62, 0.9 %), Slovakia (58, 0.9 %), Estonia (48, 0.7 %), Italy (30, 0.5 %), Czechia (19, 0.3 %), Lithuania (17, 0.3 %), Malta (17, 0.3 %), Croatia (12, 0.2 %), Hungary (7, 0.1 %), Romania (7, 0.1 %), Slovenia (6, 0.1 %) and Greece (3, <0.1 %).

Regarding the susceptibility to neuraminidase inhibitors, nine countries performed a phenotypic assessment: Germany (186), Poland (60), Spain (47), Netherlands (44), France (37), Portugal (35), Norway (14), Italy (13) and Romania (1). Reduced and highly reduced inhibition by Oseltamivir was observed for 10 (2.3 %) and 3 (0.7 %) of the 437 tested A(H1N1)pdm09 viruses (Table 9). The susceptibility of the remaining viruses was assessed genetically based on the presence of substitutions in the neuraminidase protein known to be associated with reduced inhibition. Substitutions associated with reduced and highly reduced inhibition by Oseltamivir were observed for 147 (2.4 %, associated with NA_I223V_S247N mainly, or NA_I223M/T or NA_S247R) and 15 (0.2 %, associated with NA_H275Y mainly, or NA_N295S) viruses, respectively. For Zanamivir, substitutions associated with reduced and highly reduced inhibition were observed for 1 (<0.1 %, associated with NA_S247R) and 1 (<0.1 %, associated with NA_Q136K) of the 6 089 assessed viruses, respectively.

Table 9. Number of A(H1N1)pdm09 viruses, by reporting categories, for neuraminidase inhibitor susceptibility, EU/EEA, week 40 2025 to week 33 2026

	Phenotypic			Genotypic			
Antiviral	NI	RI	HRI	AANI	AARI[a]	AAHRI[b]	Total
Oseltamivir	424	10	3	5 926	147	15	6 525
Zanamivir	435	1	0	6 087	1	1	6 525

AAHRI: amino acid mutations associated with highly reduced inhibition; AANI: amino acid mutations associated with normal inhibition; AARI: amino acid mutations associated with reduced inhibition; HRI: highly reduced inhibition; NI: normal inhibition; RI: reduced inhibition.
Amino acid substitutions associated with reduced susceptibility are listed in Annex 2.
[a] The substitutions related to reduced susceptibility were NA_I223V and S247N mainly, or NA_I223M/T or NA_S247R for oseltamivir and NA_S247R for zanamivir.
[b] The substitution related to highly reduced susceptibility was NA_H275Y mainly, or NA_N295S for oseltamivir and NA_Q136K for zanamivir.

The susceptibility to polymerase inhibitors was assessed genetically based on the presence of substitutions in the PA polymerase subunit gene that are known to confer reduced susceptibility. Sequencing data of the PA gene were reported by 22 countries: France (1 515), Netherlands (544), Spain (390), Denmark (347), Portugal (319), Norway (258), Germany (203), Belgium (95), Finland (89), Sweden (82), Luxembourg (59), Slovakia (43), Italy (23), Czechia (18), Malta (17), Lithuania (14), Croatia (8), Hungary (6), Slovenia (6), Estonia (3), Greece (3) and Ireland (3). Out of the 4 020 assessed A(H1N1)pdm09 viruses, substitutions associated with reduced susceptibility were observed for 4 (0.1 %, associated with PA_E23G or PA_A37T or PA_E199G/K) virus (Table 10).

Table 10. Number of A(H1N1)pdm09 viruses, by reporting categories, for baloxavir marboxil susceptibility, EU/EEA, week 40 2025 to week 33 2026

	Genotypic		
Antiviral	AANS	AARS[a]	Total
Baloxavir	4 016	4	4 020

AANS: amino acid mutations associated with normal susceptibility; AARS: amino acid mutations associated with reduced susceptibility. Amino acid substitutions associated with reduced susceptibility are listed in Annex 2.
[a] The substitutions related to reduced susceptibility were PA_E23G or PA_A37T or PA_E199G/K.

Age, outcome and vaccination status

Data about how the characterised viruses were distributed in age groups per subclade, what the outcome was and what proportion of individuals infected by characterised viruses had been vaccinated, are displayed in Annex 4.

A(H3N2) viruses

Antigenic characterisation

From week 40 2025 to week 33 2026, with latest data reported for week 30 2026, eight countries reported antigenic characterisation to TESSy for 1 137 A(H3N2) influenza viruses. The countries that contributed were: Germany (514, 45.2 %), France (413, 36.3 %), Denmark (79, 6.9 %), Portugal (54, 4.7 %), Slovenia (51, 4.5 %), Belgium (13, 1.1 %), Spain (9, 0.8 %) and Romania (4, 0.4 %).

Countries were asked to report antigenic characterisation results in TESSy according to the predefined categories described in Table 11.

Table 11. Predefined antigenic reporting categories for A(H3) viruses

TESSy category	Virus of reference	Clade name	Subclade name
agAH3/Darwin/9/2021	A/Darwin/9/2021-like	3C.2a1b.2a	2a(G1)
agAH3/Thailand/8/2022	A/Thailand/8/2022-like	3C.2a1b.2a.3a.1	2a.3a.1(J)
agAH3/Croatia/10136RV/2023	A/Croatia/10136RV/2023-like[a]	3C.2a1b.2a.3a.1	2a.3a.1(J.2)
agAH3/Netherlands/10685/2024	A/Netherlands/10685/2024-like	3C.2a1b.2a.3a.1	2a.3a.1(J.2.3)
agAH3/Singapore/GP20238/2024	A/Singapore/GP20238/2024-like[b]	3C.2a1b.2a.3a.1	2a.3a.1(J.2.4)
agAH3/France/IDF-IPP29542/2023	A/France/IDF-IPP29542/2023-like	3C.2a1b.2a.3a.1	2a.3a.1(J.4)
agAH3/Norway/8765/2025	A/Norway/8765/2025-like	3C.2a1b.2a.3a.1	2a.3a.1(K)
agAH3NOCAT	none	none	none

[a] WHO recommended vaccine virus from the 2025–2026 northern hemisphere influenza season.
[b] WHO recommended vaccine virus for the 2026 southern hemisphere influenza season.

Among the 1 137 characterised A(H3) viruses, the main reported categories were A/Croatia/10136RV/2023-like, clade 2a.3a.1(J.2), A/Singapore/GP20238/2024-like, clade 2a.3a.1(J.2.4) and A/Norway/8765/2025-like, clade 2a.3a.1(K), representing 43.3 %, 34.7 % and 10.6 %, respectively (Table 12).

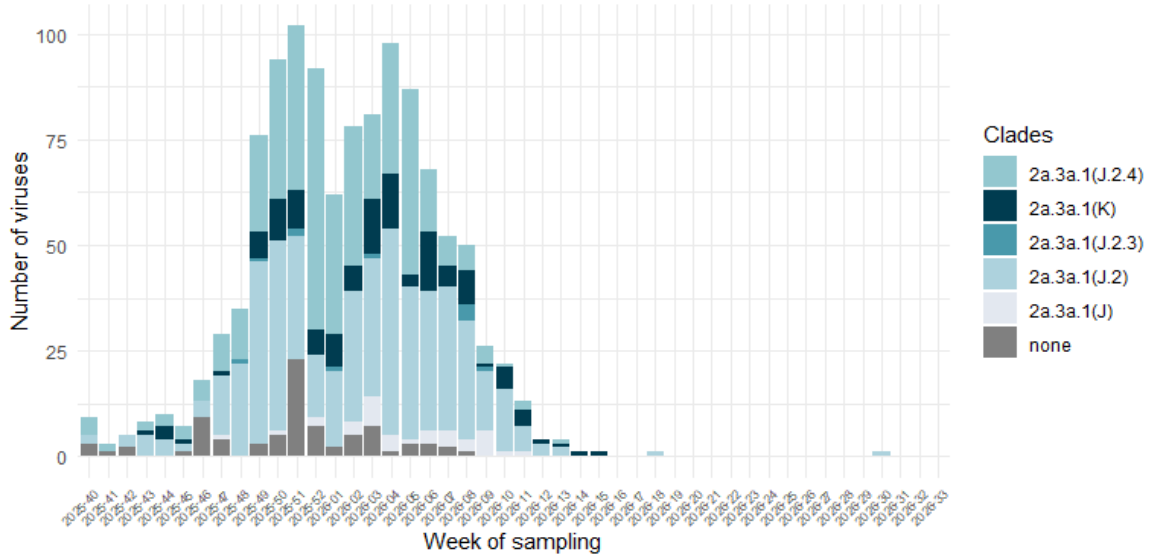
Table 12. Number of viruses by A(H3) antigenic reporting categories, EU/EEA, week 40 2025 to week 33 2026

Subclade	Virus_of_reference	nb	percent
2a.3a.1(J)	A/Thailand/8/2022-like	37	3.3
2a.3a.1(J.2)	A/Croatia/10136RV/2023-like[a]	492	43.3
2a.3a.1(J.2.3)	A/Netherlands/10685/2024-like	11	1.0
2a.3a.1(J.2.4)	A/Singapore/GP20238/2024-like[b]	394	34.7
2a.3a.1(K)	A/Norway/8765/2025-like	121	10.6
none	none	82	7.2

[a] WHO recommended vaccine virus from the 2025–2026 northern hemisphere influenza season.
[b] WHO recommended vaccine virus for the 2026 southern hemisphere influenza season.

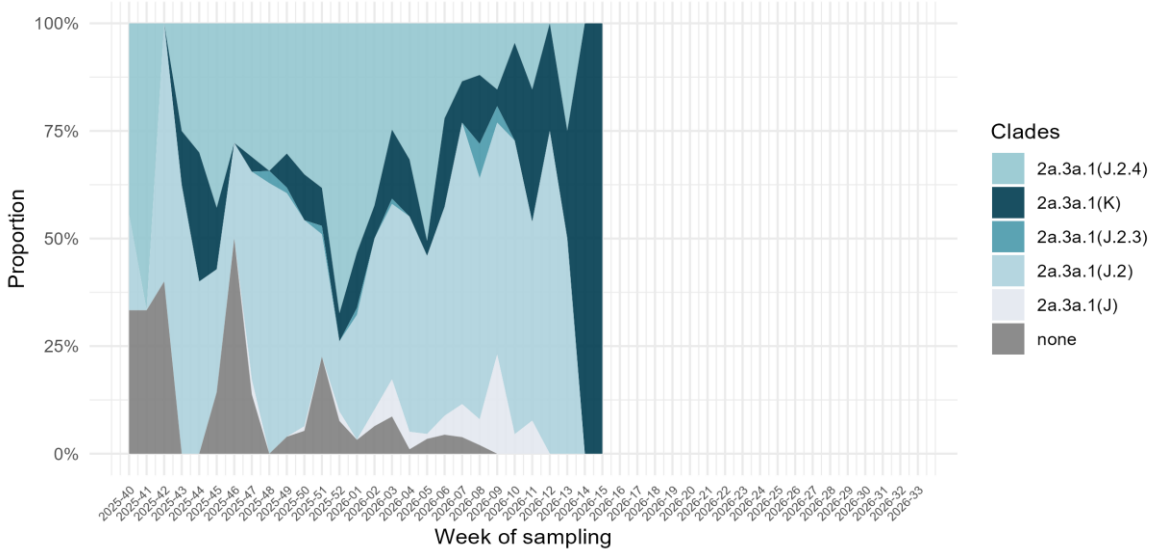
Among the viruses that could not be assigned to any of the predefined reporting antigenic categories ('none'), 55 have been tested against A/District of Columbia/27/2023 (subclade J.2) antiserum. This virus corresponds to the cell-based vaccine A(H3N2) component recommended by WHO for the 2025-2026 northern hemisphere influenza season. Only the egg-based vaccine equivalent (A/Croatia/10136RV/2023-like) was included in the TESSy reporting categories for the 2025-2026 season. The results of hemagglutination inhibition assays were provided in comments by two countries (Slovenia, Spain). Eight viruses out of the 55 were well recognised (within 8-fold difference): one was genetically assigned to subclade J.2.4 and seven to subclade K. Eight viruses among the remaining 47 A/District of Columbia/27/2023 -tested viruses belonged genetically to subclade K. No genetic information was available for the remaining 39 A/District of Columbia/27/2023 -tested viruses.

Figure 16. A(H3N2) clade weekly distribution based on antigenic characterisation, EU/EEA, week 40 2025 to week 33 2026



In the legend, the short clade name is given with the subclade in brackets.

Figure 17. A(H3) clade weekly proportion based on antigenic characterisation, EU/EEA, week 40 2025 to week 33 2026



In the legend, the short clade name is given with the subclade in brackets.

Genetic characterisation

From week 40 2025 to week 33 2026, with latest data reported for week 32 2026, 25 countries reported genetic characterisation to TESSy for 9 543 A(H3N2) influenza viruses. The countries that contributed were: Spain (3 352, 35.1 %), France (1 936, 20.3 %), Netherlands (809, 8.5 %), Ireland (617, 6.5 %), Germany (560, 5.9 %), Denmark (435, 4.6 %), Norway (434, 4.5 %), Portugal (313, 3.3 %), Romania (172, 1.8 %), Luxembourg (156, 1.6 %), Slovakia (118, 1.2 %), Sweden (117, 1.2 %), Austria (115, 1.2 %), Belgium (76, 0.8 %), Finland (64, 0.7 %), Estonia (46, 0.5 %), Croatia (45, 0.5 %), Czechia (42, 0.4 %), Italy (36, 0.4 %), Lithuania (33, 0.3 %), Slovenia (33, 0.3 %), Greece (14, 0.1 %), Poland (8, 0.1 %), Malta (7, 0.1 %) and Hungary (5, 0.1 %).

Countries were asked to report genetic characterisation results in TESSy according to the predefined categories described in Table 13.

Table 13. Predefined genetic reporting categories for A(H3) viruses

TESSy category	Virus of reference	Clade name	Subclade name
genAH3/Thailand/8/2022	A/Thailand/8/2022	3C.2a1b.2a.3a.1	2a.3a.1(J)
genAH3/Croatia/10136RV/2023	A/Croatia/10136RV/2023[a]	3C.2a1b.2a.3a.1	2a.3a.1(J.2)
genAH3/Switzerland/59652/2024	A/Switzerland/59652/2024	3C.2a1b.2a.3a.1	2a.3a.1(J.2.1)
genAH3/Lisboa/216/2023	A/Lisboa/216/2023	3C.2a1b.2a.3a.1	2a.3a.1(J.2.2)
genAH3/Netherlands/10685/2024	A/Netherlands/10685/2024	3C.2a1b.2a.3a.1	2a.3a.1(J.2.3)
genAH3/Singapore/GP20238/2024	A/Singapore/GP20238/2024[b]	3C.2a1b.2a.3a.1	2a.3a.1(J.2.4)
genAH3/Victoria/211/2025	A/Victoria/211/2025	3C.2a1b.2a.3a.1	2a.3a.1(J.2.5)
genAH3/Norway/8765/2025	A/Norway/8765/2025	3C.2a1b.2a.3a.1	2a.3a.1(K)
genAH3NOClade	none	none	none
genAH3SubgroupNotListed	other	other	other

[a] *WHO recommended vaccine virus from the 2025–2026 northern hemisphere influenza season.*
[b] *WHO recommended vaccine virus for the 2026 southern hemisphere influenza season.*

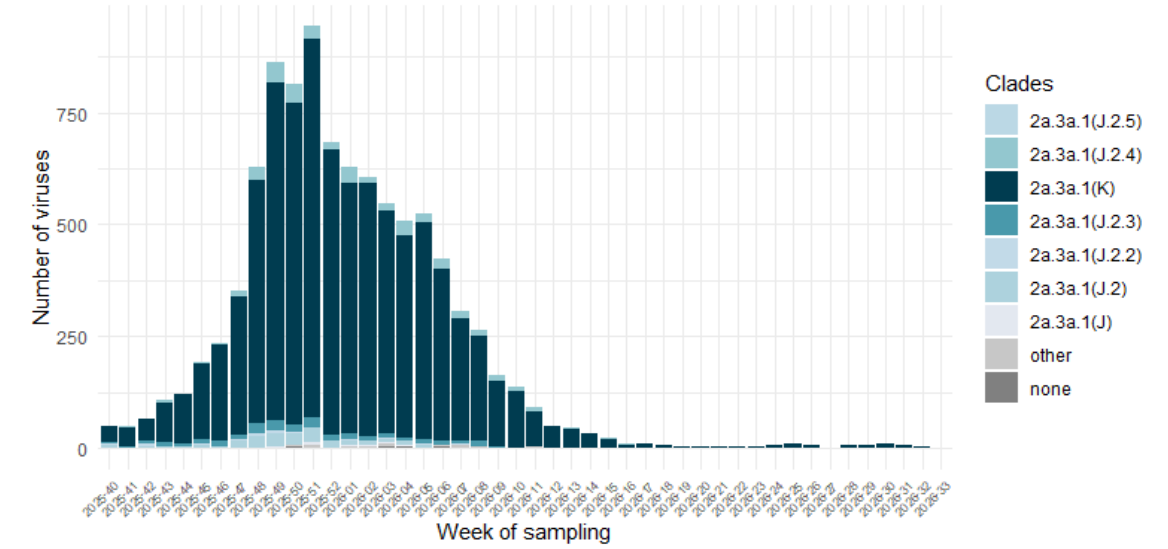
Among the 9 543 characterised A(H3) viruses, the main reported categories were A/Norway/8765/2025, clade 2a.3a.1(K) and A/Singapore/GP20238/2024, clade 2a.3a.1(J.2.4), representing 89.7 % and 4.3 %, respectively (Table 14).

