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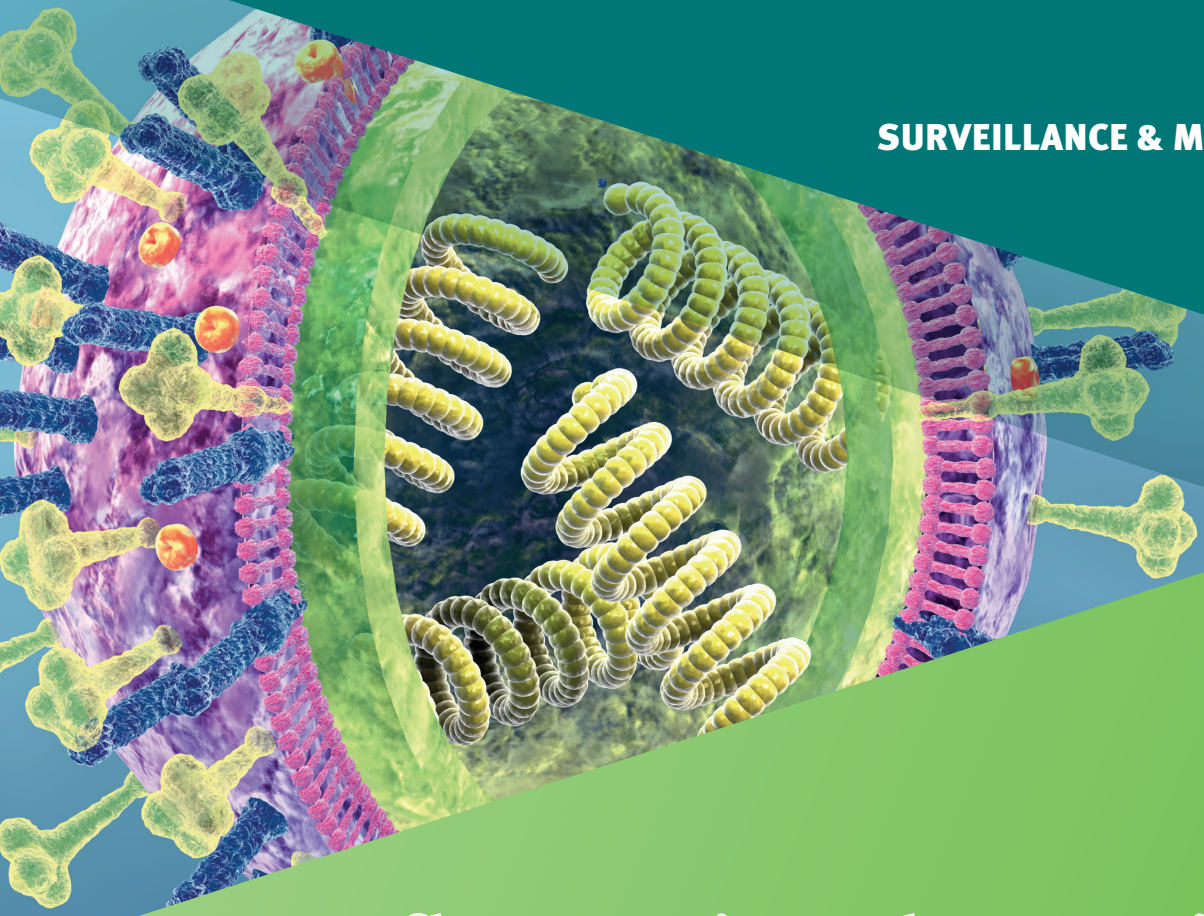

Influenza virus characteristics, week 40 2024 to week 33 2025, EU/EEA

September 2025

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

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A draft of this report was sent for consultation to EU/EEA Member State Operational Contact Points for Respiratory Viruses (Microbiology). The report was reviewed by Raquel Guiomar (National Institute of Health Doctor Ricardo Jorge, Portugal), Adam Meijer (National Institute for Public Health and the Environment, the Netherlands), Francisco Pozo (Instituto de Salud Carlos III, Spain), Katarina Prosenc Trilar (National Laboratory for Health, Environment and Food, Slovenia), Andreas Rohringer (National Public Health Institute, Norway), Karen Nahapetyan (WHO Regional Office for Europe), and Edoardo Colzani (ECDC).

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We gratefully acknowledge the work of the country representatives that have reported their data to TESSy and the originating laboratories that submitted the data and sequences to the EpiFlu database of GISAID; these are the data that were downloaded for use in the preparation of this report (those who submitted data may be contacted directly via the GISAID website). We acknowledge Marius Valentin Valcu (ECDC) for his support in TESSy data management.

Disclaimer
The data presented in this report were extracted on 22 August 2025 from the TESSy database. Any error in the database on 22 August 2025 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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Erratum: On 1 October 2025, the NA segment substitution for B/Netherlands/10658/2025 was corrected from 'Unknown' to 'NA_M464T' in Annex 2, Table 5A (last column, fourth to last row).

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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)	Victoria lineage of influenza B viruses
B(Yam)	Yamagata lineage of influenza B viruses
EISN	European Influenza Surveillance Network
ERLI-Net	European Reference Laboratory Network for Human Influenza
EU/EEA	European Union and European Economic Area
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 30 European Union and European Economic Area (EU/EEA) countries from week 40 2024 to week 33 2025, 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, 354 455 influenza virus detections (sentinel and non-sentinel combined) were reported, of which 73% (257 761) were type A and 26% (90 873) were type B virus; another 1.6% (5 821) were reported untyped.

Of the 52 442subtyped influenza A viruses (20% of detected type A viruses), 31 638 (60%) were subtype A(H1)pdm09 and 20 804 (40%) were subtype A(H3). Of the 90 873 reported influenza type B viruses, the lineage for 9 279 (10%) was determined, with all except one virus falling into the B/Victoria/2/87 lineage. One report on viral RNA belonging to the B/Yamagata/16/88 lineage was submitted. Attempts to culture or sequence this virus were unsuccessful due to a very low viral load.

A(H1N1)pdm09

For A(H1N1)pdm09 viruses, 17 countries reported 5 572 haemagglutinin (HA) sequences. All of the 5 560 sequences that passed quality filters fell in the clade 5a.2a (C.1) branch. A proportion of 16% were further characterised into clade 5a.2a.1 (D), represented by the 2023–25 northern hemisphere (NH) vaccine strain for egg-based vaccines, A/Victoria/4897/2022. Most (69%) of the 5a.2a.1 viruses carried T120A in comparison with A/Wisconsin/67/2022_Cell and belonged to subclade D.3, which is not represented by a reference strain; 19% belonged to subclade D.2, defined by the additional R113K substitution.

Among the 821 characterised A(H1)pdm09 viruses, the main reported categories were A/Sydney/5/2021-like, clade 5a.2a (C.1) and A/Victoria/4897/2022-like, clade 5a.2a.1 (D), representing 51% and 46%, respectively.

In total, 5 293 A(H1N1)pdm09 viruses were assessed for antiviral susceptibility to oseltamivir and/or zanamivir and/or baloxavir marboxil. Reduced and highly reduced inhibition by oseltamivir was detected in two (0.6%) and four (1.3%) of 317 phenotypically tested viruses. By genotypic testing, reduced and highly reduced inhibition by oseltamivir were observed for four (<0.1%) and 25 (0.5%) viruses, respectively, of the remaining 4 690 tested viruses. One of 4 714 viruses (<0.1%) showed genotypic reduced inhibition to zanamivir. Two (0.1%) of 3 048 assessed A(H1N1)pdm09 viruses carried genetic markers associated with reduced susceptibility to baloxavir marboxil.

A(H3N2)

For A(H3N2) viruses, 17 countries reported 4 279 HA sequences, of which 4 277 passed quality criteria and were analysed phylogenetically. All A(H3) HA sequences fell into the branch of clade 2a.3a defined by E50K compared with 2a.3 representative virus A/Norway/24873/2021; out of these, the majority (>99%) fell into clade 2a.3a.1 (J), represented by NH 2024–2025 egg-based vaccine strain A/Thailand/8/2022_Egg. Fifteen viruses belonged to 2a.3b and fell into subclade G.1.3.1. Within clade 2a.3a.1, the SH 2025 vaccine strain A/Croatia/10136RV/2023 represents subclade J.2, defined by N122D and K276E compared with NH 2024–2025 vaccine strain A/Massachusetts/18/2022_Cell. Most viruses (78%) fell into this subclade, 57% of which fell on a branch with the N8D amino-acid substitution that does not have a reference representative or subclade designation.

Among the 486 characterised A(H3) viruses, the main reported categories were A/Croatia/10136RV/2023-like, clade 2a.3a.1 (J.2) and A/Thailand/8/2022-like, clade 2a.3a.1 (J), representing 50% and 44%, respectively. In total, 4 267 A(H3N2) viruses were assessed for antiviral susceptibility to oseltamivir and/or zanamivir and/or baloxavir marboxil. Reduced inhibition by oseltamivir was detected in four (1.3%) of 298 phenotypically tested viruses, and reduced inhibition by zanamivir was detected in one (<0.5%) of the 292 phenotypically tested viruses. By genotypic testing, reduced and highly reduced inhibition by oseltamivir was observed for 12 (0.3%) and three (0.1%) of the 3 930 tested viruses, respectively, and reduced inhibition by zanamivir was observed for 10 (0.3%) of the 3 936 tested viruses. Three (0.1%) of 2 593 assessed A(H3N2) viruses carried genetic markers associated with reduced susceptibility to baloxavir marboxil.

B/Victoria

For B/Victoria viruses, 17 countries reported 4 292 HA sequences. Excluding 17 sequences that did not pass quality control, all B/Victoria sequences carried HA genes that fell into genetic clade V1A.3a.2 (C), represented by NH 2022–2025 vaccine strain B/Austria/1359417/2021_Egg. The majority (58%) of viruses fell in the C.5.1 subclade, followed by 22% in C.5.7 and 19% in C.5.6. Additional minor proportions below 1% also populated subclade C.3 and C.5. For the subclades present in the reported data set, each contained a reference strain. Overall, B/Victoria evolution was characterised by multiple branches absent from defining amino-acid substitutions.

Among the 684 characterised B(Victoria) viruses, the main reported category was B/Austria/1359417/2021-like, clade V1A.3a.2 (C), representing 92%. In total, 4 063 B(Victoria) viruses were assessed for antiviral susceptibility to oseltamivir and/or zanamivir and/or baloxavir marboxil. Reduced inhibition by oseltamivir was detected in eight (3.6%) of 223 phenotypically tested viruses, and reduced inhibition by zanamivir was detected in six (2.8%) of the 215 phenotypically tested viruses. By genotypic testing, reduced inhibition by oseltamivir were observed for six (0.2%) of 3 473 assessed viruses. Genotypically reduced and highly reduced inhibition to zanamivir was reported in four (0.1%) and one (<0.1%) of 3 480 tested viruses (0.1%). One (<0.1%) of 2 699 assessed B/Victoria viruses carried genetic markers associated with reduced susceptibility to baloxavir marboxil.

1 Introduction

Influenza vaccines are the principal measure for preventing influenza and reducing the impact of epidemics [1]. Influenza viruses frequently undergo genetic and antigenic changes. Therefore, based on global surveillance data, data on circulating influenza viruses are reviewed every year to inform recommendations on vaccine composition. Since 1973, the World Health Organization (WHO) publishes formal recommendations for the composition of influenza vaccines based on the information provided by the WHO Global Influenza Surveillance and Response System (GISRS) [2]. WHO updates its recommendations for vaccine composition twice a year to target the viruses expected to be the most frequently circulating in the coming influenza seasons in the northern hemisphere (NH) and southern hemisphere (SH), respectively [3,4].

This report summarises influenza virological surveillance data from all 30 European Union and European Economic Area (EU/EEA) countries from week 40 2024 to week 33 2025, 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 2024–25 influenza season (from week 40 2024 to week 33 2025);
- monitor the diversity and circulation of viruses, their geographical occurrence and frequency;
- provide feedback to the laboratories, through analysis of their antigenic and genetic characterisation results in the regional context;
- monitor, maintain and enhance the quality of the characterisations 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 Influenza Surveillance Network (EISN) 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 or B/Yamagata), 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.

2 Data sources and methods

Before this analysis was conducted, we performed initial data cleaning and provided feedback to the participating NRLs. The individual laboratories were contacted by email and asked to update and clean their weekly virus detection and characterisation data in TESSy by 22 August 2025. The data for week 40 2024 to week 33 2025 were then accessed and summarised for inclusion in this analysis.

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.

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 and, in some instances, embryonated chicken eggs [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 WHO CC Atlanta, 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 2024, 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 influenza virus characterisation guidelines for the northern hemisphere influenza season 2024–25, December 2024', available upon request).

GISAID accession numbers were also reported; sequences were either obtained 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 guidance [13,14]. 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)).

Currently, different non-standardised assays (focus, plaque, or yield reduction assay, high-content imaging neutralisation, ViroDot assay, IRINA) are mainly used by WHO CCs for the phenotypic analyses and monitoring of reduced baloxavir marboxil susceptibility and, therefore, the indicated fold changes in the WHO list are not necessarily comparable [13]. For reporting purposes, amino acid substitutions associated with IC50 fold-change of up to three-fold change in phenotypic assays are considered as 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 22 August 2025 for the period 30 September 2024 to 22 August 2025), including only sequences where the isolate could be linked to a record in the TESSy INFLANTIVIR database for the 2024–25 season. Phylogenetic analysis data are presented 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. Unsuccessful matches, duplicates and other discrepancies were addressed via communication with the NRLs.