Table 14. Number of viruses by A(H3) genetic reporting categories, EU/EEA, week 40 2025 to week 33 2026

Subclade	Virus_of_reference	nb	percent
2a.3a.1(J)	A/Thailand/8/2022	22	0.2
2a.3a.1(J.2)	A/Croatia/10136RV/2023[a]	224	2.3
2a.3a.1(J.2.2)	A/Lisboa/216/2023	44	0.5
2a.3a.1(J.2.3)	A/Netherlands/10685/2024	236	2.5
2a.3a.1(J.2.4)	A/Singapore/GP20238/2024[b]	408	4.3
2a.3a.1(J.2.5)	A/Victoria/211/2025	1	0.0
2a.3a.1(K)	A/Norway/8765/2025	8 560	89.7
none	none	10	0.1
other	other	38	0.4

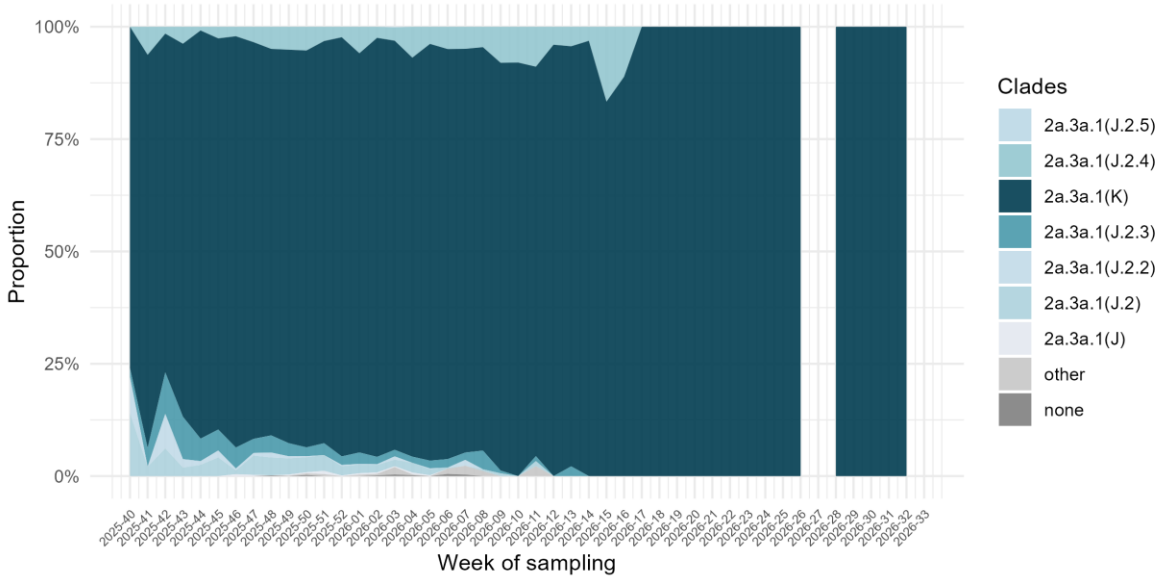
[a] *WHO recommended vaccine virus from the 2025–2026 northern hemisphere influenza season.*
[b] *WHO recommended vaccine virus for the 2026 southern hemisphere influenza season.*

Figure 18. A(H3) clade weekly distribution based on genetic characterisation, EU/EEA, week 40 2025 to week 33 2026



In the legend, the short clade name is given with the subclade in brackets.

Figure 19. A(H3) clade weekly proportion based on genetic characterisation, EU/EEA, week 40 2025 to week 33 2026



In the legend, the short clade name is given with the subclade in brackets.

Phylogenetic analysis

From week 40 2025 to week 33 2026, a total of 9 538 A(H3) HA sequences from 25 countries were reported, retrieved and included in the analyses (Figure 20). Countries that reported HA sequences are shown in Annex 3, Table 8A. There were eleven sequences that failed Nextstrain's quality control and were excluded from the phylogenetic tree (please see subsampled tree at Figure20.svg and full tree svg file at h3n2_2026_2026-09-01_1727.svg).

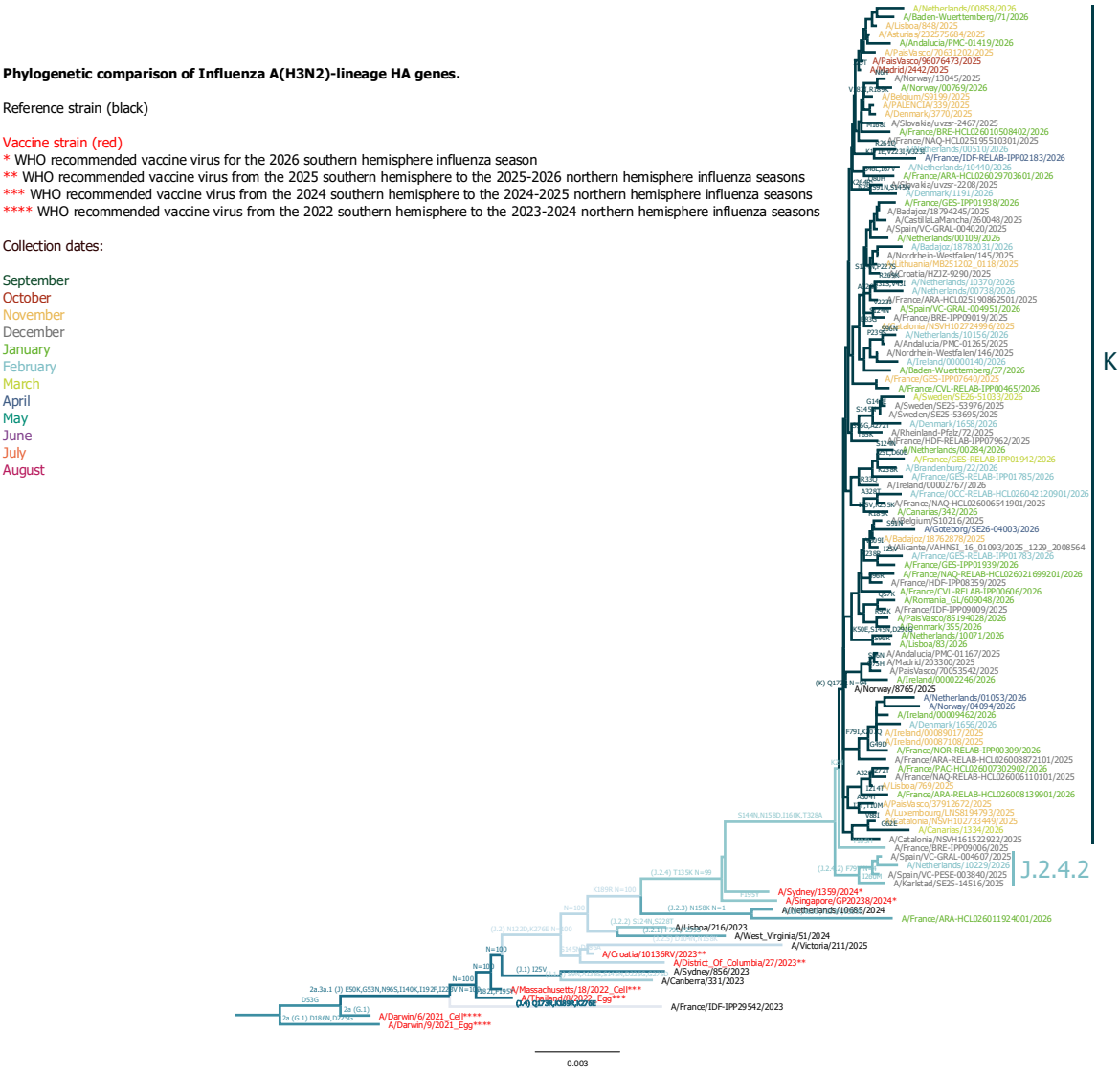
All A(H3) HA sequences fell into clade 2a.3a.1 and to one of the J.2 subclades, defined by N122D and K276E substitutions compared to A/Massachusetts/18/2022_Cell vaccine strain for NH 2024-2025. Most viruses (8 808, 92 %) fell into newly emerged subclade K (former J.2.4.1) characterised by K2N, S144N (a potential addition of an N-glycosylation site), N158D, I160K, Q173R, T328A and S378N (HA2:S49N) and represented by A/Norway/8765/2025.

The remaining 719 A(H3N2) viruses belonged to subclades J.2 (83, 0.9 %) represented by NH 2024-2025 vaccine strain A/Croatia/10136RV/2023, J.2.2 (47, 0.5 %) with substitutions S124N and S228T and represented by A/Lisboa/216/2023, J.2.3 (235, 2.5 %) represented by A/Netherlands/10685/2024 and characterised by N158K and

K189R, J.2.4 (47, 0.5 %) represented by vaccine strain A/Singapore/GP20238/2024 recommended for SH 2026 and J.2.4.2 (307, 3.2 %) which is not represented by a reference strain.

For the 9 538 viruses of A(H3) with reported clade, 9 475 (99 %) were concordant with the assigned clade and 9200 (97 %) were concordant with the subclade.

Figure 19. Phylogenetic comparison of 100 sub-samples of influenza A(H3N2) HA genes



The vaccine strains are given in red, reference strains in black and sequences reported to TESSy are coloured according to the virus collection date, by month. Please see subsampled and full tree svg here

Match between antigenic and genetic characterisations

Of the A(H3N2) viruses, 850 had both genetic and antigenic data reported (Annex 1, Table 4A). Overall, the reported A(H3N2) viruses were dispersed across five antigenic categories and six genetic clades. In addition, 44 viruses were reported distinct from all antigenic categories available for reporting.

The majority of the A(H3N2) viruses with both antigenic and genetic reports were antigenically reported as A/Croatia/10136RV/2023 -like (277, 32.6 %), the current NH season vaccine, or as A/Singapore/GP20238/2024 -like (394, 46.4 %), the SH 2026 season vaccine. Most of these viruses (255, 92.1 % and 371, 94.2 %, respectively) were however assigned genetically to the newly emerged subclade K that is antigenically distinct from the current NH season vaccine and is represented by A/Norway/8765/2025.

In addition, 117 viruses antigenically reported as A/Norway/8765/2025-like as well as 38 viruses that were not assigned to any antigenic category were classified genetically to subclade K. Further details on the reported viruses are available in Annex 1, Table 4A.

Antiviral susceptibility

From week 40 2025 to week 33 2026, with latest data reported for week 32 2026, 9 441 A(H3N2) influenza viruses were assessed genotypically and/or phenotypically for resistance to at least one drug (oseltamivir, zanamivir or baloxavir marboxil) by 25 countries. The countries that contributed were: Spain (3 314, 35.1%), France (1 941, 20.6 %), Netherlands (807, 8.5 %), Germany (592, 6.3 %), Ireland (563, 6 %), Denmark (435, 4.6 %), Norway (434, 4.6 %), Portugal (313, 3.3 %), Luxembourg (156, 1.7 %), Austria (119, 1.3 %), Poland (118, 1.2 %), Slovakia (118, 1.2 %), Sweden (117, 1.2 %), Belgium (76, 0.8 %), Finland (63, 0.7 %), Estonia (48, 0.5 %), Croatia (47, 0.5 %), Czechia (42, 0.4 %), Italy (36, 0.4 %), Lithuania (33, 0.3 %), Romania (31, 0.3 %), Greece (14, 0.1 %), Slovenia (12, 0.1 %), Malta (7, 0.1 %) and Hungary (5, 0.1 %).

Regarding the susceptibility to neuraminidase inhibitors, nine countries performed a phenotypic assessment: Germany (185), Poland (110), Netherlands (60), Spain (49), France (44), Portugal (24), Romania (14), Norway (10) and Italy (9). Reduced inhibition to Oseltamivir was observed for 1 (0.2 %) of the 505 tested A(H3N2), and reduced inhibition to Zanamivir was observed for 1 (0.2 %) of 491 tested A(H3N2) viruses (Table 15). The susceptibility of the remaining viruses was assessed genetically based on the presence of substitutions in the neuraminidase gene known to be associated with reduced inhibition. Substitutions associated with reduced and highly reduced inhibition by Oseltamivir were observed for 19 (0.2 %, associated with NA_S331R* mainly or NA_K249E or NA_N329R*) and 3 (<0.1 %, associated with NA_E119V or NA_del245-248/247-250), respectively, of the 8 869 viruses that could be assessed. Reduced inhibition by Zanamivir was observed for 17 (0.2 %, associated with NA_S331R* mainly or NA_del245-248/247-250) among the 8 883 viruses that could be assessed.

**Although these substitutions are not shown to reduce susceptibility to neuraminidase inhibitors in the currently circulating H3N2 strains [12], they have been included to raise awareness.*

Table 15. Number of A(H3N2) viruses, by reporting categories, for neuraminidase inhibitor susceptibility, EU/EEA, week 40 2025 to week 33 2026

	Phenotypic		Genotypic			
Antiviral	NI	RI	AANI	AARI[a]	AAHRI[b]	Total
Oseltamivir	504	1	8 847	19	3	9 374
Zanamivir	490	1	8 866	17	0	9 374

AAHRI: amino acid mutations associated with highly reduced inhibition; AANI: amino acid mutations associated with normal inhibition; AARI: amino acid mutations associated with reduced inhibition; NI: normal inhibition; RI: reduced inhibition.
Amino acid substitutions associated with reduced susceptibility are listed in Annex 2.
[a] The substitutions related to reduced susceptibility were NA_S331R mainly or NA_K249E or NA_N329R* for oseltamivir, and NA_S331R* or NA_del245-248/247-250 for zanamivir.*
[b] The substitution related to highly reduced susceptibility was NA_E119V or NA_del245-248/247-250 for oseltamivir.
**Although these substitutions are not shown to reduce susceptibility to neuraminidase inhibitors in the currently circulating H3N2 strains, they have been included to raise awareness.*

The susceptibility to polymerase inhibitors was assessed genetically based on the presence of substitutions in the PA polymerase subunit gene known to confer reduced susceptibility. Sequencing data were reported by 23 countries: France (1 772), Netherlands (763), Germany (538), Spain (527), Denmark (425), Norway (402), Portugal (255), Luxembourg (149), Sweden (114), Slovakia (107), Belgium (76), Finland (59), Croatia (45), Czechia (41), Lithuania (32), Italy (31), Greece (12), Slovenia (12), Estonia (10), Ireland (10), Malta (7), Hungary (5) and Poland (5). Out of the 5 397 assessed A(H3N2) viruses, substitutions associated with reduced susceptibility were observed for 7 (0.1 %, associated with PA_I38L) A(H3N2) viruses (Table 15).

Table 16. Number of A(H3N2) viruses, by reporting categories, for baloxavir marboxil susceptibility, EU/EEA, week 40 2025 to week 33 2026

	Genotypic		
Antiviral	AANS	AARS[a]	Total
Baloxavir	5 390	7	5 397

AANS: amino acid mutations associated with normal susceptibility; AARS: amino acid mutations associated with reduced susceptibility. Amino acid substitutions associated with reduced susceptibility are listed in Annex 2.
[a] The substitution related to reduced susceptibility was PA_I38L.

Age, outcome and vaccination status

Data about how the characterised viruses were distributed in age groups per subclade, what the outcome was and what proportions of individuals infected by characterised viruses had been vaccinated, are displayed in Annex 4.

B/Victoria lineage viruses

Antigenic characterisation

From week 40 2025 to week 33 2026, with latest data reported for week 19 2026, 4 countries reported antigenic characterisation to TESSy for 21 B/Victoria influenza viruses. The countries that contributed were: France (9, 42.9 %), Denmark (7, 33.3 %), Portugal (4, 19 %) and Germany (1, 4.8 %).

Countries were asked to report antigenic characterization results in TESSy according to the predefined categories described in Table 17.

Table 17. Predefined antigenic reporting categories for B(Victoria) viruses

TESSy category	Virus of reference	Clade name	Subclade name
agBVicB/Washington/02/2019	B/Washington/02/2019-like	V1A.3	V1A.3(A.3.2)
agBVicB/Austria/1359417/2021	B/Austria/1359417/2021-like[a]	V1A.3a.2	V1A.3a.2(C)
agBVicB/Stockholm/3/2022	B/Stockholm/3/2022-like	V1A.3a.2	V1A.3a.2(C.5)
agBVicNOCAT	none	none	none

[a] WHO recommended vaccine virus from the 2025–2026 northern hemisphere and the 2026 southern hemisphere influenza seasons.

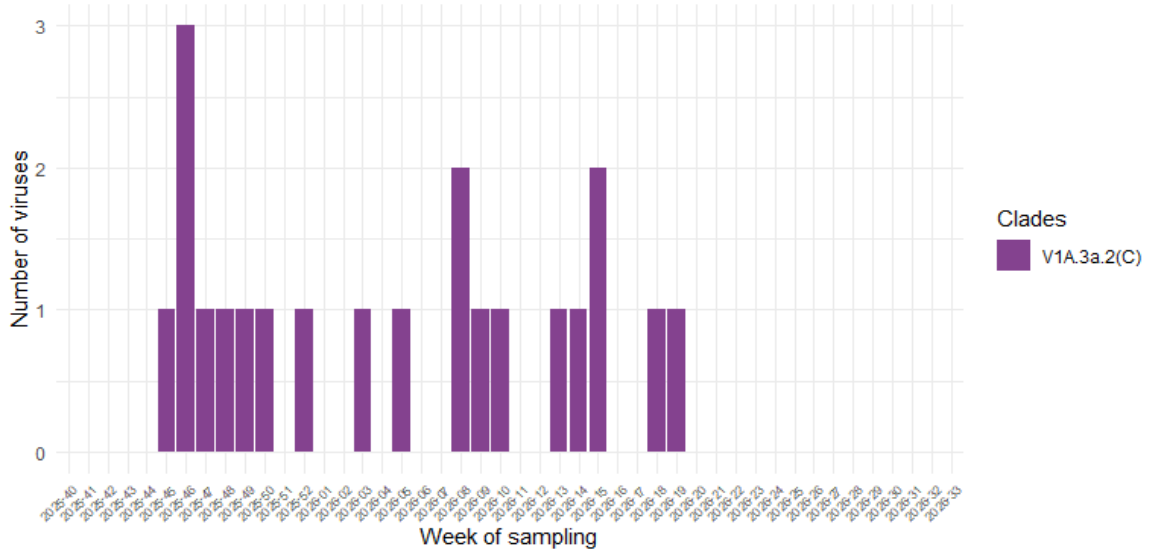
Among the 21 characterised B(Victoria) viruses, all were reported as B/Austria/1359417/2021-like, clade V1A.3a.2(C) (Table 18).

Table 18. Number of viruses by B(Victoria) antigenic reporting categories, EU/EEA, week 40 2025 to week 33 2026

Subclade	Virus_of_reference	nb	percent
V1A.3a.2(C)	B/Austria/1359417/2021-like[a]	21	100

[a] WHO recommended vaccine virus from the 2025–2026 northern hemisphere and the 2026 southern hemisphere influenza seasons.

Figure 20. B(Victoria) clade weekly distribution based on antigenic characterisation, EU/EEA, week 40 2025 to week 33 2026



In the legend, the short clade name is given with the subclade in brackets.

Genetic characterisation

From week 40 2025 to week 33 2026, with latest data reported for week 29 2026, 14 countries reported genetic characterisation to TESSy for 318 B(Victoria) influenza viruses. The countries that contributed were: Norway (69, 21.7 %), Denmark (61, 19.2 %), Sweden (52, 16.4 %), Spain (44, 13.8 %), France (43, 13.5 %), Netherlands (19, 6 %), Ireland (8, 2.5 %), Finland (7, 2.2 %), Belgium (5, 1.6 %), Italy (3, 0.9 %), Portugal (3, 0.9 %), Germany (2, 0.6 %), Austria (1, 0.3 %) and Lithuania (1, 0.3 %).

Countries were asked to report genetic characterisation results in TESSy according to the predefined categories described in Table 19.

Table 19. Predefined genetic reporting categories for B(Victoria) viruses

TESSy category	Virus of reference	Clade name	Subclade name
genBVicB/Austria/1359417/2021	B/Austria/1359417/2021[a]	V1A.3a.2	V1A.3a.2(C)
genBVicB/Kanagawa/AC2414/2025	B/Kanagawa/AC2414/2025	V1A.3a.2	V1A.3a.2(C.3.1)
genBVicB/Stockholm/3/2022	B/Stockholm/3/2022	V1A.3a.2	V1A.3a.2(C.5)
genBVicB/Catalonia/2279261NS/2023	B/Catalonia/2279261NS/2023	V1A.3a.2	V1A.3a.2(C.5.1)
genBVicB/Switzerland/329/2024	B/Switzerland/329/2024	V1A.3a.2	V1A.3a.2(C.5.6)
genBVicB/ENG/120/2025	B/ENG/120/2025	V1A.3a.2	V1A.3a.2(C.5.6.1)
genBVicB/Greece/5509/2024	B/Greece/5509/2024	V1A.3a.2	V1A.3a.2(C.5.7)
genBVicNOClade	none	none	none
genBVicSubgroupNotListed	other	other	other

[a] *WHO recommended vaccine virus from the 2025–2026 northern hemisphere and the 2026 southern hemisphere influenza seasons.*

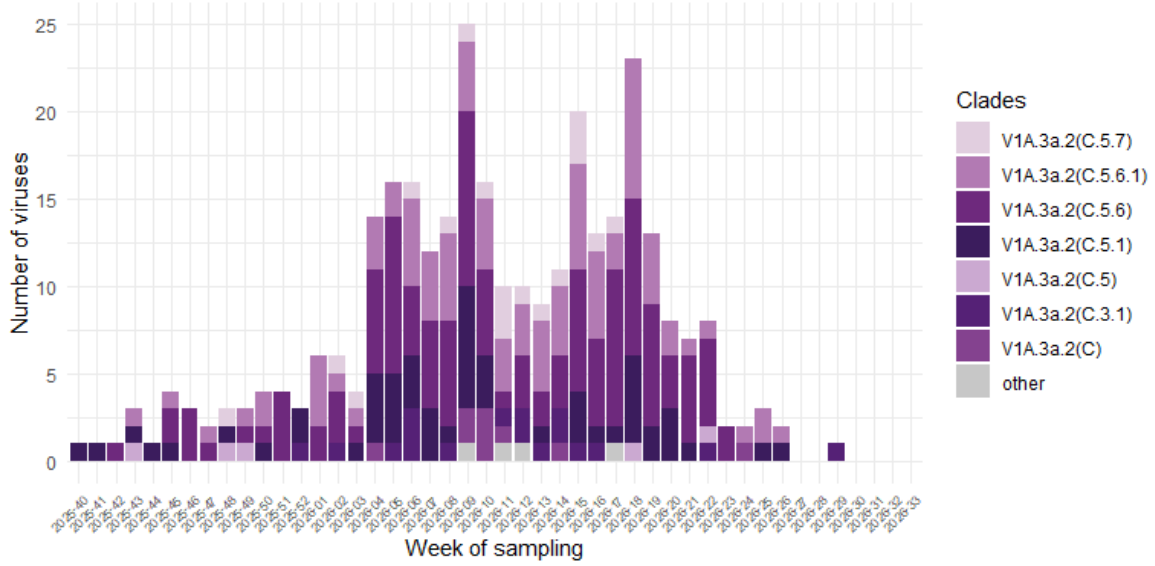
Among the 318 characterised B(Victoria) viruses, the main reported categories were B/Switzerland/329/2024, clade V1A.3a.2(C.5.6), B/ENG/120/2025, clade V1A.3a.2(C.5.6.1) and B/Catalonia/2279261NS/2023, clade V1A.3a.2(C.5.1), representing 39.3 %, 27 % and 17 %, respectively (Table 19).

Table 20. Number of viruses by B(Victoria) genetic reporting categories, EU/EEA, week 40 2025 to week 33 2026

Subclade	Virus_of_reference	nb	percent
V1A.3a.2(C)	B/Austria/1359417/2021[a]	9	2.8
V1A.3a.2(C.3.1)	B/Kanagawa/AC2414/2025	17	5.3
V1A.3a.2(C.5)	B/Stockholm/3/2022	5	1.6
V1A.3a.2(C.5.1)	B/Catalonia/2279261NS/2023	54	17.0
V1A.3a.2(C.5.6)	B/Switzerland/329/2024	125	39.3
V1A.3a.2(C.5.6.1)	B/ENG/120/2025	86	27.0
V1A.3a.2(C.5.7)	B/Greece/5509/2024	18	5.7
other	other	4	1.3

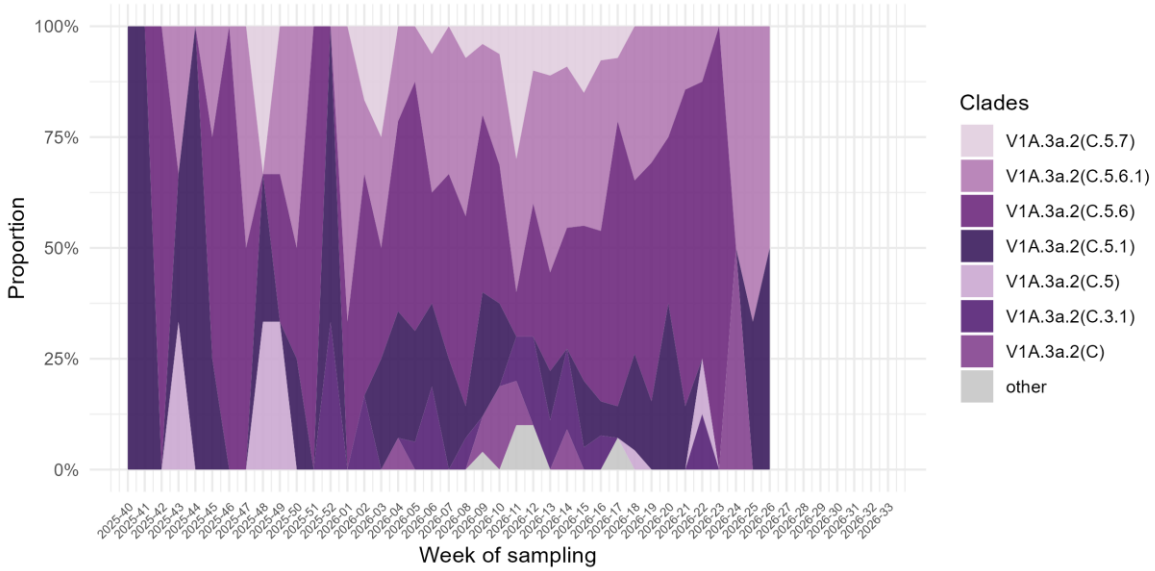
[a] *WHO recommended vaccine virus from the 2025–2026 northern hemisphere and the 2026 southern hemisphere influenza seasons.*

Figure 21. B(Victoria) clade weekly distribution based on genetic characterisation, EU/EEA, week 40 2025 to week 33 2026



In the legend, the clade name is given with the subclade in brackets.

Figure 22. B(Victoria) clade weekly proportion based on genetic characterisation, EU/EEA, week 40 2025 to week 33 2026



In the categories, the clade name is given with the subclade in brackets.

Phylogenetic analysis

From week 40 2025 to week 33 2026, a total of 318 B/Victoria HA sequences from 14 countries were reported, retrieved and included in the analyses (Figure 23). Countries that reported HA sequences are shown in Annex 3, Table 9A. There were two sequences that failed Nextstrain's quality control and were excluded from the phylogenetic tree (please see subsampled tree at Figure23.svg and full tree svg file at: vic_2026_2026-09-02_1440.svg).

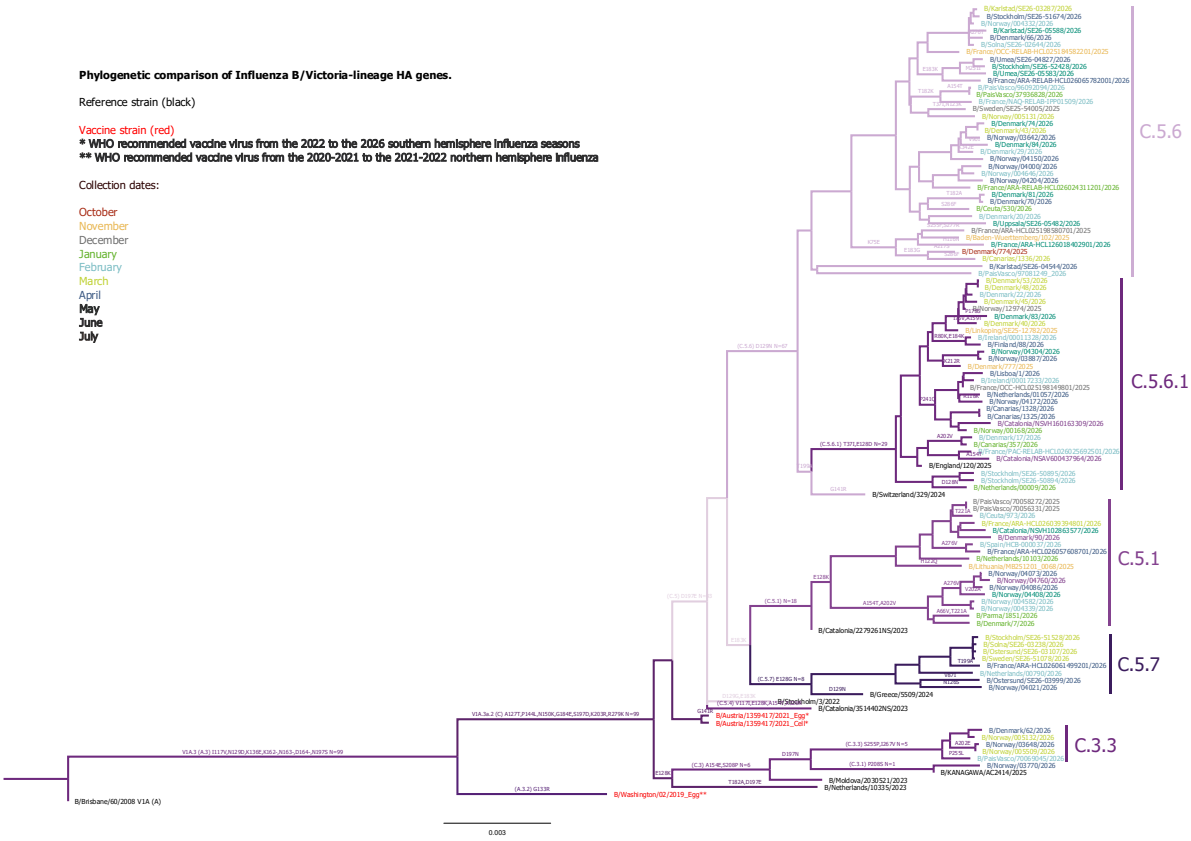
All reported viruses of B/Victoria carried HA genes that fell into genetic clade V1A.3a.2 (C) with characteristic amino acid substitutions A127T, P144L, N150K, G184E, S197D, K203R and R279K compared with previous vaccine strain B/Washington/02/2019 and represented by B/Austria/1359417/2021_Egg, the NH vaccine strain since the 2022–2023 season.

The majority (288, 91 %) of the viruses within 3a.2 fell in the branch of subclade C.5 defined by D197E, compared with B/Austria/1359417/2021_Egg, where the viruses fell into the following subclades in descending order, C.5.6 defined by D129N (126, 40 %), C.5.6.1 (89, 28 %) defined by T37I and E128D, C.5.1 (54, 17 %) additionally carrying E128K and C.5.7 (18, 6 %) defined by E128G represented by B/Switzerland/329/2024, B/England/120/2025, B/Catalonia/2279261NS/2023 and B/Greece/5509/2024, respectively.