The Nextstrain [15] 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.

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 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.

3 Results

Weekly aggregate reports of detections

From week 40 2024 to week 33 2025, 354 455 influenza virus detections were reported from sentinel and non-sentinel surveillance sources in 30 EU/EEA countries, including 257 761 (72.7%) type A influenza viruses and 90 873 (25.6%) type B influenza viruses. The type was not reported for the 5 821 remaining viruses (Table 1, Figures 1–2). Out of the 52 442 type A viruses with a defined subtype (20.3% of type A viruses), 31 638 (60.3%) were A(H1)pdm09 and 20 804 (39.7%) were A(H3).

For A(H1)pdm09, the neuraminidase subtype N1 was determined for 3 570 of the 7 310 sentinel detections (48.8%) and 9 317 of the 24 328 non-sentinel detections (38.3%). For A(H3), the neuraminidase subtype N2 was determined for 2 141 of the 5 520 sentinel detections (38.8%) and 4 671 of the 15 284 non-sentinel detections (30.6%). Out of the 9 279 type B viruses with a defined lineage (10.2% of type B viruses), 9 278 (~100%) were assigned to the Victoria lineage. The one remaining detection of HA segment viral RNA was assigned to the Yamagata lineage and was reported in week 42 2024; the NRL's attempts to culture or sequence the virus was unsuccessful due to very low viral load.

One A(H1N2) and two recombinant A(H3N2) viruses were detected as well. Please see further details in the virus characterisation section of this report.

Table 1. Number and proportion of detected influenza viruses, by type and subtype, reported to TESSy, EU/EEA, week 40 2024 to week 33 2025

Type	Subtype	Sentinel		Non-sentinel		Total	
		N	%	N	%	N	%
A	A(H1)pdm09	7 310	28.6	24 328	7.4	31 638	8.9
	A(H3)	5 520	21.6	15 284	4.6	20 804	5.9
	A unsubtyped	2 246	8.8	203 073	61.7	205 319	57.9
B	B(Vic)	4 666	18.3	4 612	1.4	9 278	2.6
	B(Yam)	1	0.0	0	0.0	1	0.0
	B lineage not determined	5 552	21.7	76 042	23.1	81 594	23.0
Untyped	Untyped	262	1.0	5 559	1.7	5 821	1.6
Total	**–**	**25 557**	**100.0**	**328 898**	**100.0**	**354 455**	**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 2024 to week 33 2025 (N = 354 455)

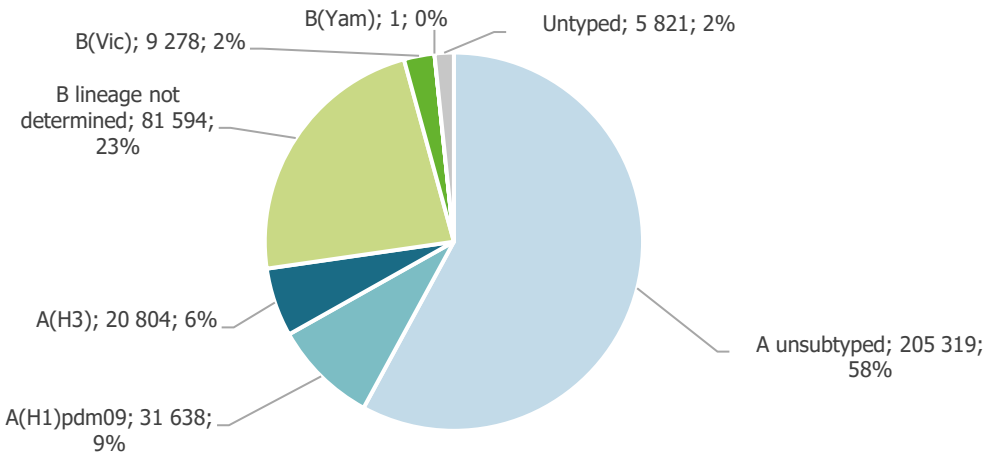
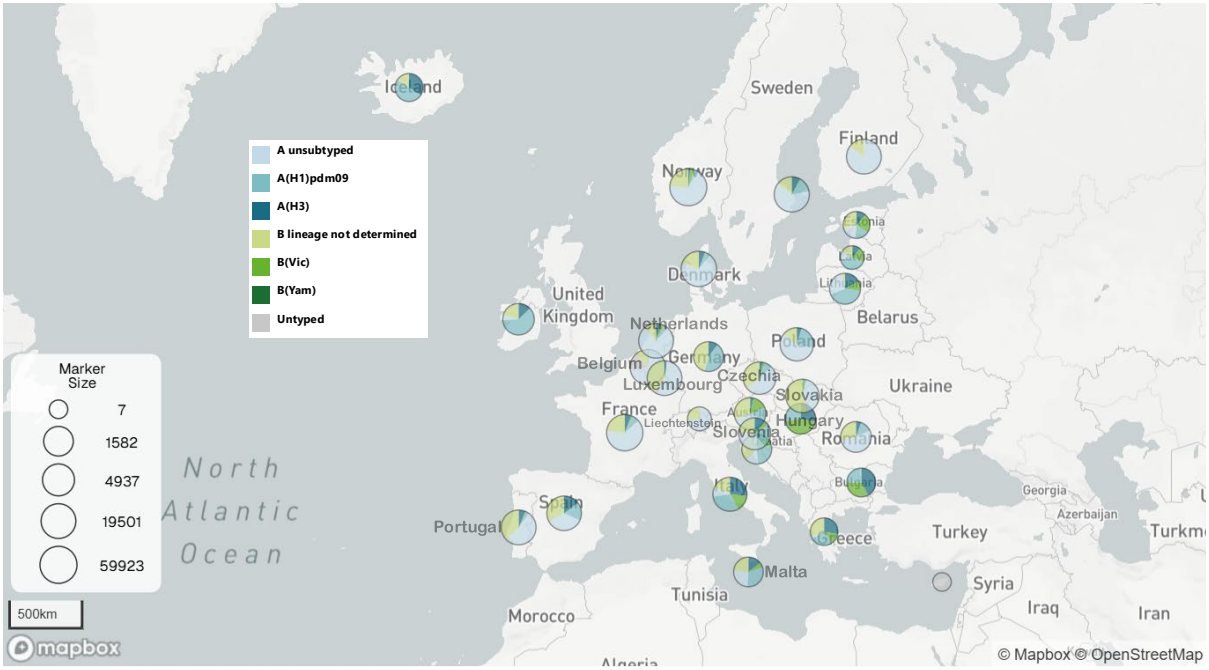


Figure 2. Proportions of influenza types and subtypes, sentinel and non-sentinel surveillance systems, EU/EEA, week 40 2024 to week 33 2025



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

Sentinel detections

Among the 25 557 virus detections reported in the sentinel surveillance systems between week 40 2024 and week 33 2025, 15 076 (59.0%) were type A and 10 219 (40.0%) were type B. The type was not reported for the 262 remaining viruses (Table 2, Figure 3). Out of the 12 830 type A viruses with a defined subtype (85.1% of type A viruses), 7 310 (57.0%) were A(H1)pdm09 and 5 520 (43.0%) were A(H3). Out of the 4 667 type B viruses with a defined lineage (45.7% of type B viruses), 4 666 (~100%) were assigned to the Victoria lineage and the one remaining RNA detection was assigned to the Yamagata lineage.

Figure 3. Number and proportion of influenza virus cumulative detections in sentinel surveillance systems by subtype, EU/EEA, week 40 2024 to week 33 2025 (N = 25 557)

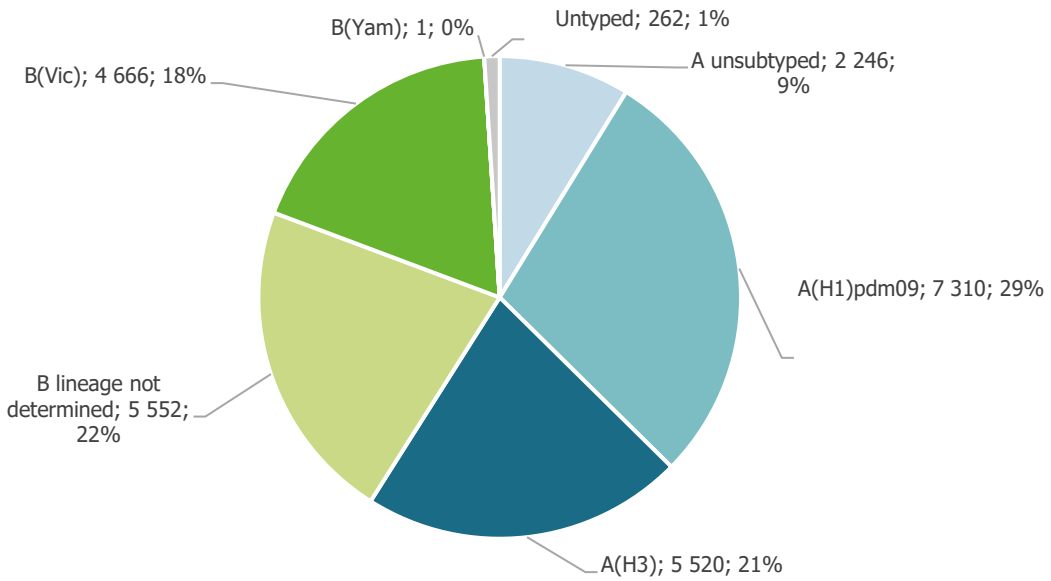
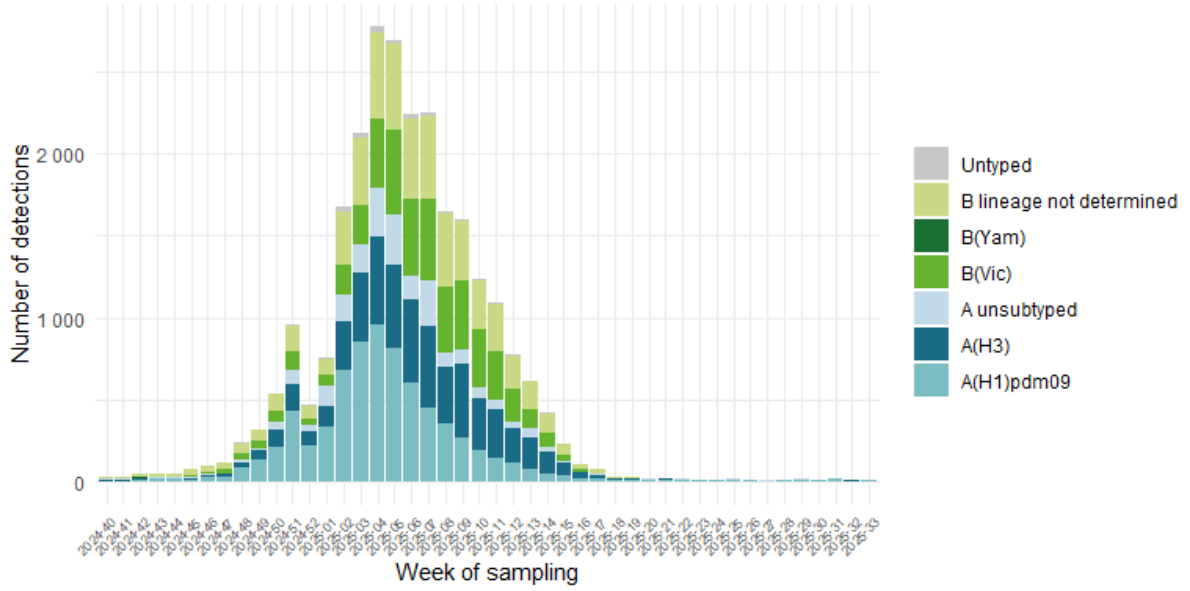


Figure 4. Distribution of detected influenza viruses in sentinel surveillance by week, subtype and lineage, EU/EEA, week 40 2024 to week 33 2025



Non-sentinel detections

Among the 328 898 virus detections reported in the non-sentinel surveillance systems between week 40 2024 and week 33 2025, 242 685 (73.8%) were type A and 80 654 (24.5%) were type B. The type was not reported for the 5 559 remaining viruses (Table 1, Figure 5). Out of the 39 612 type A viruses with a defined subtype (16.3% of type A viruses), 24 328 (61.4%) were A(H1)pdm09 and 15 284 (38.6%) were A(H3). Out of the 4 612 type B viruses with a defined lineage (5.7% 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 2024 to week 33 2025 (N=328 898)