Twenty-eight (9 %) viruses represented the subclade C.3, characterised by the combination of E128K, A154E and S208P, similar to B/Moldova/2030521/2023 where half of them belonged to subclade C.3.1 with HA substitution P208S and represented by B/KANAGAWA/AC2414/2025 and half to C.3.3 defined by S255P and I267V that does not have a representative reference strain.

The concordance between assigned clade and subclade was high for B/Victoria, where all except one (317) viruses with a reported clade matched at clade level and 310 (97 %) matched at subclade level.

Figure 23. Phylogenetic comparison of 100 sub-samples of influenza B/Victoria-lineage HA genes



The vaccine strains are given in red, reference strains in black and sequences reported to TESSy are coloured according to the virus collection date, by month. Please see subsampled and full tree svg files at at ECON Respiratory Viruses - Laboratory - 2025-2026 Influenza virus characterisation - All Documents).

Match between antigenic and genetic characterisations

The 19 B/Victoria viruses that had both genetic and antigenic data were all antigenically reported as B/Austria/1359417/2021-like, which is the current NH season 2025-26 vaccine component, but genetically these viruses were reported across five categories with nine belonging to B/Switzerland/329/2024 V1A.3a.2(C.5.6), five to B/ENG/120/2025 V1A.3a.2(C.5.6.1), three to B/Catalonia/2279261NS/2023 V1A.3a.2(C.5.1), one to B/Greece/5509/2024 V1A.3a.2(C.5.7) and one to B/Kanagawa/AC2414/2025 V1A.3a.2(C.3.1).

Antiviral susceptibility

From week 40 2025 to week 33 2026, with latest data reported for week 26 2026, 312 B(Victoria) influenza viruses were assessed genotypically and/or phenotypically for resistance to at least one drug (oseltamivir, zanamivir or baloxavir marboxil) by 14 countries. The countries that contributed were: Norway (64, 20.5 %), Denmark (61, 19.6 %), Sweden (52, 16.7 %), Spain (44, 14.1 %), France (43, 13.8 %), Netherlands (19, 6.1 %), Finland (7, 2.2 %), Ireland (7, 2.2 %), Belgium (5, 1.6 %), Italy (3, 1 %), Portugal (3, 1 %), Germany (2, 0.6 %), Austria (1, 0.3 %) and Lithuania (1, 0.3 %).

Regarding the susceptibility to neuraminidase inhibitors, six countries performed a phenotypic assessment: Netherlands (5), Spain (3), Germany (2), Portugal (2), Italy (1) and Norway (1). None of the 298 genotypically and 14 phenotypically tested B(Victoria) viruses showed reduced susceptibility (Table 21).

Table 21. Number of B(Victoria) viruses by reporting categories for neuraminidase inhibitor susceptibility, EU/EEA, week 40 2025 to week 33 2026

	Phenotypic	Genotypic	
Antiviral	NI	AANI	Total
Oseltamivir	14	298	312
Zanamivir	14	298	312

AANI: amino acid mutations associated with normal inhibition; NI: normal inhibition.

The susceptibility to polymerase inhibitor were assessed genetically based on the presence of substitutions in the PA polymerase subunit gene that are known to confer reduced susceptibility. Sequencing data were reported by 12 countries: Norway (57), Sweden (52), Denmark (49), France (41), Netherlands (17), Spain (15), Finland (6), Belgium (5), Italy (3), Portugal (3), Germany (1) and Lithuania (1). Substitutions associated with reduced susceptibility were reported for none of the 250 assessed B(Victoria) viruses (Table 22).

Table 22. Number of B(Victoria) viruses by reporting categories for baloxavir marboxil susceptibility, EU/EEA, week 40 2025 to week 33 2026

	Genotypic	
Antiviral	AANS	Total
Baloxavir	250	250

Age, outcome and vaccination status

Data about how the characterised viruses were distributed in age groups per subclade, what the outcome was and what proportions of individuals infected by characterised viruses had been vaccinated, are displayed in Annex 4.

Discussion

Detections and virus characterisation data

Influenza virus detection and characterisation data from the EU/EEA remain essential for monitoring the genetic and antigenic evolution of influenza viruses, assessing antiviral susceptibility among circulating seasonal strains, and selecting viruses for submission to WHO Collaborating Centres (WHO CCs) for further in-depth analyses. These analyses contribute to the evidence base used in the biannual WHO vaccine composition meetings, where recommendations are made on the influenza viruses to be included in seasonal vaccines.

From week 40 2025 to week 33 2026, all 30 EU/EEA countries reported 256 967 influenza virus detections to TESSy, as well as 1 996 antigenic and 16 482 genetic characterisations. This influenza season was characterised by the predominance of A(H3) viruses, however, influenza type A subtype A(H1)pdm09 and type B/Victoria lineage also co-circulated at lower levels. Among the 57 318 (sub)typed or lineage-defined viruses, 20 072 A(H1)pdm09 (35 %), 36 874 A(H3) (64 %) and 372 B/Victoria (0.6 %) viruses were reported from sentinel and non-sentinel surveillance specimens. Further surveillance data, maps and country-specific tables are available at: www.erviss.org.

NRLs have been encouraged to characterise as many of their sentinel influenza viruses as possible, with both ECDC and WHO/Europe recommending in the 2022 joint surveillance guidance that all sentinel influenza viruses should be sequenced [15]. At the moment, ECDC is in the process of drafting a new guidance for genomic surveillance which will give more nuanced advice for countries to apply sequencing in different epidemiological situations and within different sizes of surveillance systems, which has already mentioned in the 2026 ECDC surveillance guidance [2]. Clear efforts towards characterisation of a higher number of influenza viruses have been made across Europe during the past two seasons. In total, 16 482 (6.7 %) of 256 967 influenza virus detections were entered into TESSy as characterised during the reporting period, which is an increase from the 4.2 % characterised last year [16]. For the sentinel specimens, 5 263 (29 %) of 18 022 were characterised; again an increase from 20 % sentinel specimens characterised in August 2025.

In this season, of the 30 EU/EEA countries, 25 reported virus characterisation data along with influenza detection data, to varying extents. Eight countries also reported antigenic data this season at the same time, a similar number to last year. Since the 2017-18 season, the antigenic reports have either decreased or fluctuated. With 1 996 reports by week 33 2026, the numbers were comparable to the 2 016 antigenic reports in 2024-25 season.

Twenty-five countries reported genetic data this year, which is eight more countries than last year. This is another major achievement in the network to increase molecular surveillance capacity for influenza in the EU/EEA. ECDC continues to support countries in reporting virus characterisation data into TESSy. Overall numbers of genetic clade data reports made by EU/EEA countries in the 2025–26 season increased further in comparison to the reports in 2024-25, although the genetic reports had already doubled the year before. Furthermore, the country-reported genetic clade categories aligned well with ECDC Nextstrain-based phylogenetic analysis and assignment of clades.

Approximately 6 % of all detections, and 29 % of all subtyped influenza viruses were genetically characterised. Of the subtyped A(H1)pdm09, 33 % were genetically characterised. For A(H3) viruses, 26 % of subtyped viruses were characterised. Among the subtyped A viruses, A(H1)pdm09 accounted for 35 % of the subtyped A viruses, and 41 % of the genetically characterised A viruses were A(H1)pdm09 viruses. A(H3N2) accounted for 65% of the subtyped A viruses, and 59 % of genetically characterised A viruses were A(H3) viruses. Those proportions of subtyped viruses and genetic characterisations align very well with each other. B viruses represented <1 % of all the detected and subtyped/lineage-determined influenza viruses; and of the genetically characterised viruses, 2 % were B/Victoria viruses which is also aligning well with the detections. Overall, 85 % of B/Victoria viruses that were detected, were characterised genetically.

Approximately 0.8 % of all detections, and 3.5 % of the subtyped influenza viruses were antigenically characterised. The distribution of type A and B viruses that had antigenic analyses were very similar to the overall virus distribution: 97 % influenza A and 1.3 % influenza B viruses detected versus 98.9 % and 1.1% antigenically characterised, respectively. Among the A viruses, the proportion of antigenically characterised A(H3) viruses was 57.6 %, compared with 42.4 % for A(H1)pdm09 viruses. The detection rates were slightly different, with 65 % for A(H3) and 35 % for A(H1)pdm09. However, higher proportion of characterised A(H1) viruses could reflect the laboratory experts' interest towards antigenic properties of viruses that were circulating less than the predominating A(H3) viruses, as minority influenza virus types and A subtypes are more likely to cause an epidemic next season compared with the majority strains. Sequencing strategies should prioritise these minority types and A subtypes rather than adhering strictly to proportional sampling.

In this report, we also included data on age, vaccination status and outcome. Age was reported for the majority of non-sentinel specimens. The majority of the virus characterisation specimens originated from 15-65 years old persons for A(H3) and B/Victoria, while the majority of A(H1)pdm09 virus characterisation specimens were from persons 65 years and older. For A(H1)pdm09 and A(H3), the age group 15-64 years is under-represented in the specimens collected for characterisation with only 38 % of specimens coming from that group even though they comprise about 63 % of the EU population [17,18]. The age group 65 years and older was again over-represented in the specimens as 46 % and 31% of specimens were from this group, respectively, although they compose only 22 % of the EU population [17,18]. For B viruses, the age group 65 years and older was under-represented, as only 6 % of specimens were from that group. More sampling was performed in school children aged 5-14y olds (17 %). For A(H3) viruses, younger age groups <15y of age were overrepresented with 30% of sampling coming from this group even though they comprise only 14% of the EU/EEA population [17,18].

Influenza virus evolution and vaccine effectiveness

When comparing the antigenic similarity of circulating A(H1)pdm09 viruses to the 2025–26 NH vaccine strains, 51.2 % of circulating viruses were reported as similar to the NH 2025–26 vaccine strains A/Victoria/4897/2022-like or A/Wisconsin/67/2022-like, when characterised with available antisera. However, nearly half (44.2 %) of A(H1N1)pdm09 viruses circulating in Europe were reported as similar to A/Missouri/11/2025-like, which was the SH 2026 vaccine strain and antigenically distinct from the NH current season vaccine strain.

Genetically, almost all (99.6 %) of A(H1)pdm09 viruses fell into the 5a.2a.1(D.3.1) subclade represented by A/Missouri/11/2025, and furthermore, almost all those viruses (95 %) belonged to the newly emerged subclade D.3.1.1. Similar dominance of the D.3.1 and D.3.1.1 subclades was presented earlier in by the US CDC [19]. Only one of the sequenced viruses belonged to this season's NH vaccine component subclade D, represented by A/Victoria/4897/2022 and a few others (0.3 %) belonged to subclade C.1.9.3. In the February 2026 NH vaccine composition meeting (VCM) there was a conclusion to recommend a change to the A(H1)pdm09 vaccine component for the 2026–27 season to A/Missouri/11/2025-like (subclade D.3.1) viruses [20]. Interim European vaccine effectiveness data showed a varied vaccine effectiveness (VE) that ranged from 25 % to 35% protection against influenza A(H1)pdm09 across study sites [21]. Further diversification of D.3.1.1 viruses continued and global increases of viruses carrying G155E, associated with reduced ferret antisera recognition, were reported in the southern hemisphere vaccine composition consultation of WHO [22].

For A(H3), based on sequence analysis, the majority (92 %) of circulating viruses fell in subclade K represented by A/Norway/8765/2025 that emerged during the summer of 2025 and spread rapidly across the globe [23]. Available antigenic data indicate that 43.3 % of circulating viruses this season were reported as antigenically similar to the A/Croatia/10136RV/2023-like viruses of the NH 2025–2026 season vaccine strain in the EU/EEA. However, global data analysis from the 2026 NH VCM revealed reduced reactivity of 2025-2026 season vaccine component A/Croatia/10136RV/2023-like viruses against many recent strains, such as J.2.3, J.2.4 and K subclades [20]. This reduced reactivity was more pronounced in viruses with HA substitutions F79V, S144N (addition of a potential N-glycosylation site), N158D, I160K and/or T328A [20]. The VCM recommended a change to the A(H3) vaccine for the 2026–27 season to A/Darwin/1454/2025 (H3N2)-like (subclade K) viruses [20]. Somewhat surprisingly, the vaccine effectiveness against the subclade K viruses was still moderate from 38 to 50% across six study sites in Europe by January 2026 [21].

For the B/Victoria lineage, all antigenically characterised viruses were B/Austria/1359417/2021 -like (subclade C), the current NH 2025–26 season vaccine strain B/Austria/1359417/2021 [20]. Genetically, most of the B/Victoria lineage viruses were in a sub-branch of the vaccine strain (in subclade C.5) but the genetic diversification has continued. B/Victoria viruses fell into subclades C.5.6 (125, 39.3 %), C.5.6.1 (86, 27 %), C.5.1 (54, 17%) and C.5.7 (18, 5.7 %). In addition, twenty-one (6.6 %) viruses represented the subclade C.3, belonging to subclade C.3.1 and C.3.3, which were poorly recognized by the current vaccine. VCM recommended a change for the B/Victoria lineage vaccine component to B/Tokyo/EIS13-175/2025-like subclade C.3.1 viruses for the NH 2026-27 influenza season [20]. At the time of this study, final VE estimates for Europe were not available and at the time of the interim results, too few data points were available for B viruses.

Antiviral susceptibility

About 3 % of the A(H1)pdm09 viruses tested were found to have reduced susceptibility to neuraminidase inhibitors and 0.1 % against baloxavir marboxal, by either phenotypic or genotypic testing. This showed a clear increase in reduced susceptibility, especially against Oseltamivir (175 of 6 525 tested viruses classified AARI, AAHRI, RI or HRI) compared to earlier years, when around 0.1 % of A(H1)pdm09 viruses have been found to be reduced inhibited. Most viruses that showed reduced or highly reduced inhibition by oseltamivir carried amino acid substitutions NA_I223V and S247N (151 of 175), which were also present in the majority of A(H1)pdm09 viruses with reduced susceptibility in the 2023–2024 season, but were not reported during the 2024–2025 season. NA_H275Y was detected in 17 A(H1)pdm09 viruses. NA_275Y is an amino acid substitution that is well known to confer reduced or

highly reduced susceptibility to oseltamivir [12]. Other substitutions were detected in one to two viruses only (see Annex, Table 5A). One A(H1)pdm09 virus that showed reduced inhibition by oseltamivir in phenotypic assay had the double substitution NA_G147R and S247N, which is not described in WHO reference tables. Four A(H1)pdm09 viruses were carrying substitutions (PA_A37T, PA_E199G, PA_E199K or PA_E23G; one each) that confer reduced susceptibility to baloxavir marboxal.

Twenty-four A(H3) viruses (<0.3 %) were found to have reduced susceptibility to neuraminidase inhibitors. The neuraminidase sequences available for 23 of these viruses showed substitutions known to reduce susceptibility. Fifteen viruses reported this season carried the NA_S331R substitution. Although listed in WHO table as 'normal inhibition/reduced inhibition' (NI/RI) for both oseltamivir and zanamivir, this substitution has been described as not affecting neuraminidase inhibitor susceptibility in the currently circulating A(H3) viruses. It was nonetheless interpreted as conferring reduced inhibition in this report to raise awareness. In addition, one virus was found to carry the NA_N329R substitution. This substitution is also listed as conferring reduced inhibition to oseltamivir in WHO table but described as having no effect in the currently circulating A(H3) viruses. Instructions on how to report genetically assessed antiviral susceptibility based on these substitutions would require additional clarification from the WHO antiviral working group. Other substitutions potentially associated with reduced inhibition to neuraminidase inhibitors that were found and included were NA_del245_248, NA_del247_250, NA_E119V, and NA_K249E; further details on the reported viruses are presented in Annex 2, Table 5A. Seven (0.1 %) A(H3N2) viruses were detected with substitution PA_I38L that confers reduced susceptibility to baloxavir marboxal.

None of the B/Victoria viruses were reported to have reduced susceptibility to antivirals.

Limitations

There are limitations to the data presented in this report. The specimen sources (sentinel general practitioners, hospitals, intensive care units, outbreak investigations), patient characteristics (e.g. age per subtype) and selection processes for the viruses that undergo characterisation vary from country to country, and only a small percentage of total influenza detections were characterised: 0.8 % antigenically and 6.4 % genetically; which could bias the analysis. It could be that some of the countries performing sequencing do not report their genetic clade or sequence identifier information to TESSy, but only to sequence databases. If that is the case, their data would not be included in this analysis.

Furthermore, for the antigenic data reported to TESSy, only the laboratory interpretations were considered, and no direct analysis of HI-assay data was possible. Therefore, the antigenic characterisation results from the different laboratories may not be directly comparable.

For the antiviral phenotypic susceptibility analysis, the laboratories' interpretations of their antiviral test results regarding drug susceptibility were used for this report, rather than the IC50 test values from the phenotypic testing. Using these interpretations should make the data from different countries easier to compare; however, it is noted that the methods the laboratories used to reach their conclusions may vary.

Conclusions

The following conclusions are drawn from this 2025–2026 influenza virus characteristics analysis:

- EU/EEA countries continue to be a major contributor of influenza detection and virus characterisation data to the Global Influenza Surveillance and Response System with all 30 EU/EEA reporting data this season
- EU/EEA countries have had major achievements in terms of virus characterisation of influenza in season 2025-2026 by increasing the number of countries reporting.
  - Eight EU/EEA countries provided antigenic characterisation data.
  - Twenty-five countries, including eight new countries, provided genetic characterisation data for slightly increased number of viruses than the previous year, showing increasing sequencing efforts and capacity for influenza in the region.
- Influenza virus characterisation specimens originate from both sentinel and non-sentinel surveillance systems, with approximately two-thirds (67 %) reported from non-sentinel systems. Non-sentinel surveillance systems provide a large number of positive influenza virus specimens to the NRLs that are a crucial complement to the sentinel source specimens.
- Characterisation data showed that the genetic diversification of influenza viruses has continued. Antigenically, the majority of both A(H1)pdm09 and A(H3) in the EU/EEA became distinct from the 2025–26 vaccine components and molecular evolution of also B/Victoria viruses continued. Similar observations in other parts of the world prompted WHO to recommend all three components (A(H1)pdm09, A(H3) and B/Victoria) of the vaccine to be changed for the NH 2026–27 season vaccines.

- Phylogenetic analysis showed diversification within influenza A subtypes and B/Victoria viruses circulating in the EU/EEA. Several subclades, such as subclade D.3.1.1 of A(H1)pdm09, subclade K of A(H3), and C.5.6 and C.5.6.1 of B/Victoria, display an expansion.
- Overall, only a few (201/16 318 viruses analysed for neuraminidase inhibitor susceptibility, 1.2 %; 11/9 692 viruses analysed for PA-inhibitor susceptibility, 0.1 %) influenza viruses with reduced susceptibility to antiviral drugs were detected this season, however, an increase of reduced susceptibility against Oseltamivir is noted in A(H1)pdm09 viruses.

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Annex 1. Antigenic group and genetic clade category reports

Table 1A. Antigenic characterisation data by reporting category, as reported to TESSy, by country (n=8), EU/EEA, week 40 2025 to week 33 2026

	Countries								
AntigenicGroup	Belgium	Denmark	France	Germany	Portugal	Slovenia	Spain	Romania	Total
agAH1/Lisboa/188/2023						4			4
agAH1/Missouri/11/2025		1	314		55				370
agAH1/Sydney/5/2021				33					33
agAH1/Victoria/4897/2022		49	92	277		7	3		428
agAH1/Wisconsin/67/2022		1							1
agAH1NOCAT			2						2
agAH3/Croatia/10136RV/2023		2	4	478	2	2		4	492
agAH3/Netherlands/10685/2024		1	10						11
agAH3/Norway/8765/2025		69			52				121
agAH3/Singapore/GP20238/2024	12	7	375						394
agAH3/Thailand/8/2022	1			36					37
agAH3NOCAT			24			49	9		82
agBVicB/Austria/1359417/2021		7	9	1	4				21
Total	13	137	830	825	113	62	12	4	1 996

HI: haemagglutination inhibition.
To denote a virus isolate as being like a vaccine/reference virus, its HI titre with post-infection ferret antiserum raised against the vaccine/reference virus should differ by no more than four-fold (usually a decrease), in a two-fold dilution series, compared with the HI titre (homologous) with the vaccine/reference virus itself. A virus isolate is considered antigenically different ('Not categorised') from a vaccine/reference virus if the HI titre with post-infection ferret antiserum raised against the vaccine/reference virus differs by eight-fold or more (a decrease), in a two-fold dilution series, compared with the HI titre (homologous) with the vaccine/reference virus itself.

Table 2A. Genetic characterisation data by category as reported to TESSy, by country (n=25), EU/EEA, week 40 2025 to week 33 2026

	Countries																									
GeneticClade	Austria	Belgium	Croatia	Czechia	Denmark	Estonia	Finland	France	Germany	Greece	Hungary	Ireland	Italy	Lithuania	Luxembourg	Malta	Netherlands	Norway	Poland	Portugal	Romania	Slovakia	Slovenia	Spain	Sweden	Total
genAH1/Hungary/286/2024								9									3							6	1	19
genAH1/Missouri/11/2025	60	37	12	19	358	48	97	1 195	227	3	6	72	30	17	70	17	684	286	1	382	6	58	11	2 328	87	6 111
genAH1/Victoria/4897/2022		60																			26					86
genAH1NOClade																			1							1
genAH1SubgroupNotListed								404																		404
genAH3/Croatia/10136RV/2023	2	33		1	8			6	3			19				1	6	6	1	4	109			25		224
genAH3/Lisboa/216/2023					4		2	9	4	2							6	4		4				8	1	44
genAH3/Netherlands/10685/2024			1		2			50	4	1		1		2	18		1	3	2	14		1		136		236
genAH3/Norway/8765/2025	110	12	44	31	389	7	61	1 837	536	11	5	585	35	30	138	6	749	414	5	289		109	21	3 038	98	8 560
genAH3/Singapore/GP20238/2024		26		10	32		1	34	13			12	1				47	7		2	46		12	145	17	405
genAH3/Thailand/8/2022		5																			17					22
genAH3/Victoria/211/2025																									1	1
genAH3NOClade	3					1								1								8				13
genAH3SubgroupNotListed						38																				38
genBVicB/Austria/1359417/2021					1													8								9
genBVicB/Catalonia/2279261NS/2023		1			2			7					1	1			3	22						16	1	54
genBVicB/ENG/120/2025					28		5	12				3					4	13		2				8	11	86
genBVicB/Greece/5509/2024					1			4									2	2							9	18
genBVicB/Kanagawa/AC2414/2025					1		1	4	1			2					1	2						5		17
genBVicB/Stockholm/3/2022		3										1												1		5
genBVicB/Switzerland/329/2024		1			27			16	1			1	2				9	22		1				14	31	125
genBVicNOClade	1																									1
genBVicSubgroupNotListed					1		1					1														3
Total	176	178	57	61	854	94	168	3 587	789	17	11	697	69	51	226	24	1 515	789	10	698	204	176	44	5 730	257	16 482

To report a virus as belonging to a specific genetic group, the phylogenetic and amino-acid sequence analyses should meet the following criteria: i) In phylogenetic analysis of the HA gene, it should cluster within the clade represented by the indicated vaccine/reference virus; ii) It should neither contain many nor critical (i.e. those that significantly affect antigenicity) amino-acid substitutions when compared with viruses recognised as belonging to the specific group with which it associates. Viruses with sequences that fall well outside all recognised groups are entered in the 'not attributed to clade' category – this is also to be done for viruses not falling within a designated group and with evidence of antigenic drift.

Table 3A. Antigenic (A) and genetic (B) characterisation data as reported to TESSy, by week of sampling, EU/EEA, week 40 2025 to week 33 2026

A. Antigenic

Categories															
Week	agAH1/Lisboa/188/2023	agAH1/Missouri/11/2025	agAH1/Sydney/5/2021	agAH1/Victoria/4897/2022	agAH1/Wisconsin/67/2022	agAH1NOCAT	agAH3/Croatia/10136RV/2023	agAH3/Netherlands/10685/2024	agAH3/Norway/8765/2025	agAH3/Singapore/GP20238/2024	agAH3/Thailand/8/2022	agAH3NOCAT	agBVicB/Austria/1359417/2021		Total
2025-40		2		11			2			4		3			22
2025-41		10		28						2		1			41
2025-42		12		14	1		3					2			32
2025-43		10		15			5		1	2					33
2025-44		5		12			4		3	3					27
2025-45		4	1	9			2		1	3		1	1		22
2025-46		6		6			4			5		9	3		33
2025-47		10		4			14		1	9	1	4	1		44
2025-48		25	1	8			22	1		12			1		70
2025-49		20		14			43	1	6	23		3	1		111
2025-50		36		29			45		10	33	1	5	1		160
2025-51	3	38		24			29	2	9	39		23			167
2025-52		48		10		1	15		6	62	2	7	1		152
2026-01		16	1	11			18	1	8	33		2			90
2026-02	1	30	3	18			31		6	33	3	5			130
2026-03		21	5	31			33	1	13	20	7	7	1		139
2026-04		17	7	28			49		13	31	4	1			150
2026-05		32	5	28		1	36		3	44	1	3	1		154
2026-06		12	2	37			33		14	15	3	3			119
2026-07		5		12			34		5	7	4	2			69
2026-08		7	1	17			28	4	8	6	3	1	2		77
2026-09		1	3	22			14	1	1	4	6		1		53

Categories															
Week	agAH1/Lisboa/188/2023	agAH1/Missouri/11/2025	agAH1/Sydney/5/2021	agAH1/Victoria/4897/2022	agAH1/Wisconsin/67/2022	agAH1NOCAT	agAH3/Croatia/10136RV/2023	agAH3/Netherlands/10685/2024	agAH3/Norway/8765/2025	agAH3/Singapore/GP20238/2024	agAH3/Thailand/8/2022	agAH3NOCAT	agBVicB/Austria/1359417/2021		Total
2026-10		1	3	13			15		5	1	1		1		40
2026-11		1		10			6		4	2	1				24
2026-12				10			3		1						14
2026-13				2			2		1	1			1		7
2026-14				1					1				1		3
2026-15		1							1				2		4
2026-18				2			1						1		4
2026-19			1										1		2
2026-22				1											1
2026-30							1								1
2026-32				1											1
Total	4	370	33	428	1	2	492	11	121	394	37	82	21		1 996

B - Antigenic

	Categories																						
Week	genAH1/Hungary/286/2024	genAH1/Missouri/11/2025	genAH1/Victoria/4897/2022	genAH1NOClade	genAH1SubgroupNotListed	genAH3/Croatia/10136RV/2023	genAH3/Lisboa/216/2023	genAH3/Netherlands/10685/2024	genAH3/Norway/8765/2025	genAH3/Singapore/GP20238/2024	genAH3/Thailand/8/2022	genAH3/Victoria/211/2025	genAH3NOClade	genAH3SubgroupNotListed	genBVicB/Austria/1359417/2021	genBVicB/Catalonia/2279261NS/2023	genBVicB/ENG/120/2025	genBVicB/Greece/5509/2024	genBVicB/Kanagawa/AC2414/2025	genBVicB/Stockholm/3/2022	genBVicB/Switzerland/329/2024	genBVicNOClade	genBVicSubgroupNotListed	Total
2025-40	4	115	2		6	7	4	1	38							1								178
2025-41	3	149	3		13	1		2	42	3						1								217
2025-42	1	158	1		12	4	5	6	49	1											1			238
2025-43		153	4		5	2	2	10	88	4						1	1			1				271
2025-44		176	6		8	3	1	6	109	1						1								311
2025-45	1	198			5	8	3	9	168	5						1	1				2			401
2025-46	3	220	1		6	2	1	11	216	5	1										3			469
2025-47	1	259	4		3	15	2	11	309	12	1						1				1			619
2025-48	1	380	2		15	25	7	24	541	31			1			1		1		1				1 030
2025-49		471	8		18	31	4	25	754	44	2			1			1			1	1			1 361
2025-50		460	8		32	27	2	16	718	43	2		2	3		1	2				1			1 317
2025-51		388	9		29	33		25	844	29	7		1	4							4			1 373
2025-52		342	5		40	14	2	13	638	16	1					2			1					1 074
2026-01	1	335	11	1	31	12	1	16	557	36	2		1	2			4				2			1 012
2026-02	2	304	10		24	10	1	10	566	15	2		1	2			1	1	1		3			953
2026-03	1	315	7		20	8	4	8	498	16	1	1	2	9		1	1	1			1			894
2026-04	1	278	2		17	11		7	452	34	2		2	1	1	4	3				6			821
2026-05		250	2		44	7	1	9	486	20	1					4	2		1		9			836
2026-06		225	1		22	1		8	386	21			2	5		3	5	1	3		4			687
2026-07		145			20		4	5	274	15			1	6		3	4				5			482
2026-08		143			18	1		11	237	12				3		1	5	1	1		6			439
2026-09		121			4	1		1	147	13					2	7	4	1			10	1		312
2026-10		112			5				127	11					3	3	4	1			5			271
2026-11		78			2	1		1	78	8				2	1		3	3	1		1		1	180
2026-12		49							48	2							3	1	2		3		1	109
2026-13		60			2			1	43	2						1	4	1	1		2			117

	Categories																						
Week	genAH1/Hungary/286/2024	genAH1/Missouri/11/2025	genAH1/Victoria/4897/2022	genAH1NOClade	genAH1SubgroupNotListed	genAH3/Croatia/10136RV/2023	genAH3/Lisboa/216/2023	genAH3/Netherlands/10685/2024	genAH3/Norway/8765/2025	genAH3/Singapore/GP20238/2024	genAH3/Thailand/8/2022	genAH3/Victoria/211/2025	genAH3NOClade	genAH3SubgroupNotListed	genBVicB/Austria/1359417/2021	genBVicB/Catalonia/2279261NS/2023	genBVicB/ENG/120/2025	genBVicB/Greece/5509/2024	genBVicB/Kanagawa/AC2414/2025	genBVicB/Stockholm/3/2022	genBVicB/Switzerland/329/2024	genBVicNOClade	genBVicSubgroupNotListed	Total
2026-14		44			1				31	1					1		4	1	2		3			88
2026-15		37							20	4						3	6	3	1		7			81
2026-16		26							8	1						1	5	1	1		5			48
2026-17		32							9							1	2	1			9		1	55
2026-18		21							8							5	8			1	9			52
2026-19		14							4							2	4				7			31
2026-20		13			2				2							3	2				3			25
2026-21		7							3							1	1				5			17
2026-22		5							2								1		1	1	5			15
2026-23		6							4												2			12
2026-24		6							7						1		1							15
2026-25		4							10							1	2							17
2026-26		4							7							1	1							13
2026-27		2																						2
2026-28		1							7															8
2026-29		1							7										1					9
2026-30		2							9															11
2026-31		1							7															8
2026-32		1							2															3
Total	19	6 111	86	1	404	224	44	236	8 560	405	22	1	13	38	9	54	86	18	17	5	125	1	3	16 482

Table 4A. Antigenic and genetic characterisation data where both types of data were available in TESSy by categories of reporting, EU/EEA, week 40 2025 to week 33 2026

	AntigenicGroup													
GeneticClade		agAH1/Missouri/11/2025	agAH1/Sydney/5/2021	agAH1/Victoria/4897/2022	agAH1/Wisconsin/67/2022	agAH1NOCAT	agAH3/Croatia/10136RV/2023	agAH3/Netherlands/10685/2024	agAH3/Norway/8765/2025	agAH3/Singapore/GP20238/2024	agAH3/Thailand/8/2022	agAH3NOCAT	agBVicB/Austria/1359417/2021		Total
genAH1/Hungary/286/2024		1	0	1	0	0	0	0	0	0	0	0	0		2
genAH1/Missouri/11/2025		241	26	279	1	0	0	0	0	0	0	0	0		547
genAH1SubgroupNotListed		124	0	26	0	2	0	0	0	0	0	0	0		152
genAH3/Croatia/10136RV/2023		0	0	0	0	0	9	0	0	6	1	0	0		16
genAH3/Lisboa/216/2023		0	0	0	0	0	6	0	0	0	0	0	0		6
genAH3/Netherlands/10685/2024		0	0	0	0	0	2	11	0	1	1	2	0		17
genAH3/Norway/8765/2025		0	0	0	0	0	255	0	117	371	5	38	0		786
genAH3/Singapore/GP20238/2024		0	0	0	0	0	5	0	0	15	0	4	0		24
genAH3/Thailand/8/2022		0	0	0	0	0	0	0	0	1	0	0	0		1
genBVicB/Catalonia/2279261NS/2023		0	0	0	0	0	0	0	0	0	0	0	3		3
genBVicB/ENG/120/2025		0	0	0	0	0	0	0	0	0	0	0	5		5
genBVicB/Greece/5509/2024		0	0	0	0	0	0	0	0	0	0	0	1		1
genBVicB/Kanagawa/AC2414/2025		0	0	0	0	0	0	0	0	0	0	0	1		1
genBVicB/Switzerland/329/2024		0	0	0	0	0	0	0	0	0	0	0	9		9
Total		366	26	306	1	2	277	11	117	394	7	44	19		1 570

Categories listed vertically are antigenic reporting categories; categories listed horizontally indicate genetic clade reporting categories.