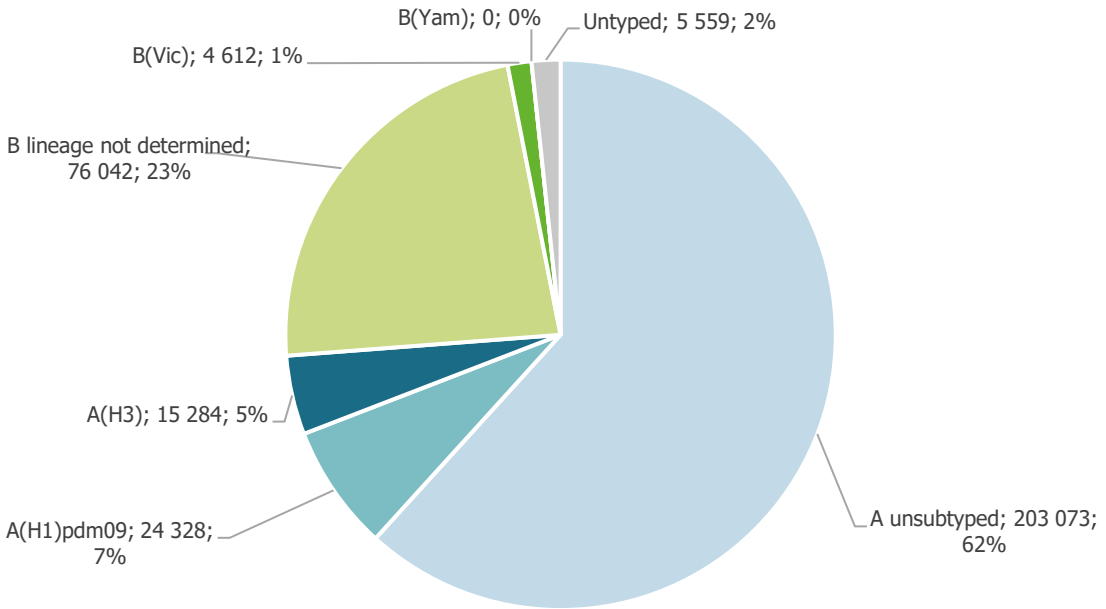


Figure 6. Distribution of detected viruses in non-sentinel surveillance by week, subtype and lineage, EU/EEA, week 40 2024 to week 33 2025

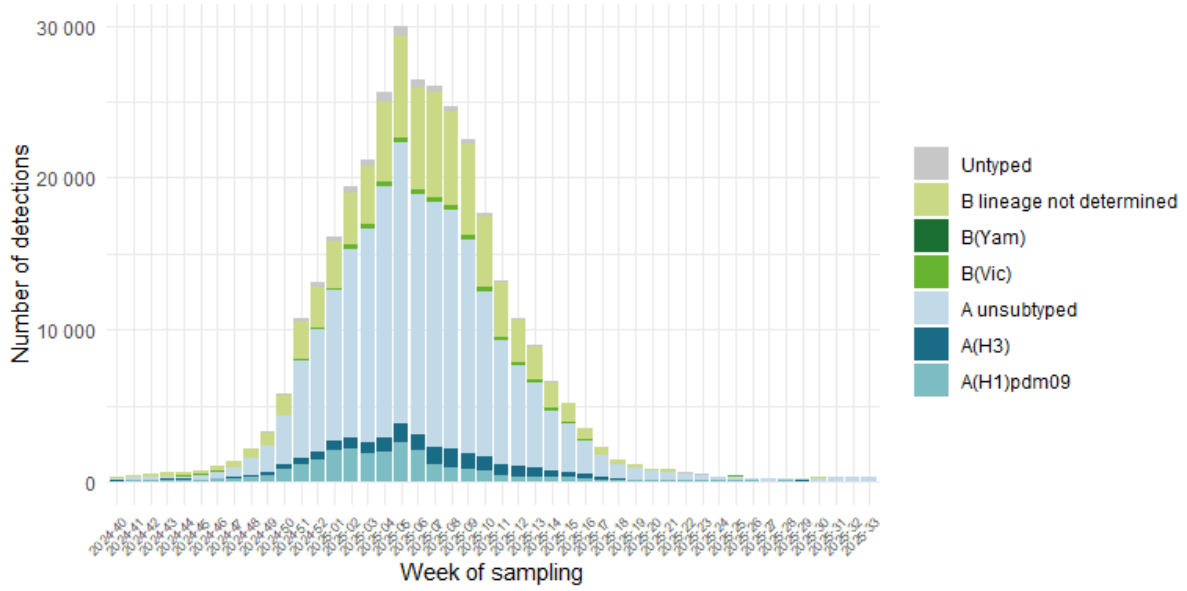
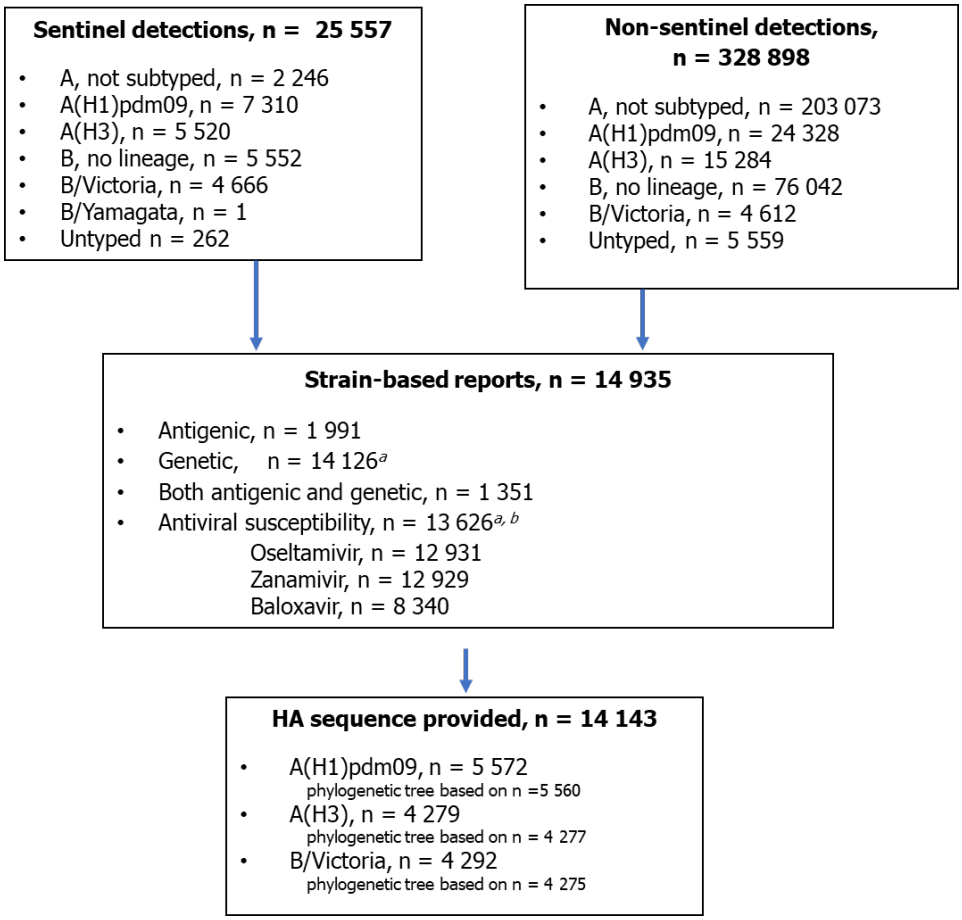


Figure 7. Flowchart of the specimens used in the analysis of this report, reported by country/territory surveillance systems, EU/EEA, week 40 2024 to week 3 2025



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

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 2024 to week 33 2025, 14 935 influenza strain-based reports from sentinel (5 013, 33.6%) and non-sentinel (9 922, 66.4%) surveillance systems were submitted by 17 countries in the EU/EEA (Table 2).

Table 2. Number of reported viruses with virus characterisation data, EU/EEA, weeks 40/2024 through 33/2025

Type	Subtype	Surveillance system		Total
		Sentinel	Non Sentinel	
A	A(H1)pdm09	2 001	3 918	5 919
	A(H3)	1 277	3 195	4 472
	A(H1)pdm09r	1	0	1
	A(H3)r	2	0	2
B	B(Vic)	1 732	2 809	4 541
Total	**–**	**5 013**	**9 922**	**14 935**

An A(H1)pdm09r: H1N2 reassortant was detected in Sweden and A(H3)r: H3N2 reassortants were detected in the Netherlands.

Out of the 10 394 type A influenza viruses, 5 919 (56.9%) were reported as subtype A(H1N1)pdm09 or A(H1)pdm09 and 4 472 (43.0%) as subtype A(H3N2) or A(H3). Of the 4 541 type B influenza viruses, virus characterisation data were reported only for viruses assigned to the Victoria lineage.

For the virus characterisation data from INFLANTIVIR record type, a majority of the A(H1) (5 260; 93%) and A(H3) (4 024; 96%) viruses were reported to TESSy with N-subtype. 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.

Sixteen countries reported antigenic and genetic characterisations to TESSy from week 40 2024 to week 33 2025 (Table 3). Eight countries (Belgium, Denmark, France, Germany, Italy, Portugal, Romania and Slovenia) reported both genetic and antigenic characterisation data, and the remaining eight countries (Finland, Greece, Ireland, Luxembourg, the Netherlands, Norway, Spain and Sweden) provided only genetic clade data during the reporting period (Table 3). In addition, Poland reported only antiviral susceptibility data.

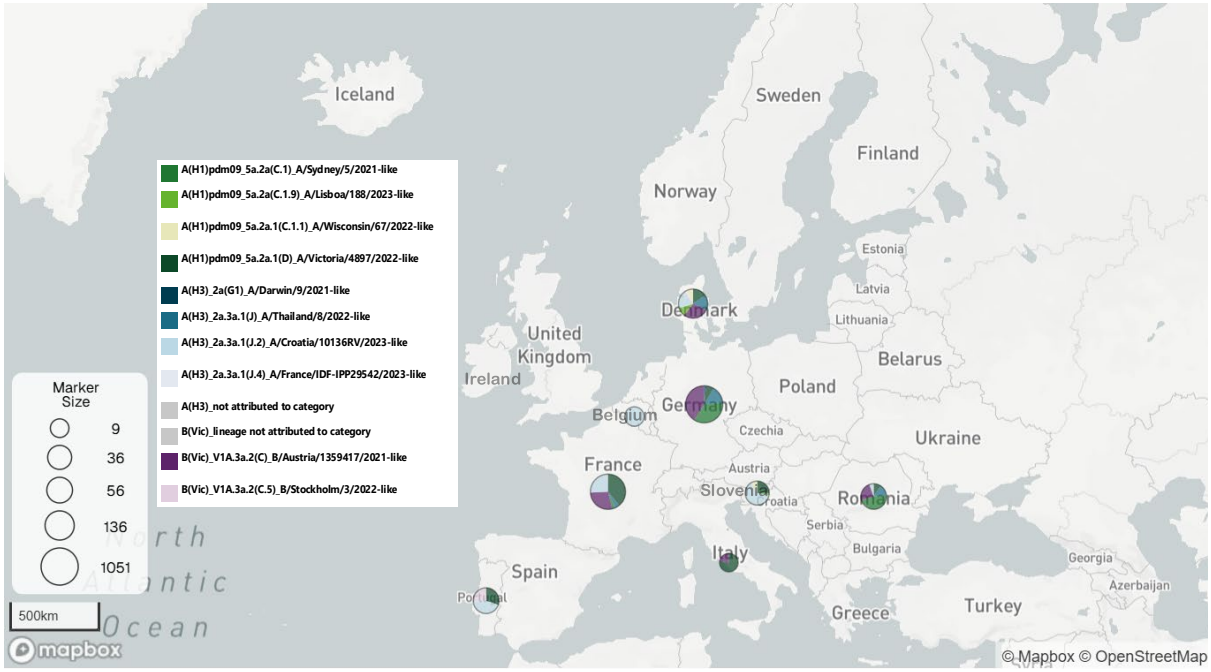
Table 3. Number of viruses characterised antigenically (AG) and genetically (GEN), as reported to TESSy by country (n=16) and week of sampling, EU/EEA, week 40 2024 to week 10 2025 (first page) and weeks 11 to 33 2025 (second page)

Country	Test	Year and week no.																						
		2024													2025									
		40	41	42	43	44	45	46	47	48	49	50	51	52	1	2	3	4	5	6	7	8	9	10
Belgium	AG	0	0	0	0	0	0	0	0	0	0	1	0	0	1	3	2	0	2	1	0	1	0	0
	GEN	0	2	2	0	2	1	2	2	0	0	2	1	5	9	10	11	4	11	5	6	3	7	13
Denmark	AG	1	2	4	2	2	0	5	0	0	2	5	19	3	8	1	20	10	4	23	5	1	6	2
	GEN	6	6	8	16	5	9	12	8	15	15	19	30	6	16	12	38	23	43	49	21	21	40	28
Finland	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	GEN	0	3	4	1	0	0	1	1	2	2	5	2	5	6	7	8	8	3	5	5	11	10	7
France	AG	4	1	8	7	10	2	6	7	15	42	36	42	34	42	50	50	65	55	39	27	28	22	9
	GEN	13	4	17	16	22	23	39	46	56	144	164	131	96	117	184	235	201	225	143	138	158	118	77
Germany	AG	0	1	3	1	2	5	0	6	7	17	18	29	14	26	69	104	120	83	68	86	52	73	71
	GEN	1	1	0	1	1	5	0	5	7	15	7	23	11	14	41	84	143	147	101	127	98	91	66
Greece	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	GEN	0	0	0	0	0	0	0	0	2	1	0	0	0	1	3	1	0	0	0	0	1	0	0
Ireland	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	GEN	0	0	5	3	6	11	10	13	24	28	72	62	27	62	45	34	31	20	23	13	9	10	13
Italy	AG	0	0	0	0	1	1	0	1	2	3	1	0	0	0	0	0	0	0	0	0	0	0	0
	GEN	0	0	0	0	3	2	1	2	3	4	2	0	0	0	0	3	0	1	1	3	1	3	5
Luxembourg	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	GEN	1	0	2	0	1	0	1	1	2	13	15	28	9	9	25	29	32	36	34	34	13	11	17
Netherlands	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	GEN	4	3	5	9	11	4	6	9	31	43	58	56	57	72	97	118	139	171	131	121	99	105	79
Norway	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	GEN	5	13	22	20	19	23	10	12	11	2	1	16	4	9	11	23	46	27	15	20	36	22	6
Portugal	AG	0	1	0	1	2	2	2	0	3	4	0	0	0	1	0	1	2	3	2	4	3	10	5
	GEN	4	4	0	6	5	9	6	8	16	16	27	41	29	56	84	59	103	82	75	65	35	23	16
Romania	AG	0	0	0	0	0	0	1	1	0	2	1	2	1	2	1	8	2	5	11	5	5	2	3
	GEN	0	0	0	0	1	1	1	2	1	3	4	4	15	25	6	38	18	25	20	18	15	10	13
Slovenia	AG	0	0	0	0	0	0	1	0	1	0	0	0	0	1	1	1	3	0	4	1	4	3	0
	GEN	0	0	0	0	0	0	1	1	1	0	2	1	0	0	2	0	1	1	1	1	0	0	2
Spain	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	GEN	34	39	36	41	43	48	45	66	74	78	103	165	184	308	405	412	434	419	299	308	243	184	186
Sweden	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	GEN	3	6	7	9	11	5	6	3	6	8	16	13	4	11	7	14	9	17	19	12	26	16	16
Total	**AG**	**5**	**5**	**15**	**11**	**17**	**10**	**15**	**15**	**28**	**70**	**62**	**92**	**52**	**81**	**125**	**186**	**202**	**152**	**148**	**128**	**94**	**116**	**90**
	GEN	**71**	**81**	**108**	**122**	**130**	**141**	**141**	**179**	**251**	**372**	**497**	**573**	**452**	**715**	**939**	**1 107**	**1 192**	**1 228**	**921**	**892**	**769**	**650**	**544**