Annex 2. Antiviral susceptibility testing

Table 5A. List of viruses reported with reduced inhibition or susceptibility[a] by antiviral, subtypes and lineages, phenotypic or genotypic testing as well as available corresponding GISAID sequence number (ID) and interpretation defining mutation, TESSy, EU/EEA, week 40 2025 to week 33 2026

Antiviral	Country	Subtype	Virus	Clade	Treated	Setting	Age	Assessment	Interpretation	GISAID	Substitution
Oseltamivir	BE	A(H1)pdm09	A/Belgium/H0023/2026	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AARI	EPI5432074	NA_I223V_S247N
		A(H1)pdm09	A/Belgium/S0794/2026	5a.2a.1(D)	-	Hospital	>=65y	Genotypic	AARI	EPI5060754	NA_I223V_S247N
		A(H1)pdm09	A/Belgium/S10060/2025	5a.2a.1(D)	-	Hospital	>=65y	Genotypic	AARI	EPI4975782	NA_I223V_S247N
		A(H1)pdm09	A/Belgium/S1731/2026	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AARI	EPI5191745	NA_I223V_S247N
	DE	A(H1)pdm09	A/Thueringen/26/2026	5a.2a.1(D.3.1)	-	Community	[15y,65y)	Phenotypic	RI		NA_I223T
	DK	A(H1)pdm09	A/Denmark/1122/2026	5a.2a.1(D.3.1)	-	-	-	Genotypic	AARI	EPI5276146	NA_I223V_S247N
		A(H1)pdm09	A/Denmark/3779/2025	5a.2a.1(D.3.1)	-	-	-	Genotypic	AARI	EPI4932088	NA_I223V_S247N
		A(H1)pdm09	A/Denmark/3902/2025	5a.2a.1(D.3.1)	-	-	-	Genotypic	AARI	EPI4932234	NA_I223V_S247N
	EE	A(H1)pdm09	A/Estonia/739/2026	5a.2a.1(D.3.1)	-	Hospital	[5y,15y)	Genotypic	AARI	EPI5498996	NA_I223V_S247N
		A(H1)pdm09	A/Estonia/755/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5499059	NA_I223V_S247N
	ES	A(H1)pdm09	A/Canarias/261035/2025	5a.2a.1(D.3.1)	-	Community	[15y,65y)	Genotypic	AAHRI	EPI5420408	NA_H275Y
		A(H1)pdm09	A/Catalonia/NSVH102747116/2025	5a.2a.1(D.3.1)	Yes	Hospital	>=65y	Genotypic	AAHRI	EPI4899277	NA_H275Y
		A(H1)pdm09	A/Madrid/654/2026	5a.2a.1(D.3.1)	Yes	Hospital	[15y,65y)	Genotypic	AAHRI	EPI5420166	NA_H275Y
		A(H1)pdm09	A/Madrid/HRYC-13891646/2025	5a.2a.1(D.3.1)	-	-	-	Genotypic	AAHRI	EPI5287952	NA_H275Y
		A(H1)pdm09	A/Madrid/HRYC-13897573/2025	5a.2a.1(D.3.1)	Yes	Hospital	[15y,65y)	Genotypic	AAHRI	EPI4923688	NA_H275Y
		A(H1)pdm09	A/VALLADOLID/277/2025	5a.2a.1(D.3.1)	-	Community	>=65y	Genotypic	AAHRI	EPI5098293	NA_H275Y
		A(H1)pdm09	A/Andalucia/PMC-01661/2025	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AARI	EPI5424069	NA_I223V_S247N
		A(H1)pdm09	A/Badajoz/18733937/2025	5a.2a.1(D.3.1)	-	-	-	Genotypic	AARI	EPI4894289	NA_I223V_S247N
		A(H1)pdm09	A/Badajoz/18779328/2025	5a.2a.1(D.3.1)	-	-	-	Genotypic	AARI	EPI4894347	NA_I223V_S247N
		A(H1)pdm09	A/Badajoz/18793325/2025	5a.2a.1(D.3.1)	-	-	-	Genotypic	AARI	EPI4894409	NA_I223V_S247N
		A(H1)pdm09	A/Badajoz/18793364/2025	5a.2a.1(D.3.1)	-	Hospital	[15y,65y)	Genotypic	AARI	EPI5022928	NA_I223V_S247N
		A(H1)pdm09	A/Badajoz/18793370/2025	5a.2a.1(D.3.1)	-	-	-	Genotypic	AARI	EPI5000188	NA_I223V_S247N
		A(H1)pdm09	A/Badajoz/18793614/2025	5a.2a.1(D.3.1)	-	-	-	Genotypic	AARI	EPI5022804	NA_I223V_S247N
		A(H1)pdm09	A/Badajoz/18793791/2025	5a.2a.1(D.3.1)	-	-	-	Genotypic	AARI	EPI4976579	NA_I223V_S247N
		A(H1)pdm09	A/Badajoz/18801946/2025	5a.2a.1(D.3.1)	-	Hospital	-	Genotypic	AARI	EPI5000254	NA_I223V_S247N
		A(H1)pdm09	A/Badajoz/18804808/2025	5a.2a.1(D.3.1)	-	Hospital	-	Genotypic	AARI	EPI4976486	NA_I223V_S247N
		A(H1)pdm09	A/Badajoz/18808836/2026	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AARI	EPI5133015	NA_S247R
		A(H1)pdm09	A/Canarias/2341/2025	5a.2a.1(D.3.1)	No	Community	[15y,65y)	Genotypic	AARI	EPI4855246	NA_I223V_S247N

Antiviral	Country	Subtype	Virus	Clade	Treated	Setting	Age	Assessment	Interpretation	GISAID	Substitution
		A(H1)pdm09	A/Canarias/2343/2025	5a.2a.1(D.3.1)	Yes	Hospital	[15y,65y)	Genotypic	AARI	EPI4855263	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/260324/2025	5a.2a.1(D.3.1)	No	Community	>=65y	Genotypic	AARI	EPI5446807	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/260335/2025	5a.2a.1(D.3.1)	No	Community	[15y,65y)	Genotypic	AARI	EPI5446844	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/260341/2025	5a.2a.1(D.3.1)	No	Community	<5y	Genotypic	AARI	EPI5446868	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/260352/2025	5a.2a.1(D.3.1)	Yes	Community	<5y	Genotypic	AARI	EPI5446908	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/260353/2025	5a.2a.1(D.3.1)	Yes	Hospital	>=65y	Genotypic	AARI	EPI5446916	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/260360/2025	5a.2a.1(D.3.1)	Yes	Hospital	[15y,65y)	Genotypic	AARI	EPI5446956	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/260365/2025	5a.2a.1(D.3.1)	No	Community	[15y,65y)	Genotypic	AARI	EPI5446972	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/260382/2025	5a.2a.1(D.3.1)	Yes	Hospital	[15y,65y)	Genotypic	AARI	EPI5447028	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/315/2026	5a.2a.1(D.3.1)	Yes	Hospital	>=65y	Genotypic	AARI	EPI5447108	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/322/2026	5a.2a.1(D.3.1)	Yes	Hospital	>=65y	Genotypic	AARI	EPI5447124	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/333/2026	5a.2a.1(D.3.1)	Yes	Hospital	>=65y	Genotypic	AARI	EPI5447153	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/348/2026	5a.2a.1(D.3.1)	Yes	Hospital	>=65y	Genotypic	AARI	EPI5447169	NA_I223V_S247N
		A(H1)pdm09	A/Canarias/349/2026	5a.2a.1(D.3.1)	Yes	Hospital	[15y,65y)	Genotypic	AARI	EPI5447177	NA_I223V_S247N
		A(H1)pdm09	A/CastillaLaMancha/FLUCEN25-26_91/2025	5a.2a.1(D.3.1)	-	Community	>=65y	Genotypic	AARI	EPI5413273	NA_I223V_S247N
		A(H1)pdm09	A/CastillaLaMancha/FLUCEN25-26_92/2025	5a.2a.1(D.3.1)	-	Community	[15y,65y)	Genotypic	AARI	EPI5413281	NA_I223V_S247N
		A(H1)pdm09	A/Catalonia/NSVH160154446/2025	5a.2a.1(D.3.1)	-	-	-	Genotypic	AARI	EPI4832982	NA_I223V_S247N
		A(H1)pdm09	A/Galicia/CHUVI/22939382/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5078908	NA_I223V_S247N
		A(H1)pdm09	A/Galicia/GA-CHUAC-535/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI4786706	NA_I223V_S247N
		A(H1)pdm09	A/Galicia/GA-CHUAC-643/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI4967214	NA_I223V_S247N
		A(H1)pdm09	A/Galicia/LUGO/80554535/2026	5a.2a.1(D.3.1)	-	-	[5y,15y)	Genotypic	AARI	EPI5384863	NA_I223V_S247N
		A(H1)pdm09	A/Galicia/SCQ/120829/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5476213	NA_I223V_S247N
		A(H1)pdm09	A/Murcia/260079/2025	5a.2a.1(D.3.1)	-	Hospital	<5y	Genotypic	AARI	EPI5239340	NA_I223V_S247N
		A(H1)pdm09	A/Navarra/601/2026	5a.2a.1(D.3.1)	Yes	Hospital	>=65y	Genotypic	AARI	EPI5420138	NA_I223V_S247N
		A(H1)pdm09	A/PaisVasco/67969169/2025	5a.2a.1(D.3.1)	-	Community	[5y,15y)	Genotypic	AARI	EPI4867619	NA_I223V_S247N
		A(H1)pdm09	A/Spain/VC-GRAL-004714/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5374683	NA_I223V_S247N
	FI	A(H1)pdm09	A/Finland/19/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5545804	NA_I223V_S247N
		A(H1)pdm09	A/Finland/20/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5545813	NA_I223V_S247N
		A(H1)pdm09	A/Finland/25/2026	5a.2a.1(D.3.1)	-	-	<5y	Genotypic	AARI	EPI5545837	NA_I223V_S247N
		A(H1)pdm09	A/Finland/26/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5545840	NA_I223V_S247N
		A(H1)pdm09	A/Finland/28/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5545846	NA_I223V_S247N
		A(H1)pdm09	A/Finland/34/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5545864	NA_I223V_S247N
		A(H1)pdm09	A/Finland/38/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5545876	NA_I223V_S247N

Antiviral	Country	Subtype	Virus	Clade	Treated	Setting	Age	Assessment	Interpretation	GISAID	Substitution
		A(H1)pdm09	A/Finland/46/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5545900	NA_I223V_S247N
		A(H1)pdm09	A/Finland/48/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5545906	NA_I223V_S247N
		A(H1)pdm09	A/Finland/53/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5545921	NA_I223V_S247N
		A(H1)pdm09	A/Finland/64/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5545974	NA_I223V_S247N
		A(H1)pdm09	A/Finland/68/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5546006	NA_I223V_S247N
		A(H1)pdm09	A/Finland/71/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5546030	NA_I223V_S247N
		A(H1)pdm09	A/Finland/72/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5546038	NA_I223V_S247N
		A(H1)pdm09	A/Finland/74/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5546054	NA_I223V_S247N
		A(H1)pdm09	A/Finland/75/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5546062	NA_I223V_S247N
		A(H1)pdm09	A/Finland/84/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5546087	NA_I223V_S247N
		A(H1)pdm09	A/Finland/85/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5546090	NA_I223V_S247N
		A(H1)pdm09	A/Finland/873/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI4885535	NA_I223V_S247N
		A(H1)pdm09	A/Finland/876/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI4885544	NA_I223V_S247N
		A(H1)pdm09	A/Finland/881/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI4885555	NA_I223V_S247N
		A(H1)pdm09	A/Finland/882/2025	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI4885558	NA_I223V_S247N
		A(H1)pdm09	A/Finland/898/2025	5a.2a.1(D.3.1)	-	-	[5y,15y)	Genotypic	AARI	EPI5091381	NA_I223V_S247N
		A(H1)pdm09	A/Finland/899/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5091384	NA_I223V_S247N
		A(H1)pdm09	A/Finland/900/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5091387	NA_I223V_S247N
		A(H1)pdm09	A/Finland/903/2025	5a.2a.1(D.3.1)	-	-	<5y	Genotypic	AARI	EPI5091395	NA_I223V_S247N
		A(H1)pdm09	A/Finland/904/2025	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5091397	NA_I223V_S247N
		A(H1)pdm09	A/Finland/908/2025	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5091406	NA_I223V_S247N
		A(H1)pdm09	A/Finland/909/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5098230	NA_I223V_S247N
		A(H1)pdm09	A/Finland/914/2025	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5091421	NA_I223V_S247N
		A(H1)pdm09	A/Finland/926/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5091457	NA_I223V_S247N
		A(H1)pdm09	A/Finland/927/2025	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5091460	NA_I223V_S247N
		A(H1)pdm09	A/Finland/931/2025	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5091472	NA_I223V_S247N
		A(H1)pdm09	A/Finland/932/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5091475	NA_I223V_S247N
		A(H1)pdm09	A/Finland/933/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5091478	NA_I223V_S247N
		A(H1)pdm09	A/Finland/936/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5091487	NA_I223V_S247N
		A(H1)pdm09	A/Finland/937/2025	5a.2a.1(D.3.1)	-	-	<5y	Genotypic	AARI	EPI5091490	NA_I223V_S247N
		A(H1)pdm09	A/Finland/942/2025	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5091504	NA_I223V_S247N
	FR	A(H1)pdm09	A/France/ARA-HCL025201425501/2025	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AAHRI	EPI5314509	NA_H275Y
		A(H1)pdm09	A/France/ARA-HCL026016581001/2026	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AAHRI	EPI5353306	NA_H275Y

Antiviral	Country	Subtype	Virus	Clade	Treated	Setting	Age	Assessment	Interpretation	GISAID	Substitution
		A(H1)pdm09	A/France/ARA-HCL026020227501/2026	5a.2a.1(D.3.1)	Yes	Hospital	>=65y	Genotypic	AAHRI	EPI5375732	NA_H275Y
		A(H1)pdm09	A/France/BFC-RELAB-HCL025170198201/2025	5a.2a.1(D.3.1)	-	Community	>=65y	Genotypic	AAHRI	EPI4777165	NA_N295S
		A(H1)pdm09	A/France/ARA-HCL026013304501/2025	5a.2a.1(D.3.1)	-	Hospital	[15y,65y)	Genotypic	AARI	EPI5157930	NA_I223V_S247N
		A(H1)pdm09	A/France/ARA-HCL026030700602/2025	5a.2a.1(D.3.1)	-	Hospital	[15y,65y)	Genotypic	AARI	EPI5199414	NA_I223V_S247N
		A(H1)pdm09	A/France/ARA-RELAB-HCL025193801001/2025	5a.2a.1(D.3.1)	-	Community	>=65y	Genotypic	AARI	EPI4901080	NA_I223V_S247N
		A(H1)pdm09	A/France/HDF-IPP08205/2025	other	-	Community	>=65y	Genotypic	AARI	EPI5038097	NA_I223V_S247N
		A(H1)pdm09	A/France/HDF-IPPG1273/2025	other	-	Hospital	>=65y	Genotypic	AARI	EPI5185037	NA_I223V_S247N
		A(H1)pdm09	A/France/HDF-RELAB-IPP00307/2026	other	-	Community	<5y	Genotypic	AARI	EPI5038641	NA_I223V_S247N
		A(H1)pdm09	A/France/IDF-RELAB-IPPG0224/2025	other	-	Community	[15y,65y)	Genotypic	AARI	EPI5082887	NA_I223T
		A(H1)pdm09	A/France/PAC-RELAB-HCL025206162501/2025	5a.2a.1(D.3.1)	-	Community	[15y,65y)	Genotypic	AARI	EPI5017846	NA_I223V_S247N
		A(H1)pdm09	A/France/BRE-IPP01724/2026	other	-	Hospital	[15y,65y)	Phenotypic	HRI	EPI5249496	NA_H275Y
		A(H1)pdm09	A/France/GES-IPP00352/2026	other	-	Hospital	[15y,65y)	Phenotypic	HRI	EPI5071268	NA_H275Y
		A(H1)pdm09	A/France/PDL-IPP01611/2026	other	-	Hospital	>=65y	Phenotypic	HRI	EPI5249256	NA_H275Y
	IT	A(H1)pdm09	A/Parma/153/2025	5a.2a.1(D.3.1)	No	Community	[15y,65y)	Phenotypic	RI	EPI5508240	NA_G147R_S247N
	LT	A(H1)pdm09	A/Lithuania/MB260127_0065/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AAHRI		NA_H275Y
		A(H1)pdm09	A/Lithuania/MB260126_0279/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI		NA_I223V_S247N
	LU	A(H1)pdm09	A/Luxembourg/LNS7818945/2026	5a.2a.1(D.3.1)	-	Community	<5y	Genotypic	AARI	EPI5264004	NA_I223V_S247N
	NL	A(H1)pdm09	A/Netherlands/00716/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AAHRI	EPI5221291	NA_H275Y
		A(H1)pdm09	A/Netherlands/02557/2025	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AAHRI	EPI4994652	NA_H275Y
		A(H1)pdm09	A/Netherlands/00055/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5035386	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00062/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5035394	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00210/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5106967	NA_I223M
		A(H1)pdm09	A/Netherlands/00303/2026	5a.2a.1(D.3.1)	-	-	[5y,15y)	Genotypic	AARI	EPI5107036	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00350/2026	5a.2a.1(D.3.1)	-	-	[5y,15y)	Genotypic	AARI	EPI5144752	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00408/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5144859	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00460/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5161250	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00495/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5161267	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00581/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5199669	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00596/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5200190	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00700/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5221277	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00708/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5212618	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00722/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5235477	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00735/2026	5a.2a.1(D.3.1)	-	-	[5y,15y)	Genotypic	AARI	EPI5235609	NA_I223V_S247N