Country	Test	Year and week no.																						
		2025																						
		11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	Total	%
Belgium	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**11**	**0.6**
	GEN	3	1	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**105**	**0.7**
Denmark	AG	0	8	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**136**	**6.8**
	GEN	23	35	38	34	17	32	23	1	0	0	0	0	0	0	0	0	0	0	0	0	0	**649**	**4.6**
Finland	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**0**	**0.0**
	GEN	6	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**109**	**0.8**
France	AG	11	10	0	4	4	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**638**	**32.0**
	GEN	57	48	43	29	13	8	2	3	3	2	3	0	0	0	0	0	0	0	0	0	0	**2 578**	**18.3**
Germany	AG	52	51	36	22	13	12	1	0	2	2	1	2	0	0	0	0	0	0	0	0	2	**1 051**	**52.8**
	GEN	51	45	35	18	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1 148**	**8.1**
Greece	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**0**	**0.0**
	GEN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**9**	**0.1**
Ireland	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**0**	**0.0**
	GEN	17	5	6	4	10	4	7	3	3	0	3	0	0	0	0	0	0	0	0	0	0	**583**	**4.1**
Italy	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**9**	**0.5**
	GEN	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**44**	**0.3**
Luxembourg	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**0**	**0.0**
	GEN	11	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**330**	**2.3**
Netherlands	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**0**	**0.0**
	GEN	82	56	47	34	20	13	9	10	3	4	4	3	5	1	1	0	0	0	1	0	0	**1 721**	**12.2**
Norway	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**0**	**0.0**
	GEN	28	22	22	16	35	11	2	20	33	16	0	0	0	0	0	0	0	0	0	0	0	**578**	**4.1**
Portugal	AG	7	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**56**	**2.8**
	GEN	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**779**	**5.5**
Romania	AG	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**54**	**2.7**
	GEN	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**228**	**1.6**
Slovenia	AG	3	5	1	5	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	**36**	**1.8**
	GEN	4	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**24**	**0.2**
Spain	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**0**	**0.0**
	GEN	185	176	109	106	79	30	46	18	7	8	11	7	7	5	2	1	0	0	0	0	0	**4 951**	**35.0**
Sweden	AG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**0**	**0.0**
	GEN	9	10	9	6	4	4	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	**290**	**2.1**
Total	**AG**	**75**	**75**	**39**	**33**	**18**	**21**	**1**	**0**	**3**	**2**	**1**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**1 991**	**100**
	GEN	**503**	**411**	**316**	**248**	**189**	**103**	**91**	**56**	**49**	**31**	**21**	**10**	**12**	**6**	**3**	**1**	**0**	**0**	**1**	**0**	**0**	**1 4126**	**100.0**

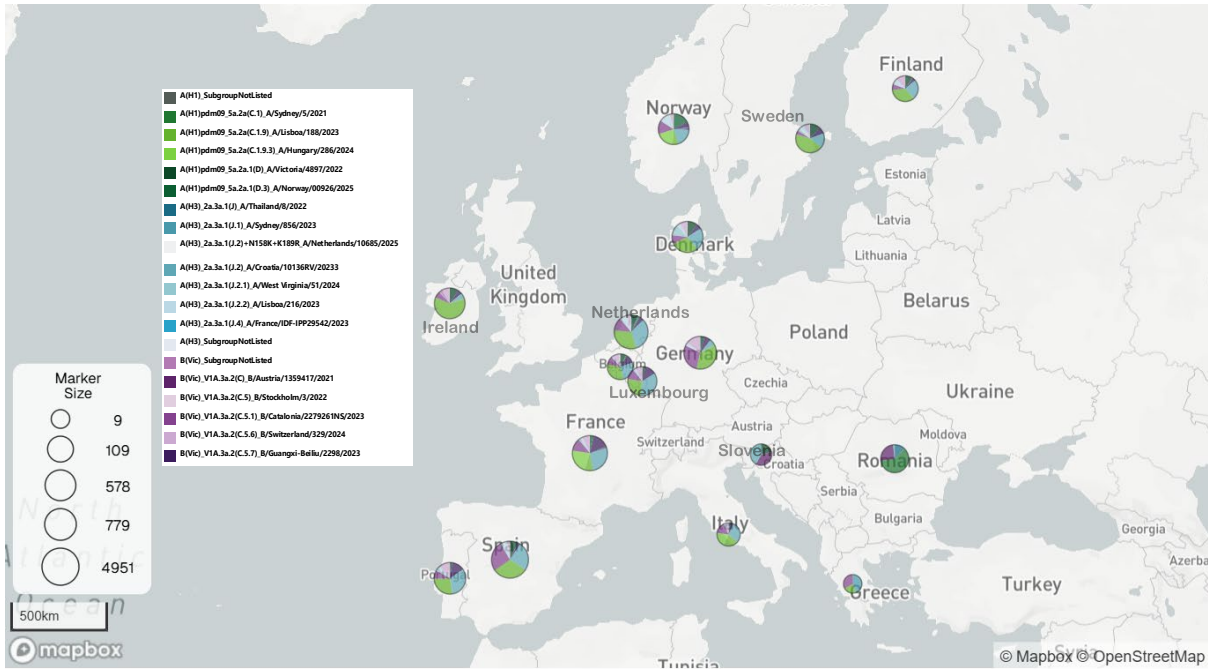
AG: antigenic characterisation; GEN: genetic characterisation.

Figure 8. Proportions of antigenic categories reported by countries, EU/EEA, week 40 2024 to week 33 2025



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

Figure 9. Proportions of genetic groups reported by countries, EU/EEA, week 40 2024 to week 33 2025



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

A(H1N1)pdm09 viruses

Antigenic characterisation

From week 40 2024 to week 33 2025, with latest data reported for week 22 2025, seven countries reported antigenic characterisation to TESSy for 821 A(H1N1)pdm09 influenza viruses. The countries that contributed were Germany (54.2%), France (32.3%), Denmark (5.4%), Romania (3.7%), Portugal (2.1%), Slovenia (1.6%) and Italy (0.9%). Countries were asked to report antigenic characterisation results according to the predefined categories described in Table 4.

Table 4. 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[a]	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[b]	6B.1A.5a.2a.1	5a.2a.1 (C.1.1)
agAH1/Victoria/4897/2022	A/Victoria/4897/2022-like [b]	6B.1A.5a.2a.1	5a.2a.1 (D)
agAH1NOCAT	None	None	None

[a] WHO recommended vaccine virus for the 2023 southern hemisphere influenza season.
[b] WHO recommended vaccine virus from the 2023–2024 northern hemisphere to the 2025 southern hemisphere influenza seasons.

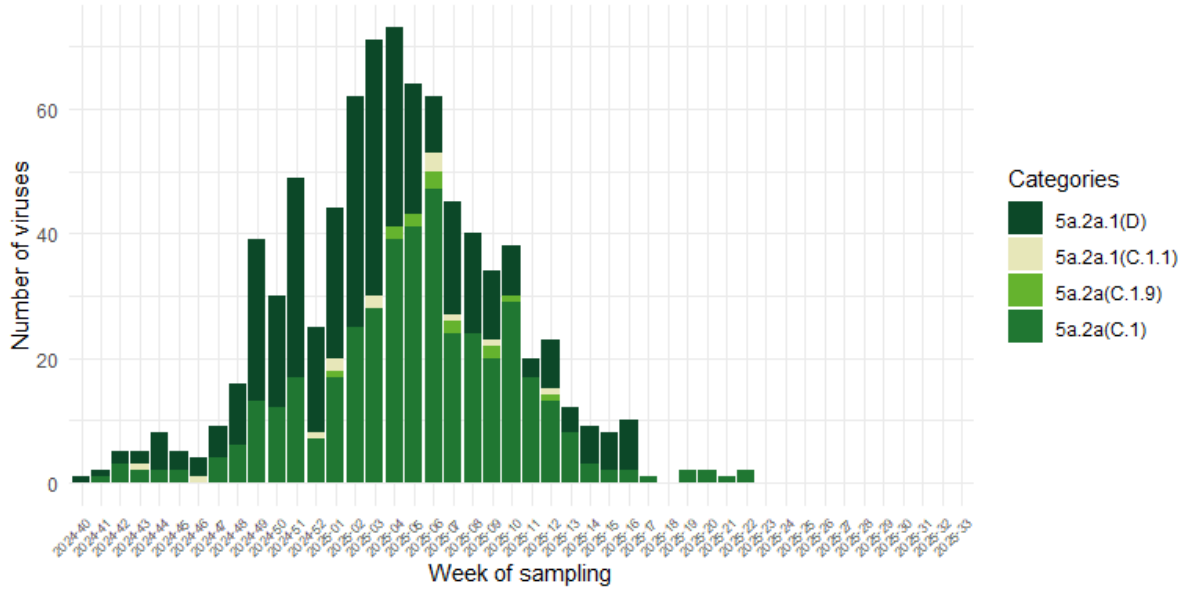
Among the 821 characterised A(H1)pdm09 viruses, the main reported categories were A/Sydney/5/2021-like, clade 5a.2a (C.1) and A/Victoria/4897/2022-like, clade 5a.2a.1 (D), representing 50.7% and 46%, respectively (Table 5).

Table 5. Number of viruses by A(H1)pdm09 antigenic reporting categories, EU/EEA, week 40 2024 to week 33 2025

Subclade	Virus of reference	N	%
5a.2a (C.1)	A/Sydney/5/2021-like[a]	416	50.7
5a.2a (C.1.9)	A/Lisboa/188/2023-like	14	1.7
5a.2a.1 (C.1.1)	A/Wisconsin/67/2022-like[b]	13	1.6
5a.2a.1 (D)	A/Victoria/4897/2022-like[b]	378	46.0

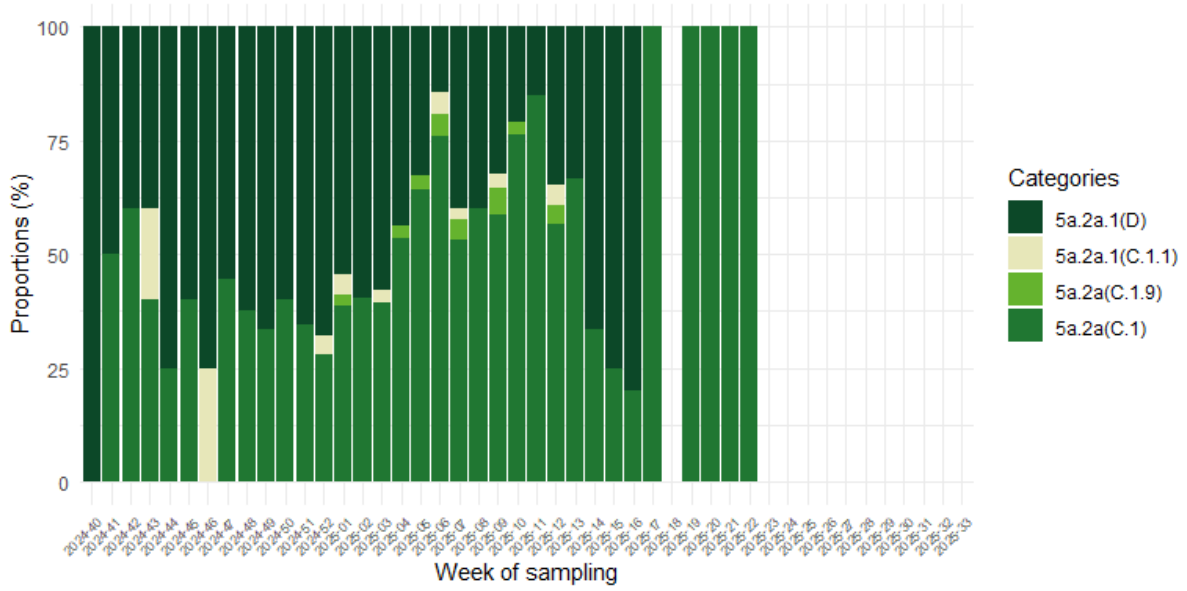
a WHO recommended vaccine virus for the 2023 southern hemisphere influenza season.
b WHO recommended vaccine virus from the 2023–2024 northern hemisphere to the 2025 southern hemisphere influenza seasons.