Antiviral	Country	Subtype	Virus	Clade	Treated	Setting	Age	Assessment	Interpretation	GISAID	Substitution
		A(H1)pdm09	A/Netherlands/00779/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5235547	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00815/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5249703	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00828/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5249961	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00879/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5250117	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00880/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5249803	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00900/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5279152	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00909/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5279169	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00925/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5279332	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00930/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5279363	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/00940/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5279387	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/01002/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5313604	NA_I223T
		A(H1)pdm09	A/Netherlands/01007/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5313616	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/01023/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5369411	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/01122/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5486821	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/02347/2025	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI4859322	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/02468/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI4909749	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/02561/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI4937189	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/02562/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI4937193	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/02568/2025	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI4937200	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/02621/2025	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI4994673	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/02638/2025	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI4994679	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/10054/2026		-	-	>=65y	Genotypic	AARI	EPI5046175	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/10212/2026	5a.2a.1(D.3.1)	-	-	>=65y	Genotypic	AARI	EPI5149772	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/10238/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5191924	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/10076/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Phenotypic	RI	EPI5082066	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/10089/2026	5a.2a.1(D.3.1)	-	-	-	Phenotypic	RI	EPI5046283	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/10206/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Phenotypic	RI	EPI5149725	NA_I223V_S247N
		A(H1)pdm09	A/Netherlands/10240/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Phenotypic	RI	EPI5178188	NA_I223V_S247N
	NO	A(H1)pdm09	A/Norway/04915/2026	5a.2a.1(D.3.1)	-	Community	[15y,65y)	Genotypic	AAHRI	EPI5579069	NA_H275Y
		A(H1)pdm09	A/Norway/005210/2026	5a.2a.1(D.3.1)	-	Community	>=65y	Genotypic	AARI	EPI5285722	NA_I223V_S247N
		A(H1)pdm09	A/Norway/04196/2026	5a.2a.1(D.3.1)	-	Community	>=65y	Genotypic	AARI	EPI5428189	NA_I223V_S247N
		A(H1)pdm09	A/Norway/04197/2026	5a.2a.1(D.3.1)	-	Community	>=65y	Genotypic	AARI	EPI5428197	NA_I223V_S247N
	PT	A(H1)pdm09	A/Lisboa/129/2026	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AAHRI		NA_H275Y

Antiviral	Country	Subtype	Virus	Clade	Treated	Setting	Age	Assessment	Interpretation	GISAID	Substitution
		A(H1)pdm09	A/Lisboa/1126/2025	5a.2a.1(D.3.1)	-	Hospital	-	Genotypic	AARI		NA_I223V_S247N
		A(H1)pdm09	A/Lisboa/120/2026	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AARI		NA_I223V_S247N
		A(H1)pdm09	A/Lisboa/121/2026	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AARI		NA_I223V_S247N
		A(H1)pdm09	A/Lisboa/61/2026	5a.2a.1(D.3.1)	-	Community	>=65y	Genotypic	AARI		NA_I223V_S247N
		A(H1)pdm09	A/Lisboa/789/2025	5a.2a.1(D.3.1)	-	Community	>=65y	Genotypic	AARI		NA_I223V_S247N
		A(H1)pdm09	A/Lisboa/802/2025	5a.2a.1(D.3.1)	-	Hospital	[5y,15y)	Genotypic	AARI		NA_I223V_S247N
		A(H1)pdm09	A/Lisboa/983/2025	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AARI		NA_I223V_S247N
		A(H1)pdm09	A/Lisboa/1002/2025	5a.2a.1(D.3.1)	-	Hospital	>=65y	Phenotypic	RI		NA_I223V_S247N
		A(H1)pdm09	A/Lisboa/967/2025	5a.2a.1(D.3.1)	-	Hospital	>=65y	Phenotypic	RI		NA_I223V_S247N
		A(H1)pdm09	A/Lisboa/980/2025	5a.2a.1(D.3.1)	-	Hospital	>=65y	Phenotypic	RI		NA_I223V_S247N
		A(H1)pdm09	A/Lisboa/988/2025	5a.2a.1(D.3.1)	-	Community	[15y,65y)	Phenotypic	RI		NA_I223V_S247N
	SE	A(H1)pdm09	A/Linkoping/SE26-03498/2026	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AARI	EPI_5336167	NA_I223V_S247N
	SE	A(H1)pdm09	A/Solna/SE26-03724/2026	5a.2a.1(D.3.1)	-	Hospital	[15y,65y)	Genotypic	AARI	EPI_5337205	NA_I223V_S247N
	SE	A(H1)pdm09	A/Stockholm/SE26-51670/2026	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AARI	EPI_5384989	NA_I223V_S247N
	SK	A(H1)pdm09	A/Slovakia/uvzsr-2411/2026	5a.2a.1(D.3.1)	-	-	[15y,65y)	Genotypic	AARI	EPI5186337	NA_I223V_S247N
	AT	A(H3)	A/Austria/1873228/2026	2a.3a.1(K)	-	-	>=65y	Genotypic	AAHRI	EPI_ISL_5211783	NA_del245_248; NA_del247_250
	DE	A(H3)	A/Saarland/16/2025	2a.3a.1(K)	-	Community	[15y,65y)	Genotypic	AAHRI		NA_del247_250
	DE	A(H3)	A/Nordrhein-Westfalen/6/2026	2a.3a.1(K)	-	Community	[15y,65y)	Genotypic	AARI		NA_S331R
	ES	A(H3)	A/Catalonia/NSVH102758815/2025	2a.3a.1(K)	-	-	-	Genotypic	AAHRI	EPI4966101	NA_E119V
	ES	A(H3)	A/Madrid/179583/2025	2a.3a.1(K)	-	Community	[15y,65y)	Genotypic	AARI	EPI5405775	NA_S331R
	ES	A(H3)	A/Melilla/01819204/2026	2a.3a.1(K)	-	-	<5y	Genotypic	AARI	EPI5363973	NA_N329R
	ES	A(H3)	A/Spain/VC-GRAL-004122/2025	2a.3a.1(K)	-	-	<5y	Genotypic	AARI	EPI5218820	NA_S331R
	ES	A(H3)	A/Spain/VC-GRAL-004134/2025	2a.3a.1(K)	-	-	[15y,65y)	Genotypic	AARI	EPI5218916	NA_S331R
	ES	A(H3)	A/Spain/VC-GRAL-004448/2025	2a.3a.1(K)	-	-	-	Genotypic	AARI	EPI5264908	NA_S331R
	ES	A(H3)	A/Spain/VC-GRAL-004460/2025	2a.3a.1(K)	-	-	>=65y	Genotypic	AARI	EPI5265002	NA_S331R
	ES	A(H3)	A/Spain/VC-GRAL-004500/2025	2a.3a.1(K)	-	-	[5y,15y)	Genotypic	AARI	EPI5265265	NA_S331R
	ES	A(H3)	A/Spain/VC-GRAL-004727/2025	2a.3a.1(K)	-	-	>=65y	Genotypic	AARI	EPI5374719	NA_S331R
	ES	A(H3)	A/Spain/VC-GRAL-004933/2026	2a.3a.1(K)	-	-	[15y,65y)	Genotypic	AARI	EPI5451640	NA_S331R
	FI	A(H3)	A/Finland/63/2026	2a.3a.1(K)	-	-	[15y,65y)	Genotypic	AARI	EPI5545966	NA_S331R
	FR	A(H3)	A/France/NAQ-HCL026012738301/2026	2a.3a.1(K)	-	Hospital	>=65y	Genotypic	AARI	EPI5157862	NA_K249E
	FR	A(H3)	A/France/HDF-IPP01699/2026	2a.3a.1(K)	-	Hospital	>=65y	Phenotypic	RI	EPI5236253	NA_E119V
	NL	A(H3)	A/Netherlands/00653/2026	2a.3a.1(K)	-	-	[5y,15y)	Genotypic	AARI	EPI5221243	NA_K249E
	NL	A(H3)	A/Netherlands/00963/2026	2a.3a.1(K)	-	-	[15y,65y)	Genotypic	AARI	EPI5303780	NA_K249E

Antiviral	Country	Subtype	Virus	Clade	Treated	Setting	Age	Assessment	Interpretation	GISAID	Substitution
	SE	A(H3)	A/Goteborg/SE26-03100/2026	2a.3a.1(K)	-	Hospital	>=65y	Genotypic	AARI	EPI_5336087	NA_S331R
		A(H3)	A/Solna/SE26-02783/2026	2a.3a.1(K)	-	Hospital	>=65y	Genotypic	AARI	EPI_5335948	NA_S331R
		A(H3)	A/Solna/SE26-03494/2026	2a.3a.1(K)	-	Hospital	>=65y	Genotypic	AARI	EPI_5336143	NA_S331R
		A(H3)	A/Stockholm/SE26-51587/2026	2a.3a.1(K)	-	Hospital	-	Genotypic	AARI	EPI_5336243	NA_S331R
	SK	A(H3)	A/Slovakia/uvzsr-2616/2026	2a.3a.1(K)	-	-	>=65y	Genotypic	AARI	EPI5428610	NA_S331R
Zanamivir	DE	A(H1)pdm09	A/Bayern/81/2025	5a.2a.1(D.3.1)	-	Community	[15y,65y)	Phenotypic	RI		
	ES	A(H1)pdm09	A/Badajoz/18808836/2026	5a.2a.1(D.3.1)	-	Hospital	>=65y	Genotypic	AARI	EPI5133015	NA_S247R
	FR	A(H1)pdm09	A/France/ARA-HCL025161699501/2025	5a.2a.1(D.3.1)	No	Hospital	>=65y	Genotypic	AAHRI	EPI4768361	NA_Q136K
	AT	A(H3)	A/Austria/1873228/2026	2a.3a.1(K)	-	-	>=65y	Genotypic	AARI	EPI_ISL_5211783	NA_del245_248; NA_del247_250
	DE	A(H3)	A/Nordrhein-Westfalen/6/2026	2a.3a.1(K)	-	Community	[15y,65y)	Genotypic	AARI		NA_S331R
		A(H3)	A/Saarland/16/2025	2a.3a.1(K)	-	Community	[15y,65y)	Genotypic	AARI		NA_del247_250
	ES	A(H3)	A/Madrid/179583/2025	2a.3a.1(K)	-	Community	[15y,65y)	Genotypic	AARI	EPI5405775	NA_S331R
		A(H3)	A/Spain/VC-GRAL-004122/2025	2a.3a.1(K)	-	-	<5y	Genotypic	AARI	EPI5218820	NA_S331R
		A(H3)	A/Spain/VC-GRAL-004134/2025	2a.3a.1(K)	-	-	[15y,65y)	Genotypic	AARI	EPI5218916	NA_S331R
		A(H3)	A/Spain/VC-GRAL-004448/2025	2a.3a.1(K)	-	-	-	Genotypic	AARI	EPI5264908	NA_S331R
		A(H3)	A/Spain/VC-GRAL-004460/2025	2a.3a.1(K)	-	-	>=65y	Genotypic	AARI	EPI5265002	NA_S331R
		A(H3)	A/Spain/VC-GRAL-004500/2025	2a.3a.1(K)	-	-	[5y,15y)	Genotypic	AARI	EPI5265265	NA_S331R
		A(H3)	A/Spain/VC-GRAL-004727/2025	2a.3a.1(K)	-	-	>=65y	Genotypic	AARI	EPI5374719	NA_S331R
		A(H3)	A/Spain/VC-GRAL-004933/2026	2a.3a.1(K)	-	-	[15y,65y)	Genotypic	AARI	EPI5451640	NA_S331R
	FI	A(H3)	A/Finland/63/2026	2a.3a.1(K)	-	-	[15y,65y)	Genotypic	AARI	EPI5545966	NA_S331R
	PL	A(H3)	A/Gdansk/428/2026		-	-	[5y,15y)	Phenotypic	RI		
	SE	A(H3)	A/Goteborg/SE26-03100/2026	2a.3a.1(K)	-	Hospital	>=65y	Genotypic	AARI	EPI_5336087	NA_S331R
		A(H3)	A/Solna/SE26-02783/2026	2a.3a.1(K)	-	Hospital	>=65y	Genotypic	AARI	EPI_5335948	NA_S331R
		A(H3)	A/Solna/SE26-03494/2026	2a.3a.1(K)	-	Hospital	>=65y	Genotypic	AARI	EPI_5336143	NA_S331R
		A(H3)	A/Stockholm/SE26-51587/2026	2a.3a.1(K)	-	Hospital	-	Genotypic	AARI	EPI_5336243	NA_S331R
	SK	A(H3)	A/Slovakia/uvzsr-2616/2026	2a.3a.1(K)	-	-	>=65y	Genotypic	AARI	EPI5428610	NA_S331R
Baloxavir	FI	A(H1)pdm09	A/Finland/888/2025		-	-	>=65y	Genotypic	AARS	EPI5091509	PA_E23G
	FR	A(H1)pdm09	A/France/PAC-HCL025160915001/2025	5a.2a.1(D.3.1)	No	-	<5y	Genotypic	AARS	EPI4768266	PA_E199G
		A(H1)pdm09	A/France/PAC-RELAB-HCL026009249501/2026	5a.2a.1(D.3.1)	-	Community	[15y,65y)	Genotypic	AARS	EPI5097160	PA_E199K
	LU	A(H1)pdm09	A/Luxembourg/LNS7818945/2026	5a.2a.1(D.3.1)	-	Community	<5y	Genotypic	AARS	EPI5264005	PA_A37T
	DK	A(H3)	A/Denmark/3608/2025	2a.3a.1(K)	-	-	-	Genotypic	AARS	EPI4844702	PA_I38L
	IE	A(H3)	A/Ireland/00000164/2026	2a.3a.1(K)	-	Hospital	[5y,15y)	Genotypic	AARS	EPI5256653	PA_I38L
		A(H3)	A/Ireland/00005495/2026	2a.3a.1(K)	-	Hospital	<5y	Genotypic	AARS	EPI5229075	PA_I38L

Antiviral	Country	Subtype	Virus	Clade	Treated	Setting	Age	Assessment	Interpretation	GISAID	Substitution
		A(H3)	A/Ireland/00025697/2026	2a.3a.1(K)	-	Hospital	>=65y	Genotypic	AARS	EPI5419757	PA_I38L
		A(H3)	A/Ireland/00081280/2025	2a.3a.1(K)	-	Community	[15y,65y)	Genotypic	AARS	EPI4801932	PA_I38L
		A(H3)	A/Ireland/00084706/2025	2a.3a.1(K)	-	Community	[15y,65y)	Genotypic	AARS	EPI4833173	PA_I38L
		A(H3)	A/Ireland/00094515/2025	2a.3a.1(K)	-	Hospital	>=65y	Genotypic	AARS	EPI5161815	PA_I38L

AA: amino acid (refers to genotypic testing result); AAHRI: amino acid mutations associated with highly reduced inhibition; AARI: amino acid mutations associated with reduced inhibition; HRI: highly reduced inhibition; RI: reduced inhibition; RS: reduced susceptibility, as defined in the WHO documentation [12,13].