Figure 10. A(H1)pdm09 clade weekly distribution based on antigenic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Figure 11. A(H1)pdm09 clade weekly proportion based on antigenic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Genetic characterisation

From week 40 2024 to week 33 2025, with latest data reported for week 26 2025, 16 countries reported genetic characterisation to TESSy for 5 564 A(H1N1)pdm09 influenza viruses. The three main countries that contributed were Spain (33.5%), France (16.4%) and the Netherlands (12.0%).

Countries were asked to report genetic characterisation results in TESSy according to the predefined categories described in Table 6.

Table 6. Predefined genetic reporting categories for A(H1)pdm09 viruses

TESSy category	Virus of reference	Clade name	Subclade name
genAH1/Sydney/5/2021	A/Sydney/5/2021[a]	6B.1A.5a.2a	5a.2a (C.1)
genAH1/Netherlands/10468/2023	A/Netherlands/10468/2023	6B.1A.5a.2a	5a.2a (C.1)418V
genAH1/Michigan/62/2023	A/Michigan/62/2023	6B.1A.5a.2a	5a.2a (C.1.8)
genAH1/Lisboa/188/2023	A/Lisboa/188/2023	6B.1A.5a.2a	5a.2a (C.1.9)
genAH1/Hungary/286/2024	A/Hungary/286/2025	6B.1A.5a.2a	5a.2a (C.1.9.3)
genAH1/Victoria/4897/2022	A/Victoria/4897/2022[b]	6B.1A.5a.2a.1	5a.2a.1 (D)
genAH1/Norway/00926/2025	A/Norway/00926/2025	6B.1A.5a.2a.1	5a.2a.1 (D.3)
genAH1NOClade	None	None	None
genAH1SubgroupNotListed	Other	Other	Other

[a] *WHO recommended vaccine virus for the 2023 southern hemisphere influenza season.*
[b] *WHO recommended vaccine virus from the 2023–2024 northern hemisphere to the 2025 southern hemisphere influenza seasons.*

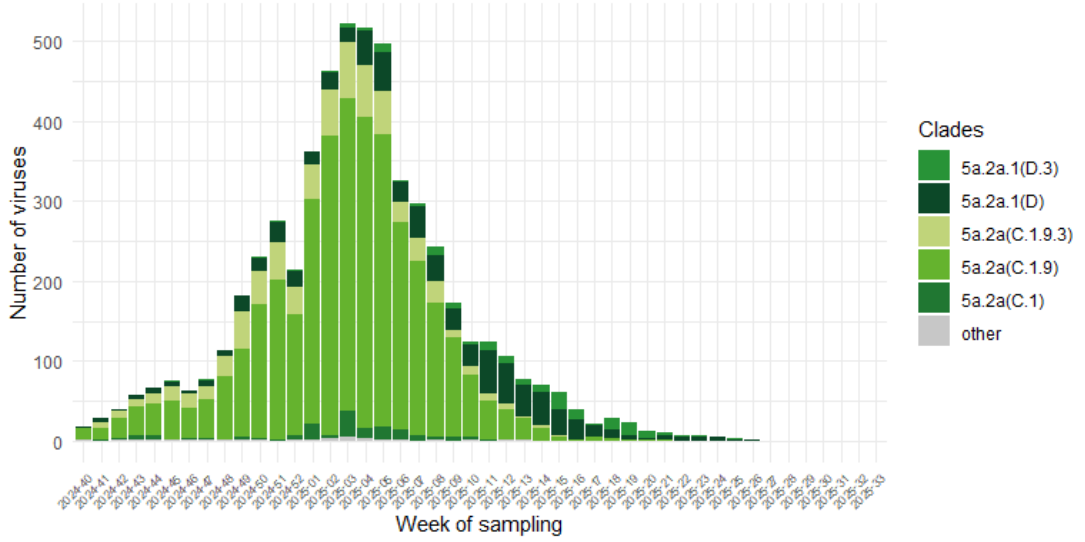
Among the 5 564 characterised A(H1)pdm09 viruses, the main reported categories were A/Lisboa/188/2023, clade 5a.2a(C.1.9), A/Victoria/4897/2022, clade 5a.2a.1(D) and A/Hungary/286/2025, clade 5a.2a(C.1.9.3), representing 67.6%, 13.2% and 12.5%, respectively (Table 7).

Table 7. Number of viruses by A(H1)pdm09 genetic reporting categories, EU/EEA, week 40 2024 to week 33 2025

Subclade	Virus of reference	N	%
5a.2a (C.1)	A/Sydney/5/2021[a]	157	2.8
5a.2a (C.1.9)	A/Lisboa/188/2023	3 762	67.6
5a.2a (C.1.9.3)	A/Hungary/286/2025	696	12.5
5a.2a.1 (D)	A/Victoria/4897/2022[b]	734	13.2
5a.2a.1 (D.3)	A/Norway/00926/2025	177	3.2
Other	Other	38	0.7

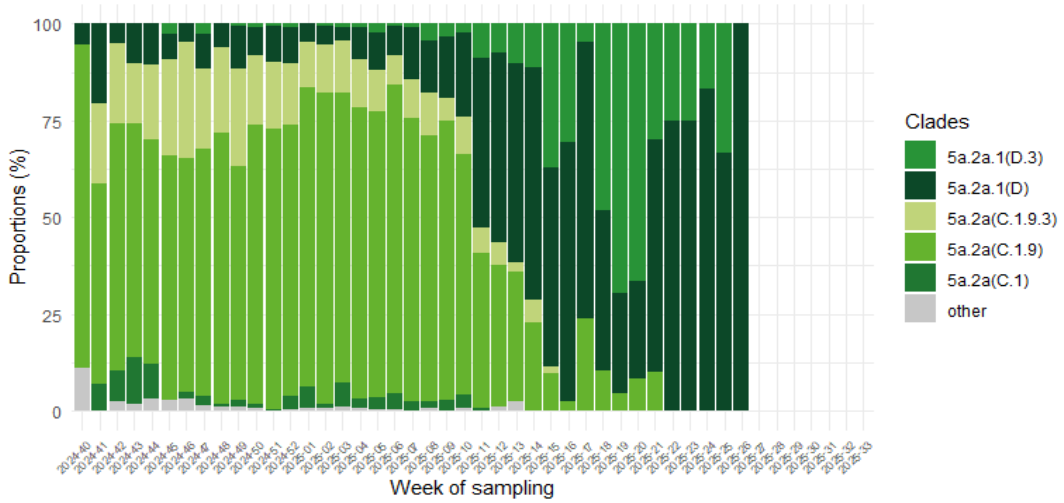
[a] *WHO recommended vaccine virus for the 2023 southern hemisphere influenza season.*
[b] *WHO recommended vaccine virus from the 2023–2024 northern hemisphere to the 2025 southern hemisphere influenza seasons.*

Figure 12. A(H1)pdm09 clade weekly distribution based on genetic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Figure 13. A(H1)pdm09 clade weekly proportion based on genetic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Phylogenetic analysis

From week 40 2024 to week 33 2025, a total of 5 572 A(H1)pdm09 HA sequences from 17 countries were reported, retrieved and included in the analyses (Figure 14). Countries that reported HA sequences are shown in Annex 3, Table 6A. There were 12 sequences that failed Nextstrain's quality control and were excluded from the phylogenetic tree (please see subsampled tree in Figure 14 and full tree svg files at https://www.ecdc.europa.eu/en/publications-data/influenza-virus-characteristics-week-40-2024-week-33-2025).

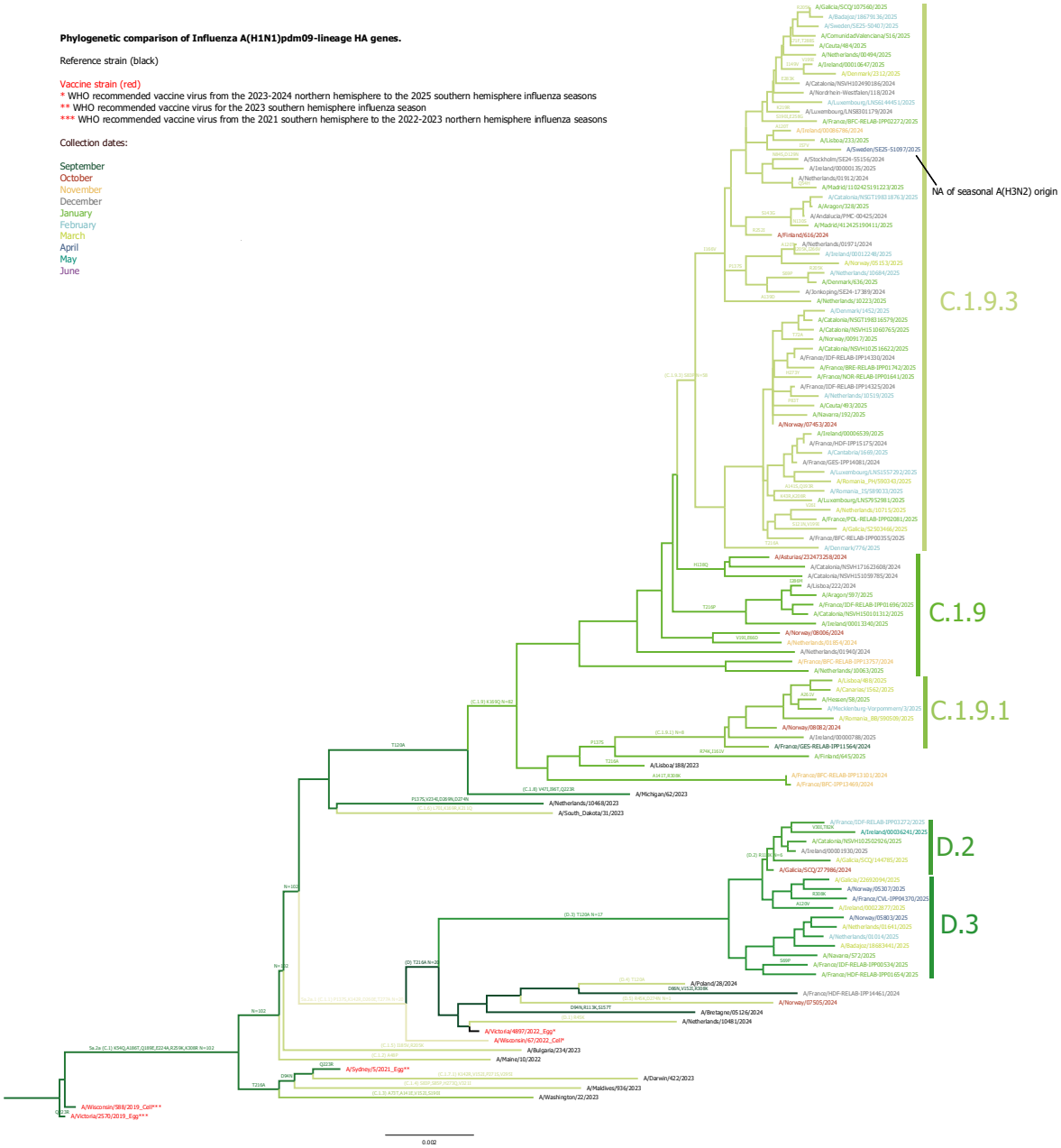
All A(H1)pdm09 viruses fell into the branch of clade 5a.2a, which is defined by the amino acid substitutions K54Q, A186T, Q189E, E224A, R259K and K308R compared with 5a.2 former (NH 2022/23) vaccine strain A/Wisconsin/588/2019_Cell and represented by A/Sydney/5/2021_Egg (SH 2023 vaccine strain).

All (4 648, 83.6%) viruses within clade 5a.2a (subclade C.1) carried the T120A and K169Q that define subclade C.1.9, represented by A/Lisboa/188/2023. The majority of 5a.2a (4 062, 87%) fell into subclade C.1.9.3, defined by S83P and 335 (7.2%) fell into subclade C.1.9.1 with the P137S amino-acid substitution that is not represented by any reference strain. The reassortant virus A/Sweden/SE25-51097/2025 with an NA of seasonal A(H3N2) origin belonged to subclade C.1.9.3 and closely related strains have no indications of reassortment.

Of the viruses within clade 5a.2a, 912 (16%) were further characterised into clade 5a.2a.1 subclade D that has the additional T216A amino acid substitution and is represented by A/Victoria/4897/2022_Egg, the NH 2024-25 vaccine strain for egg-based vaccines. Within the genetic diversification of subclade D, most carried T120A and belonged to D.3 (631; 69%) and 177 (19%) carried R113K that defines subclade D.2. Few 5a.2a.1 viruses fell into subclades D.5 (32; 3.5%) and D.1 (18; 2.0%), both having R45K. Two (0.2%) viruses belonged to subclade D.4 represented by A/Poland/28/2024. No viruses fell into subclade C.1.1, represented by A/Wisconsin/67/2022_Cell, NH 2024–25 vaccine strain for cell culture- or recombinant-based vaccines.

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 only differed for nine of 5 496 viruses and 5 449 (>99%) of these were also concordant at the subclade level.

Figure 14. 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 at: https://www.ecdc.europa.eu/en/publications-data/influenza-virus-characteristics-week-40-2024-week-33-2025).

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 546 A(H1N1)pdm09 viruses that had both genetic and antigenic data reported, the majority (332; 61%) were reported antigenically as 5a.2a.1 subclade D A/Victoria/4897/2022-like, the NH 2024-25 egg-based vaccine strain (Annex 1, Table 4A). Of these, nearly half (148; 45%) were reported as genetic subgroup 5a.2a subclade C.1.9.3 represented by A/Hungary/286/2024, while 129 viruses (39%) were assigned to the subclade C.1.9 A/Lisboa/188/2023.

Another large group of A(H1N1)pdm09 viruses (190; 35%) were antigenically assigned as 5a.2a subclade C.1 A/Sydney/5/2021-like. The majority of these (141; 74%) were genetically assigned as 5a.2a subclade C.1.9 represented by A/Lisboa/188/2023.

Only 11 A(H1N1)pdm09 viruses were reported as antigenically similar to A/Wisconsin/67/2022, the NH 2024–25 vaccine strain for cell culture- or recombinant-based vaccines, and eight of those were assigned genetically as A/Lisboa/188/2023 and three as A/Victoria/4897/2022.

Antiviral susceptibility

From week 40 2024 to week 33 2025, with latest data reported for week 25 2025, 5 293 A(H1N1)pdm09 influenza viruses were assessed genotypically and/or phenotypically for susceptibility to at least one drug (oseltamivir, zanamivir or baloxavir marboxil) by 17 countries. The three main countries that contributed were Spain (34.6%), France (17.2%) and the Netherlands (12.6%).

Regarding the susceptibility to neuraminidase inhibitors, eight countries performed a phenotypic assessment: France, Germany, Italy, the Netherlands, Poland, Portugal, Romania and Spain. Reduced and highly reduced inhibition by oseltamivir was observed for two (0.6%) and four (1.3%) of the 317 tested A(H1N1)pdm09 viruses (Table 8). The susceptibility of the remaining 4 690 viruses was assessed genetically based on the presence of substitutions in the neuraminidase known to be associated with reduced inhibition. Substitutions associated with reduced and highly reduced inhibition by oseltamivir were observed for four (<0.1%; associated with NA_D199Y/E or NA_I223T/K) and 25 (0.5%; associated with NA_H275Y) viruses, respectively (Annex 2). For zanamivir, substitutions associated with reduced inhibition were observed for one (<0.1%; associated with NA_D199Y) of the 4 714 assessed viruses (Annex 2).

Table 8. Number of A(H1N1)pdm09 viruses, by reporting categories, for neuraminidase inhibitor susceptibility, EU/EEA, week 40 2024 to week 33 2025

Antiviral	Phenotypic			Genotypic		
	NI	RI	HRI[a]	AANI	AARI[b]	AAHRI[a]
Oseltamivir	311	2	4	4 661	4	25
Zanamivir	292	0	0	4 713	1	0

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 substitution related to highly reduced susceptibility was NA_H275Y.
[b] The substitutions related to reduced susceptibility were NA_D199Y or NA_D199E or NA_I223T or NA_I223K.

The susceptibility to polymerase inhibitors was assessed genetically based on the presence of substitutions in the PA polymerase subunit that are known to confer reduced susceptibility. Sequencing data of the PA gene were reported by 14 countries; the three main contributors were France, the Netherlands and Spain. Of the 3 048 assessed A(H1N1)pdm09 viruses, substitutions associated with reduced susceptibility (PA_E199G or PA_A37T) were observed for two (<0.1%) viruses (Table 9, Annex 2).

Table 9. Number of A(H1N1)pdm09 viruses, by reporting categories, for baloxavir marboxil susceptibility, EU/EEA, week 40 2024 to week 33 2025

Antiviral	Genotypic		Total
	AANS	AARSa	
Baloxavir	3 046	2	3 048

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_E199G or PA_A37T.

A(H3N2) viruses

Antigenic characterisation

From week 40 2024 to week 33 2025, with latest data reported for week 31 2025, seven countries reported antigenic characterisation to TESSy for 486 A(H3N2) influenza viruses. The countries that contributed were France (39.3%), Germany (36.2%), Denmark (10.3%), Portugal (4.9%), Slovenia (4.7%), Belgium (2.3%) and Romania (2.3%).

Countries were asked to report antigenic characterisation results in TESSy according to the predefined categories described in Table 10.

Table 10. 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[a]	3C.2a1b.2a	2a(G1)
agAH3/Thailand/8/2022	A/Thailand/8/2022-like[b]	3C.2a1b.2a.3a.1	2a.3a.1(J)
agAH3/Croatia/10136RV/2023	A/Croatia/10136RV/2023-like[c]	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)158K189R
agAH3/France/IDF-IPP29542/2023	A/France/IDF-IPP29542/2023-like	3C.2a1b.2a.3a.1	2a.3a.1(J.4)
agAH3NOCAT	None	None	None

[a] WHO recommended vaccine virus from the 2022 southern hemisphere to the 2023–2024 northern hemisphere influenza seasons.
[b] WHO recommended vaccine virus from the 2024 southern hemisphere to the 2024–2025 northern hemisphere influenza seasons.
[c] WHO recommended vaccine virus for the 2025 southern hemisphere influenza season (Trivalent vaccine).

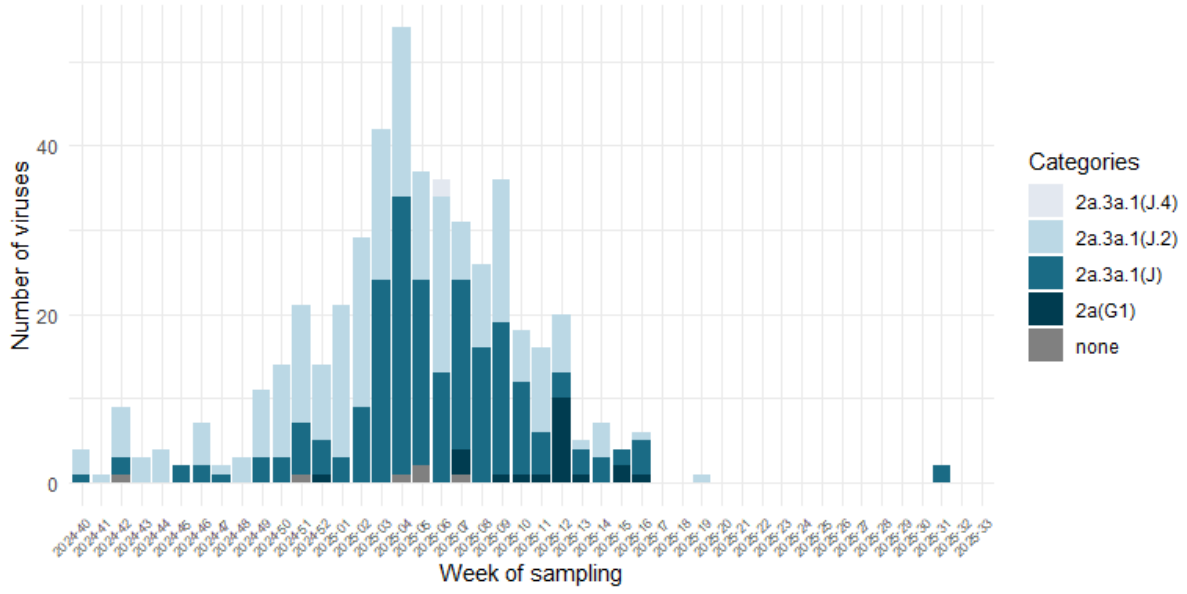
Among the 486 characterised A(H3) viruses, the main reported categories were A/Croatia/10136RV/2023-like, clade 2a.3a.1(J.2) and A/Thailand/8/2022-like, clade 2a.3a.1(J), representing 49.8% and 44.2%, respectively (Table 11).

Table 11. Number of viruses by A(H3) antigenic reporting categories, EU/EEA, week 40 2024 to week 33 2025

Subclade	Virus of reference	N	%
2a(G1)	A/Darwin/9/2021-like[a]	21	4.3
2a.3a.1(J)	A/Thailand/8/2022-like[b]	215	44.2
2a.3a.1(J.2)	A/Croatia/10136RV/2023-like[c]	242	49.8
2a.3a.1(J.4)	A/France/IDF-IPP29542/2023-like	2	0.4
None	None	6	1.2

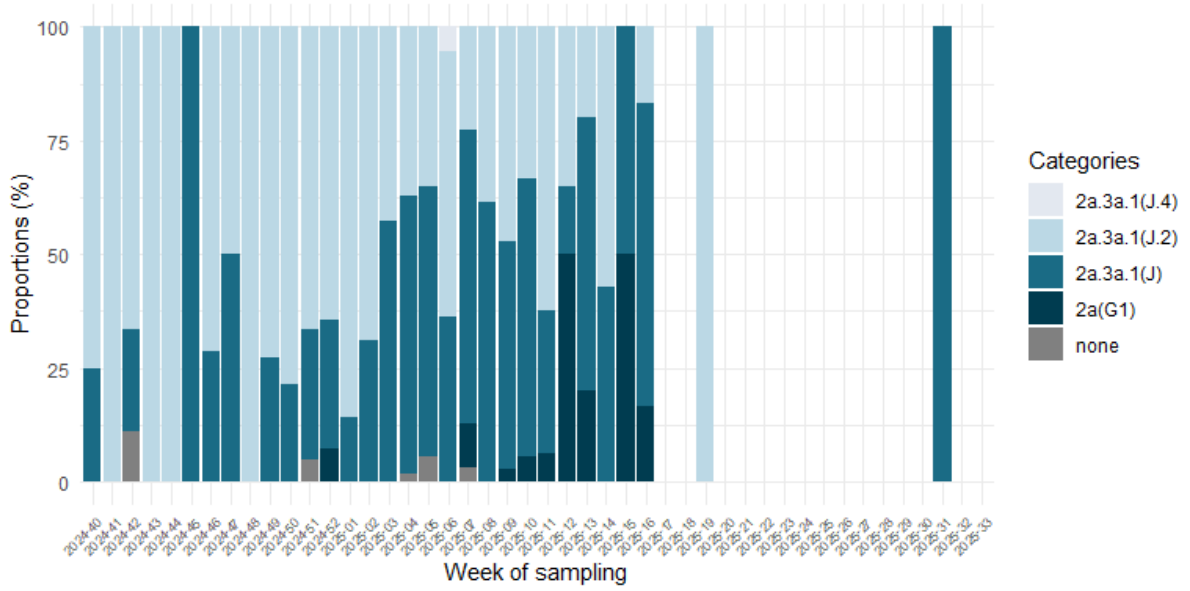
[a] WHO recommended vaccine virus from the 2022 southern hemisphere to the 2023–2024 northern hemisphere influenza seasons.
[b] WHO recommended vaccine virus from the 2024 southern hemisphere to the 2024–2025 northern hemisphere influenza seasons.
[c] WHO recommended vaccine virus for the 2025 southern hemisphere influenza season (Trivalent vaccine).

Figure 15. A(H3N2) clade weekly distribution based on antigenic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Figure 16. A(H3) clade weekly proportion based on antigenic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Genetic characterisation

From week 40 2024 to week 33 2025, with latest data reported for week 29 2025, 16 countries reported genetic characterisation to TESSy for 4 272 A(H3N2) influenza viruses. The three main countries that contributed were Spain (36.5%), France (18.7%) and the Netherlands (16.5%).

Countries were asked to report genetic characterisation results in TESSy according to the predefined categories described in Table 12.

Table 12. Predefined genetic reporting categories for A(H3) viruses

TESSy category	Virus of reference	Clade name	Subclade name
genAH3/Darwin/9/2021	A/Darwin/9/2021[a]	3C.2a1b.2a	2a(G1)
genAH3/Thailand/8/2022	A/Thailand/8/2022[b]	3C.2a1b.2a.3a.1	2a.3a.1(J)
genAH3/Sydney/856/2023	A/Sydney/856/2023	3C.2a1b.2a.3a.1	2a.3a.1(J.1)
genAH3/Croatia/10136RV/2023	A/Croatia/10136RV/2023[c]	3C.2a1b.2a.3a.1	2a.3a.1(J.2)
genAH3/Netherlands/10685/2024	A/Netherlands/10685/2024	3C.2a1b.2a.3a.1	2a.3a.1(J.2)158K189R
genAH3/West Virginia/51/2024	A/West Virginia/51/2024	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/France/IDF-IPP29542/2023	A/France/IDF-IPP29542/2023	3C.2a1b.2a.3a.1	2a.3a.1(J.4)
genAH3NOClade	None	None	None
genAH3SubgroupNotListed	Other	Other	Other

[a] WHO recommended vaccine virus from the 2022 southern hemisphere to the 2023–2024 northern hemisphere influenza seasons.
[b] WHO recommended vaccine virus from the 2024 southern hemisphere to the 2024–2025 northern hemisphere influenza seasons.
[c] WHO recommended vaccine virus for the 2025 southern hemisphere influenza season (Trivalent vaccine).

Among the 4 272 characterised A(H3) viruses, the main reported categories were A/Croatia/10136RV/2023, clade 2a.3a.1(J.2) and A/Lisboa/216/2023, clade 2a.3a.1(J.2.2), representing 78.3% and 13.5%, respectively (Table 13).