Annex 3. Phylogenetic analysis

Table 6A. Number of influenza virus haemagglutinin gene sequences retrieved with GISAID EpiFlu database accession number and analysed in this report by subtype/lineage and country (n = 25), EU/EEA, weeks 40 2025 to week 33 2026

	HA sequences				
Country	A(H1N1)pdm09	A(H3N2)	B/Victoria	Total	% of total sequences
Austria	60	115	1	**176**	1.07%
Belgium	96	74	5	**175**	1.06%
Croatia	12	45		**57**	0.35%
Czechia	19	42		**61**	0.37%
Denmark	358	435	61	**854**	5.18%
Estonia	48	46		**94**	0.57%
Finland	97	64	7	**168**	1.02%
France	1607	1936	43	**3586**	21.74%
Germany	227	561	2	**790**	4.79%
Greece	3	14		**17**	0.10%
Hungary	7	5		**13**	0.08%
Ireland	72	617	8	**697**	4.23%
Italy	30	36	3	**69**	0.42%
Lithuania	17	33	1	**51**	0.31%
Luxembourg	70	156		**226**	1.37%
Malta	17	7		**24**	0.15%
Netherlands	687	807	19	**1513**	9.17%
Norway	286	434	69	**789**	4.78%
Poland	18	9		**27**	0.16%
Portugal	382	312	3	**697**	4.23%
Romania	32	172		**204**	1.24%
Slovakia	58	118		**176**	1.07%
Slovenia	11	33		**44**	0.27%
Spain	2334	3350	44	**5728**	34.73%
Sweden	88	117	52	**257**	1.56%
Total	**6636**	**9538**	**318**	**16493**	**100%**

HA: haemagglutinin.

Table 7A. Number and proportion of A(H1N1)pdm09 reported genetic clades and assigned clades based on phylogenetic analysis, EU/EEA, week 40 2025 to week 33 2026

Clade	Reference virus	Reported clade	%	Assigned clade	%
5a.2a.1(D.3.1)	A/Missouri/11/2025_Egg	6105	92.0%	6609	99.6%
5a.2a.1(D)	A/Victoria/4897/2022_Egg	89	1.3%	1	0.0%
5a.2a(C.1.9.3)	A/Hungary/286/2024	19	0.3%	19	0.3%
Undefined		422	6.4%	6	0.0%
none		1	0.0%	-	-
Total	–	**6636**		**6635**	

5a.2a.1(D.3.1) included sub-clades: D.3.1,D.3.1.1
5a.2a.1(D) included sub-clades: D,D.1,D.2,D.3,D.4,D.5

Table 8A. Number and proportion of A(H3N2) reported genetic clades and assigned clades based on phylogenetic analysis, EU/EEA, week 40 2025 to week 33 2026

Clade	Reference virus	Reported clade	%	Assigned clade	%2
2a.3a.1(J)	A/Thailand/8/2022_Egg	23	0.2%	0	0.0%
2a.3a.1(J.2)	A/District_Of_Columbia/27/2023	226	2.4%	83	0.9%
2a.3a.1(J.2.2)	A/Lisboa/216/2023	44	0.5%	47	0.5%
2a.3a.1(J.2.3)	A/Netherlands/10685/2024	235	2.5%	235	2.5%
2a.3a.1(J.2.4)	A/Sydney/1359/2024	405	4.2%	354	3.7%
2a.3a.1(J.2.5)	A/Victoria/211/2025	1	0.0%	0	0.0%
2a.3a.1(K)	A/Norway/8765/2025	8550	89.6%	8808	92.3%
Undefined	–	41	0.4%	11	0.1%
none	–	13	0.1%	0	0.0%
Total		**9538**		**9538**	

2a.3a.1(J) included sub-clades: J.3,J.4,J,G.1

2a.3a.1(J.1) included sub-clades: J.1.1,J.1
2a.3a.1(J.2) included sub-clades: J.2,J.2.1
2a.3a.1(J.2.4) included sub-clades: J.2.4,J.2.4.2

Table 9A. Number and proportion of B/Victoria reported genetic clades and assigned clades based on phylogenetic analysis, EU/EEA, week 40 2025 to week 33 2026

Clade	Reference virus	Reported clade	%	Assigned clade	%2
V1A.3a.2(C)	B/Austria/1359417/2021_Egg	9	2.8%	14	4.4%
V1A.3a.2(C.3.1)	B/KANAGAWA/AC2414/2025	17	5.3%	14	4.4%
V1A.3a.2(C.5)	B/Stockholm/3/2022	5	1.6%	1	0.3%
V1A.3a.2(C.5.1)	B/Catalonia/2279261NS/2023	54	17.0%	54	17.0%
V1A.3a.2(C.5.6)	B/Switzerland/329/2024	125	39.3%	126	39.6%
V1A.3a.2(C.5.6.1)	B/England/120/2025	86	27.0%	89	28.0%
V1A.3a.2(C.5.7)	B/Greece/5509/2024	18	5.7%	18	5.7%
Undefined	-	3	0.9%	2	0.6%
none	-	1	0.3%	-	-
Total		318		318	

V1A.3a.2(C) included sub-clades: C,C.3,C.3.3
V1A.3a.2(C.5) included sub-clades: C.5,C.5.4

Table 10A. Reference strains included in the phylogenetic analysis and trees

Isolate Name	Subtype	Clade	Subclade	Collection Date	HA Segment Id
A/Victoria/2570/2019_Egg	A(H1N1)pdm09	5a.2	C	2019-11-22	EPI1718610
A/Sydney/5/2021_Egg	A(H1N1)pdm09	5a.2a	C.1	2021-10-16	EPI2020645
A/Netherlands/10468/2023	A(H1N1)pdm09	5a.2a	C.1	2023-03-13	EPI2660407
A/Michigan/62/2023	A(H1N1)pdm09	5a.2a	C.1	2023-10-16	EPI3351800
A/Lisboa/188/2023	A(H1N1)pdm09	5a.2a	C.1	2023-11-22	EPI3506999
A/Hungary/286/2024	A(H1N1)pdm09	5a.2a	C.1	2024-11-05	EPI3836459
A/Wisconsin/67/2022_Cell	A(H1N1)pdm09	5a.2a.1	C.1.1	2022-10-25	EPI2224978
A/Victoria/4897/2022_Egg	A(H1N1)pdm09	5a.2a.1	D	2022-10-02	EPI2437457
A/Netherlands/10481/2024	A(H1N1)pdm09	5a.2a.1	D	2024-02-12	EPI3425497
A/Poland/28/2024	A(H1N1)pdm09	5a.2a.1	D	2024-03-04	EPI3379561
A/Bretagne/05126/2024	A(H1N1)pdm09	5a.2a.1	D	2024-03-29	EPI3551548
A/Norway/06906/2024	A(H1N1)pdm09	5a.2a.1	D	2024-09-23	EPI3610057
A/Norway/00926/2025	A(H1N1)pdm09	5a.2a.1	D.3.1	2025-01-20	EPI3960099
A/Missouri/11/2025_Egg	A(H1N1)pdm09	5a.2a.1	D.3.1	2025-01-30	EPI4496474
A/Missouri/11/2025_Cell	A(H1N1)pdm09	5a.2a.1	D.3.1	2025-01-30	EPI4043935
A/Darwin/6/2021_Cell	A(H3N2)	2a	G.1	2021-03-16	EPI1885402
A/Darwin/9/2021_Egg	A(H3N2)	2a	G.1	2021-04-17	EPI1888006
A/Massachusetts/18/2022_Cell	A(H3N2)	2a.3a.1	J	2022-06-04	EPI2415918
A/Thailand/8/2022_Egg	A(H3N2)	2a.3a.1	J	2022-07-11	EPI2236266
A/Croatia/10136RV/2023	A(H3N2)	2a.3a.1	J.2	2023-04-12	EPI3251398
A/Canberra/331/2023	A(H3N2)	2a.3a.1	J.1.1	2023-10-29	EPI3180038
A/France/IDF-IPP29542/2023	A(H3N2)	2a.3a.1	J.4	2023-11-30	EPI3087141
A/District_Of_Columbia/27/2023	A(H3N2)	2a.3a.1	J.2	2023-12-09	EPI3351804
A/Sydney/856/2023	A(H3N2)	2a.3a.1	J.1	2023-12-09	EPI3251106
A/Lisboa/216/2023	A(H3N2)	2a.3a.1	J.2.2	2023-12-15	EPI3490023
A/West_Virginia/51/2024	A(H3N2)	2a.3a.1	J.2.1	2024-07-04	EPI3530536
A/Sydney/1359/2024	A(H3N2)	2a.3a.1	J.2.4	2024-11-29	EPI3902415
A/Netherlands/10685/2024	A(H3N2)	2a.3a.1	J.2.3	2024-12-12	EPI4065328
A/Singapore/GP20238/2024	A(H3N2)	2a.3a.1	J.2.4	2024-12-26	EPI4357487
A/Victoria/211/2025	A(H3N2)	2a.3a.1	J.2.5	2025-01-12	EPI4448160
A/Norway/8765/2025	A(H3N2)	2a.3a.1	K	2025-08-14	EPI4742502

Isolate Name	Subtype	Clade	Subclade	Collection Date	HA Segment Id
B/Brisbane/60/2008	B/Victoria	V1A	A	2008-08-15	EPI173277
B/Washington/02/2019_Egg	B/Victoria	V1A.3	A.3.2	2019-01-19	EPI1482046
B/Austria/1359417/2021_Egg	B/Victoria	V1A.3a.2	C	2021-01-09	EPI1987381
B/Austria/1359417/2021_Cell	B/Victoria	V1A.3a.2	C	2021-01-09	EPI1845793
B/Stockholm/3/2022	B/Victoria	V1A.3a.2	C.5	2022-03-22	EPI2100743
B/Catalonia/3514402NS/2023	B/Victoria	V1A.3a.2	C.5.4	2023-01-03	EPI2690374
B/Catalonia/2279261NS/2023	B/Victoria	V1A.3a.2	C.5.1	2023-01-03	EPI2690180
B/Netherlands/10335/2023	B/Victoria	V1A.3a.2	C	2023-02-17	EPI2690190
B/Moldova/2030521/2023	B/Victoria	V1A.3a.2	C.3	2023-03-22	EPI2649398
B/Greece/5509/2024	B/Victoria	V1A.3a.2	C.5.7	2024-01-03	EPI3474246
B/Switzerland/329/2024	B/Victoria	V1A.3a.2	C.5.6	2024-01-16	EPI3474254
B/England/120/2025	B/Victoria	V1A.3a.2	C.5.6.1	2025-02-21	EPI4620784
B/KANAGAWA/AC2414/2025	B/Victoria	V1A.3a.2	C.3.1	2025-05-19	EPI4450481

HA: haemagglutinin.

Annex 4. Age, outcome and vaccination status

A(H1N1)pdm09

Table 11A. Number of reported viruses per reporting antigenic category and age group, EU/EEA, week 40 2025 to week 33 2026

	Age group				
Subclade	<5y	[5y,15y)	[15y,65y)	>=65y	Total
5a.2a(C.1)	6	12	9	6	33
5a.2a(C.1.9)	2	0	1	1	4
5a.2a.1(D)	70	64	171	70	375
5a.2a.1(D.3.1)	18	19	159	166	362
none	0	0	1	1	2

Table 11B. Number of reported A(H1N1)pdm09 viruses per reporting genetic category and age group, EU/EEA, week 40 2025 to week 33 2026

	Age group				
Subclade	<5y	[5y,15y)	[15y,65y)	>=65y	Total
5a.2a(C.1.9.3)	1	0	6	10	17
5a.2a.1(D)	12	5	25	41	83
5a.2a.1(D.3.1)	411	335	1 860	2 412	5 018
none	0	0	1	0	1
other	29	26	208	138	401

Table 11C. Number of reported A(H1N1)pdm09 viruses per reporting genetic category and outcome, , EU/EEA, week 40 2025 to week 33 2026 EU/EEA

	Outcome			
Subclade	Alive	Deceased	Total	% Dead
5a.2a(C.1.9.3)	1	0	1	0.0
5a.2a.1(D.3.1)	657	46	703	6.5

Table 11D. Number of reported A(H1N1)pdm09 viruses per reporting genetic category and vaccination status, EU/EEA, week 40 2025 to week 33 2026

	Vaccination			
Subclade	Yes	No	Total	% Vaccinated
5a.2a(C.1.9.3)	0	5	5	0.0
5a.2a.1(D.3.1)	444	1 051	1 495	29.7
other	54	182	236	22.9

A(H3N2)

Table 12A. Number of reported viruses per reporting antigenic category and age group, EU/EEA, week 40 2025 to week 33 2026

	Age group				
Subclade	<5y	[5y,15y)	[15y,65y)	>=65y	Total
2a.3a.1(J)	7	14	8	6	35
2a.3a.1(J.2)	137	161	142	45	485
2a.3a.1(J.2.3)	0	0	4	5	9
2a.3a.1(J.2.4)	42	48	169	123	382
2a.3a.1(K)	0	4	32	16	52
none	18	20	35	8	81

Table 12B. Number of reported A(H3N2) viruses per reporting genetic category and age group, EU/EEA, week 40 2025 to week 33 2026

	Age group				
Subclade	<5y	[5y,15y)	[15y,65y)	>=65y	Total
2a.3a.1(J)	0	3	11	8	22
2a.3a.1(J.2)	22	22	87	65	196
2a.3a.1(J.2.2)	6	5	17	9	37
2a.3a.1(J.2.3)	28	35	54	71	188
2a.3a.1(J.2.4)	55	52	100	129	336
2a.3a.1(J.2.5)	0	0	1	0	1
2a.3a.1(K)	844	1 167	2 748	2 147	6 906
none	1	2	4	3	10
other	6	2	17	12	37

Table 12C. Number of reported A(H3N2) viruses per reporting genetic category and outcome, EU/EEA, week 40 2025 to week 33 2026

	Outcome			
Subclade	Alive	Deceased	Total	% Dead
2a.3a.1(J.2)	24	0	24	0.0
2a.3a.1(J.2.2)	2	0	2	0.0
2a.3a.1(J.2.3)	25	1	26	3.8
2a.3a.1(J.2.4)	24	3	27	11.1
2a.3a.1(K)	1 277	68	1 345	5.1

Table 12D. Number of reported A(H3N2) viruses per reporting genetic category and vaccination status, EU/EEA, week 40 2025 to week 33 2026

	Vaccination			
Subclade	Yes	No	Total	% Vaccinated
2a.3a.1(J.2)	6	11	17	35.3
2a.3a.1(J.2.2)	2	12	14	14.3
2a.3a.1(J.2.3)	28	55	83	33.7
2a.3a.1(J.2.4)	12	57	69	17.4
2a.3a.1(J.2.5)	0	1	1	0.0
2a.3a.1(K)	650	2 175	2 825	23.0

B/Victoria

Table 13A. Number of reported viruses per reporting antigenic category and age group, EU/EEA, week 40 2025 to week 33 2026

	Age group				
Subclade	<5y	[5y,15y)	[15y,65y)	>=65y	Total
V1A.3a.2(C)	0	1	11	0	12

Table 13B. Number of reported viruses per reporting genetic category and age group, EU/EEA, week 40 2025 to week 33 2026

	Age group				
Subclade	<5y	[5y,15y)	[15y,65y)	>=65y	Total
V1A.3a.2(C)	0	1	7	0	8
V1A.3a.2(C.3.1)	2	2	5	0	9
V1A.3a.2(C.5)	1	0	2	1	4
V1A.3a.2(C.5.1)	3	9	27	3	42
V1A.3a.2(C.5.6)	3	13	64	5	85
V1A.3a.2(C.5.6.1)	5	9	38	2	54
V1A.3a.2(C.5.7)	1	2	13	1	17
other	0	1	1	1	3

Table 13C. Number of reported viruses per reporting genetic category and outcome, EU/EEA, week 40 2025 to week 33 2026

	Outcome			
Subclade	Alive	Deceased	Total	% Dead
V1A.3a.2(C.3.1)	2	0	2	0
V1A.3a.2(C.5)	1	0	1	0
V1A.3a.2(C.5.1)	1	0	1	0
V1A.3a.2(C.5.6)	5	0	5	0
V1A.3a.2(C.5.6.1)	9	0	9	0
other	1	0	1	0

Table 13D. Number of reported viruses per reporting genetic category and vaccination status, EU/EEA, week 40 2025 to week 33 2026

	Vaccination			
Subclade	Yes	No	Total	% Vaccinated
V1A.3a.2(C.3.1)	0	1	1	0.0
V1A.3a.2(C.5.1)	0	7	7	0.0
V1A.3a.2(C.5.6)	2	14	16	12.5
V1A.3a.2(C.5.6.1)	0	6	6	0.0
V1A.3a.2(C.5.7)	0	1	1	0.0

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