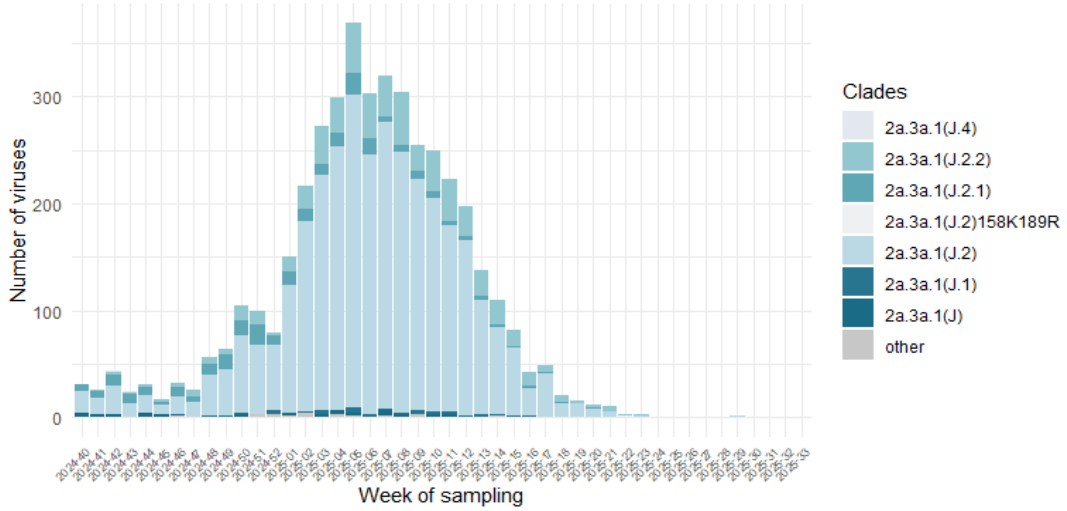
Three countries reported nineteen A(H3) viruses as 'Subgroup not listed'. Sequence information was available for all of these viruses, 15 of which clustered within subclade G.1.3.1 and four within subclade J.1.1.

Table 13. Number of viruses by A(H3) genetic reporting categories, EU/EEA, week 40 2024 to week 33 2025

Subclade	Virus of reference	N	%
2a.3a.1(J)	A/Thailand/8/2022[a]	43	1.0
2a.3a.1(J.1)	A/Sydney/856/2023	39	0.9
2a.3a.1(J.2)	A/Croatia/10136RV/2023[b]	3 343	78.3
2a.3a.1(J.2)158K189R	A/Netherlands/10685/2025	2	0.0
2a.3a.1(J.2.1)	A/West Virginia/51/2024	247	5.8
2a.3a.1(J.2.2)	A/Lisboa/216/2023	576	13.5
2a.3a.1(J.4)	A/France/IDF-IPP29542/2023	3	0.1
Other	Other	19	0.4

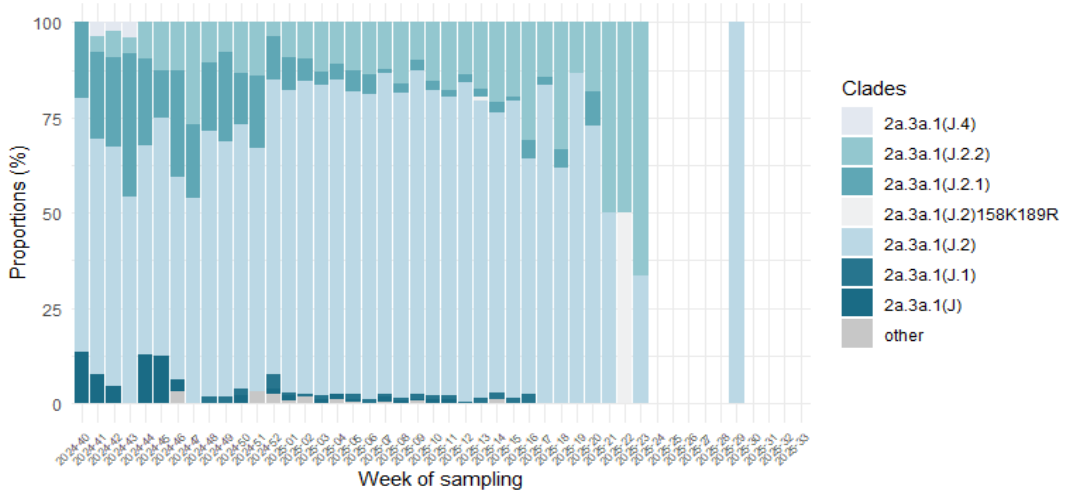
[a] WHO recommended vaccine virus from the 2024 southern hemisphere to the 2024–2025 northern hemisphere influenza seasons.
[b] WHO recommended vaccine virus for the 2025 southern hemisphere influenza season (Trivalent vaccine).

Figure 17. A(H3) clade weekly distribution based on genetic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Figure 18. A(H3) clade weekly proportion based on genetic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Phylogenetic analysis

From week 40 2024 to week 33 2025, a total of 4 279 A(H3) HA sequences from 17 countries were reported, retrieved and included in the analyses (Figure 19). Countries that reported HA sequences are shown in Annex 3, Table 6A. There were two sequences that failed Nextstrain's quality control and were excluded from the phylogenetic tree (please see subsampled and full tree svg files at https://www.ecdc.europa.eu/en/publications-data/influenza-virus-characteristics-week-40-2024-week-33-2025).

All A(H3) HA sequences fell into 2a.3, which is defined by D53N, N96S (addition of potential N-glycosylation site) and I192F amino acid substitutions compared with 2023–2024 NH influenza season vaccine strain A/Darwin/9/2021_Egg. Within 2a.3, all fell into 2a.3a defined by E50K compared with 2a.3 representative virus A/Norway/24873/2021. Of these, most (4 263; >99%) fell into clade 2a.3a.1 (J) characterised by I140K and I223V and represented by NH 2024-2025 egg-based vaccine strain A/Thailand/8/2022_Egg.

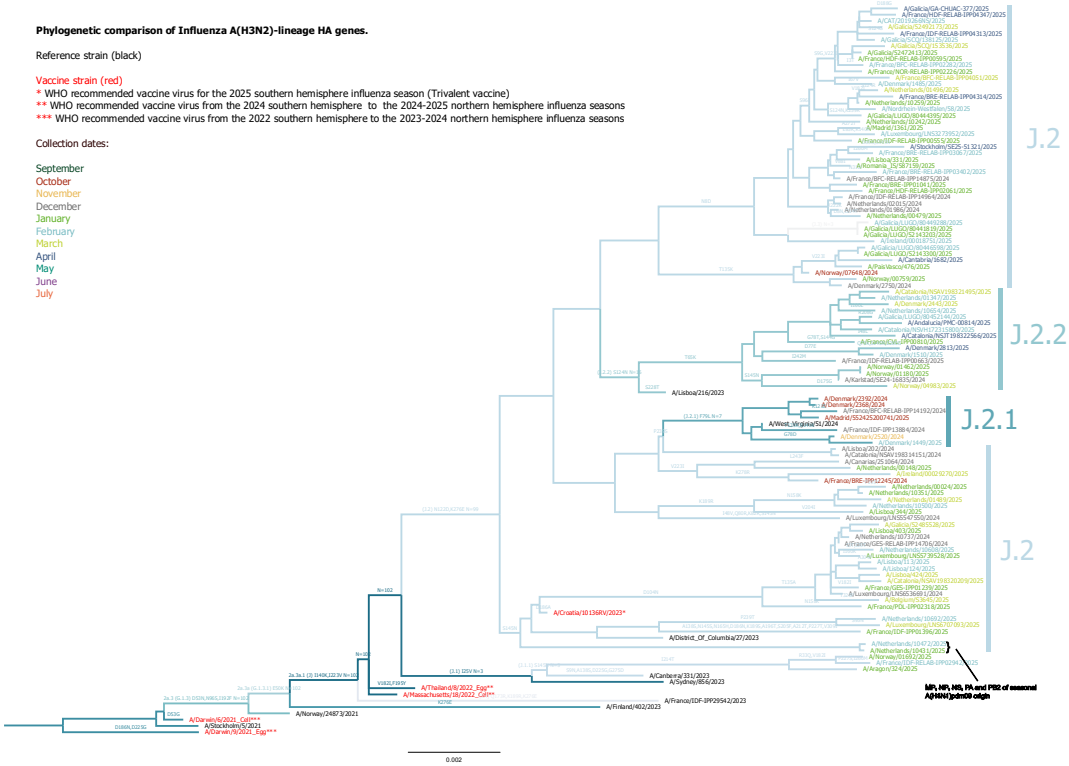
Within clade 2a.3a.1, 3 321 (78%) fell into subclade J.2 defined by N122D and K276E compared with NH 2024–2025 cell culture- or recombinant-based vaccine strain A/Massachusetts/18/2022_Cell, represented by SH 2025 vaccine strain A/Croatia/10136RV/2023. Additional diversification on the J.2 branch occurred with 1 880 viruses that had acquired an N8D mutation and were assigned as subclade J.2.2 (591; 14%), defined by S124N and represented by A/Lisboa/216/2023, and as subclade J.2.1 (208; 4.9%), defined by P239S, carrying F79L and represented by A/West_Virginia/51/2024.

Within J.2, 115 viruses had acquired the combination of N158K and K189R. Most were from the Netherlands, but there were also a few detections from Spain (6), Denmark (1), France (1), Germany (2), Norway (1) and Sweden (1). One virus within 2a.3a.1 belonged to subclade J.1 with I25V and 44 (1.0%) belonged to J.1.1 that has S145N in addition I25V. Four (<1%) viruses within 2a.3a.1 fell into subclade J.4, represented by A/France/IDF-IPP29542/2023 characterised by Q173R, K189R and K276E. Two reassortant viruses from the Netherlands with MP, NP, NS, PA and PB2 of seasonal A(H1N1)pdm09 origin fell into a subbranch within J.2.

Fifteen viruses belonged to 2a.3b, subclade G.1.3.1, represented by A/Finland/402/2023.

For the 4 249 viruses of A(H3) with reported clade, all were concordant with the assigned clade and 4 112 (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 files at https://www.ecdc.europa.eu/en/publications-data/influenza-virus-characteristics-week-40-2024-week-33-2025).

Match between antigenic and genetic characterisations

Of the 364 A(H3N2) viruses that had both genetic and antigenic data reported, the majority (214; 59%) were antigenically A/Croatia/10136RV/2023-like, representing the egg-based vaccine component for the upcoming NH 2025–26 season and distinct from the current season vaccine A/Thailand/8/2022-like viruses. The majority of these (171; 80%) were assigned genetically to homologous J.2 subclade with 22 additional viruses (10%) assigned as subclade J.2.2 A/Lisboa/216/2023, 19 (9%) as subclade J.2.1 A/West Virginia/51/2024, one as subclade J.4 A/France/IDF-IPP29542/2023 and one that could not be assigned to any of the predefined subclades.

In addition, 133 (37%) of the A(H3N2) viruses were reported antigenically as A/Thailand/8/2022-like, representing the NH egg-based vaccine strain for season 2024–25 (Table Annex 1, Table 4A). However, genetically, these viruses were assigned across five different clade 2a.3a.1 J-subclades: 86 (65%) as J.2 A/Croatia/10136RV/2023, 31 (23%) as J.2.2 A/Lisboa/216/2023, eight (6%) as J.2.1 A/West Virginia/51/2024, six (5%) as homologous J A/Thailand/8/2022 and two (2%) as J.1 A/Sydney/856/2023.

Six A(H3N2) viruses were reported antigenically without category but were genetically similar to J.2 A/Croatia/10136RV/2023.

Antiviral susceptibility

From week 40 2024 to week 33 2025, with latest data reported for week 29 2025, 4 267 A(H3N2) influenza viruses were assessed genotypically and/or phenotypically for susceptibility to at least one drug (oseltamivir, zanamivir or baloxavir marboxil) by 17 countries. The three main countries that contributed were Spain (35.2%), France (18.6%) and the Netherlands (16.5%).

Eight countries performed a phenotypic assessment of susceptibility to neuraminidase inhibitors: France, Germany, Italy, the Netherlands, Poland, Portugal, Romania and Spain. Reduced inhibition to oseltamivir and zanamivir was observed for four (1.3%) of the 298 and one (<0.5%) of the 292 tested A(H3N2) viruses, respectively (Table 14). The susceptibility of the remaining viruses was assessed genetically based on the presence of substitutions in the neuraminidase known to be associated with reduced inhibition. Substitutions associated with reduced and highly reduced inhibition by oseltamivir was observed for 12 (0.3%, associated with NA_S331R and NA_K249E) and 3 (0.1%, associated with NA_E119V) of the 3 930 viruses that could be assessed (Annex 2). Reduced inhibition by zanamivir was observed for 10 (0.3%, associated with NA_S331R) among the 3 936 viruses that could be assessed (Annex 2).

Table 14. Number of A(H3N2) viruses, by reporting categories, for neuraminidase inhibitor susceptibility, EU/EEA, week 40 2024 to week 33 2025

Antiviral	Phenotypic		Genotypic			Total
	NI	RI	AANI	AARI[a]	AAHRI[b]	
Oseltamivir	294	4	3 915	12	3	4 228
Zanamivir	291	1	3 926	10	0	4 228

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 and NA_K249E.*

[b] *The substitution related to highly reduced susceptibility was NA_E119V.*

The susceptibility to polymerase inhibitors was assessed genetically based on the presence of substitutions in the PA polymerase subunit known to confer reduced susceptibility. Sequencing data were reported by 14 countries; the three main contributors were France, the Netherlands and Spain. Of the 2 593 assessed A(H3N2) viruses, substitutions associated with reduced susceptibility were observed for three (0.1%, associated with PA_I38M; Table 15, Annex 2).

Table 15. Number of A(H3N2) viruses, by reporting categories, for baloxavir marboxil susceptibility, EU/EEA, week 40 2024 to week 33 2025

Antiviral	Genotypic		Total
	AANS	AARS[a]	
Baloxavir	2 590	3	2 593

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_I38M.*

B/Victoria lineage viruses

Antigenic characterisation

From week 40 2024 to week 33 2025, with latest data reported for week 16 2025, six countries reported antigenic characterisation to TESSy for 684 B(Victoria) influenza viruses: Germany (62.9%), France (26.6%), Denmark (6.1%), Portugal (2.2%), Romania (1.9%) and Italy (0.3%).

Countries were asked to report antigenic characterisation results in TESSy according to the predefined categories described in Table 16.

Table 16. 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

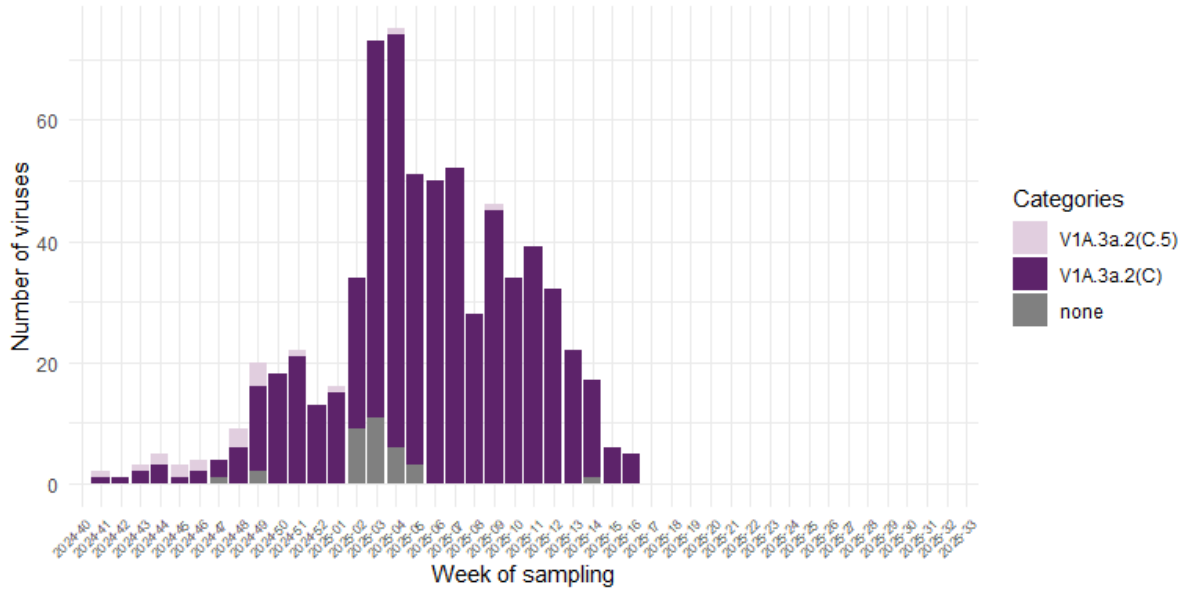
[a] *WHO recommended vaccine virus from the 2022–2025 southern hemisphere influenza seasons.*

Among the 684 characterised B(Victoria) viruses, the main reported category was B/Austria/1359417/2021-like, clade V1A.3a.2(C), representing 92.4% (Table 17).

Table 17. Number of viruses by B(Victoria) antigenic reporting categories, EU/EEA, week 40 2024 to week 33 2025

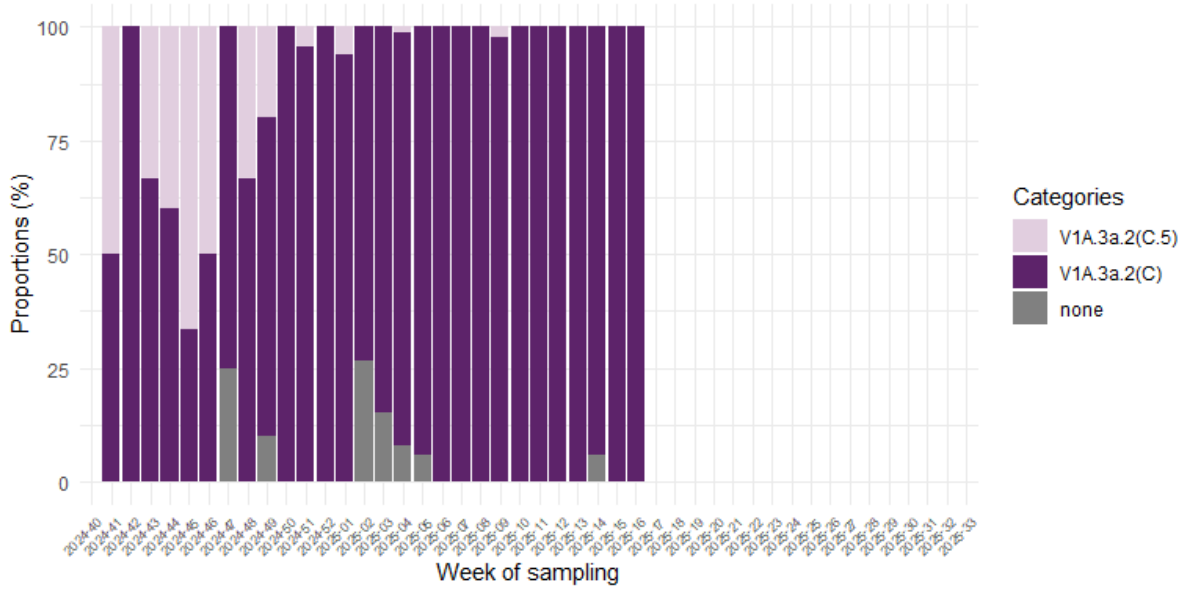
Subclade	Virus of reference	N	%
V1A.3a.2(C)	B/Austria/1359417/2021-like	632	92.4
V1A.3a.2(C.5)	B/Stockholm/3/2022-like	19	2.8
None	None	33	4.8

Figure 20. B(Victoria) clade weekly distribution based on antigenic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Figure 21. B(Victoria) clade weekly proportion based on antigenic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Genetic characterisation

From week 40 2024 to week 33 2025, with latest data reported for week 23 2025, 16 countries reported genetic characterisation to TESSy for 4 287 B(Victoria) influenza viruses. The three main countries that contributed were: Spain (35.7%), France (20.3%) and Germany (13.3%).

Countries were asked to report genetic characterisation results in TESSy according to the predefined categories described in Table 18.

Table 18. Predefined genetic reporting categories for B(Victoria) viruses

TESSy category	Virus of reference	Clade name	Subclade name
genBVicB/Washington/02/2019	B/Washington/02/2019	V1A.3	V1A.3(A.3.2)
genBVicB/Austria/1359417/2021	B/Austria/1359417/2021[a]	V1A.3a.2	V1A.3a.2(C)
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/Guangxi-Beiliu/2298/2023	B/Guangxi-Beiliu/2298/2023	V1A.3a.2	V1A.3a.2(C.5.7)
genBVicNOClade	None	None	None
genBVicSubgroupNotListed	Other	Other	Other

[a] *WHO recommended vaccine virus from the 2022–2025 southern hemisphere influenza seasons.*

Among the 4 287 characterised B(Victoria) viruses, all belonged to clade V1A.3a.2 and the main reported categories were B/Catalonia/2279261NS/2023, clade V1A.3a.2(C.5.1), B/Guangxi-Beiliu/2298/2023, clade V1A.3a.2(C.5.7), and B/Switzerland/329/2024, clade V1A.3a.2(C.5.6), representing 57.7%, 21.5% and 18.2%, respectively (Table 19).

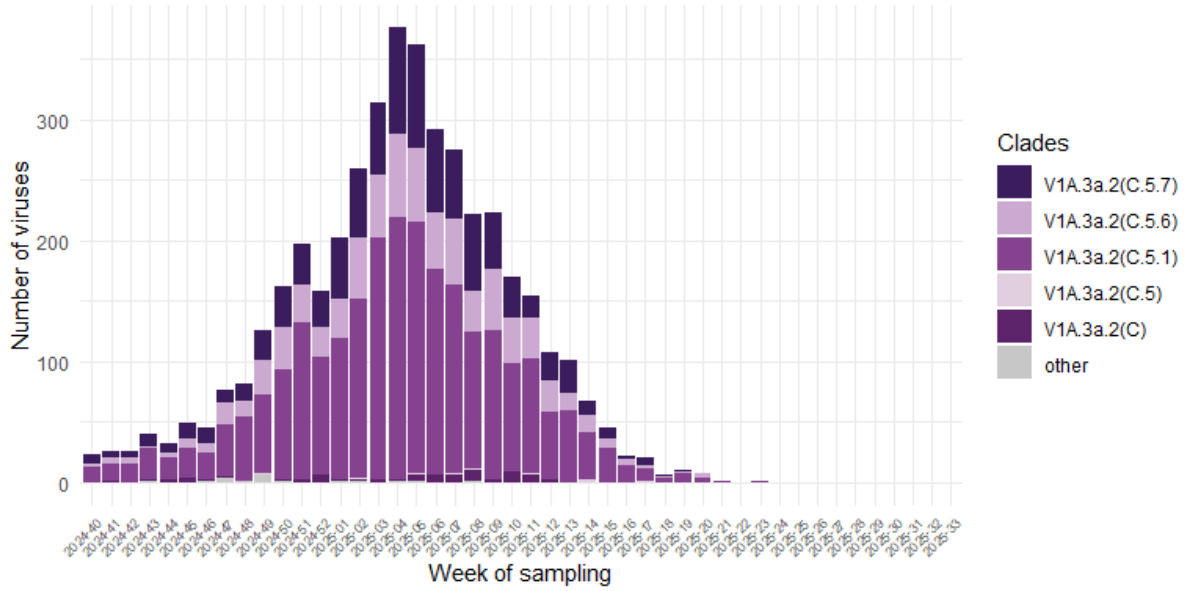
Nineteen B(Victoria) viruses were reported as 'Subgroup not listed' and all of them had sequence information available. Thirteen belonged to V1A.3a.2 subclade C.5.7., three to subclade C.5.1 and two to subclade C.3. One was unassigned due to poor sequence quality.

Table 19. Number of viruses by B(Victoria) genetic reporting categories, EU/EEA, week 40 2024 to week 33 2025

Clade	Virus of reference	N	%
V1A.3a.2(C)	B/Austria/1359417/2021[a]	78	1.8
V1A.3a.2(C.5)	B/Stockholm/3/2022	17	0.4
V1A.3a.2(C.5.1)	B/Catalonia/2279261NS/2023	2 473	57.7
V1A.3a.2(C.5.6)	B/Switzerland/329/2024	779	18.2
V1A.3a.2(C.5.7)	B/Guangxi-Beiliu/2298/2023	921	21.5
Other	Other	19	0.4

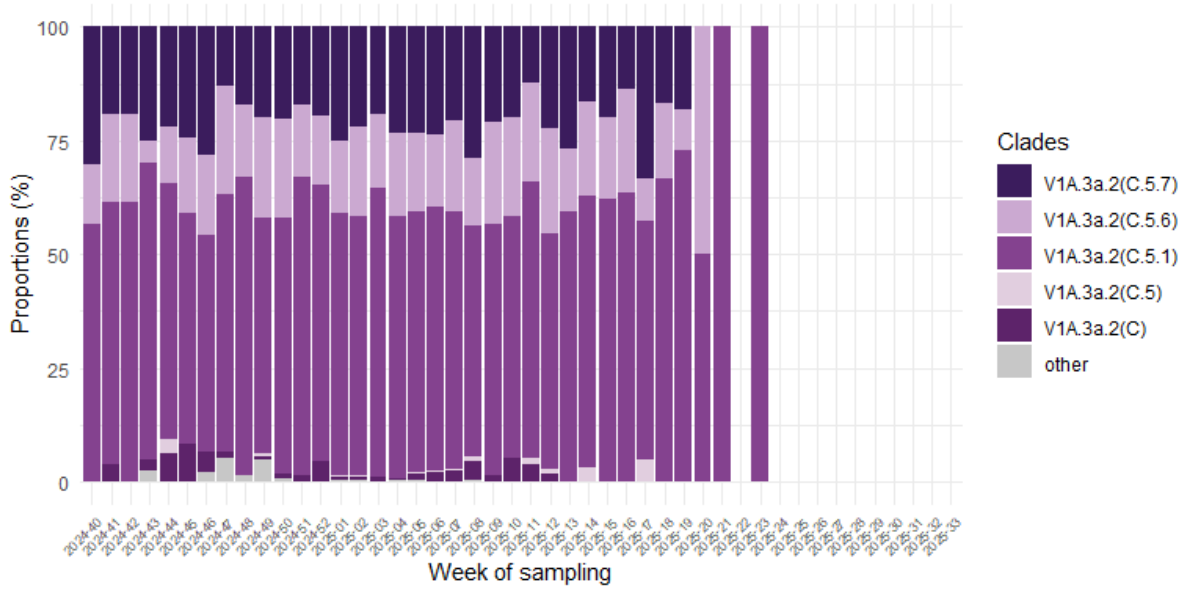
[a] *WHO recommended vaccine virus from the 2022–2025 southern hemisphere influenza seasons.*

Figure 22. B(Victoria) clade weekly distribution based on genetic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Figure 23. B(Victoria) clade weekly proportion based on genetic characterisation, EU/EEA, week 40 2024 to week 33 2025



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

Phylogenetic analysis

From week 40 2024 to week 33 2025, a total of 4 292 B/Victoria HA sequences from 17 countries were reported, retrieved and included in the analyses (Figure 24). Countries that reported HA sequences are shown in Annex 3, Table 6A. There were 17 sequences that failed Nextstrain's quality control and were excluded from the phylogenetic tree (please see subsampled and full tree svg files at: https://www.ecdc.europa.eu/en/publications-data/influenza-virus-characteristics-week-40-2024-week-33-2025).

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.

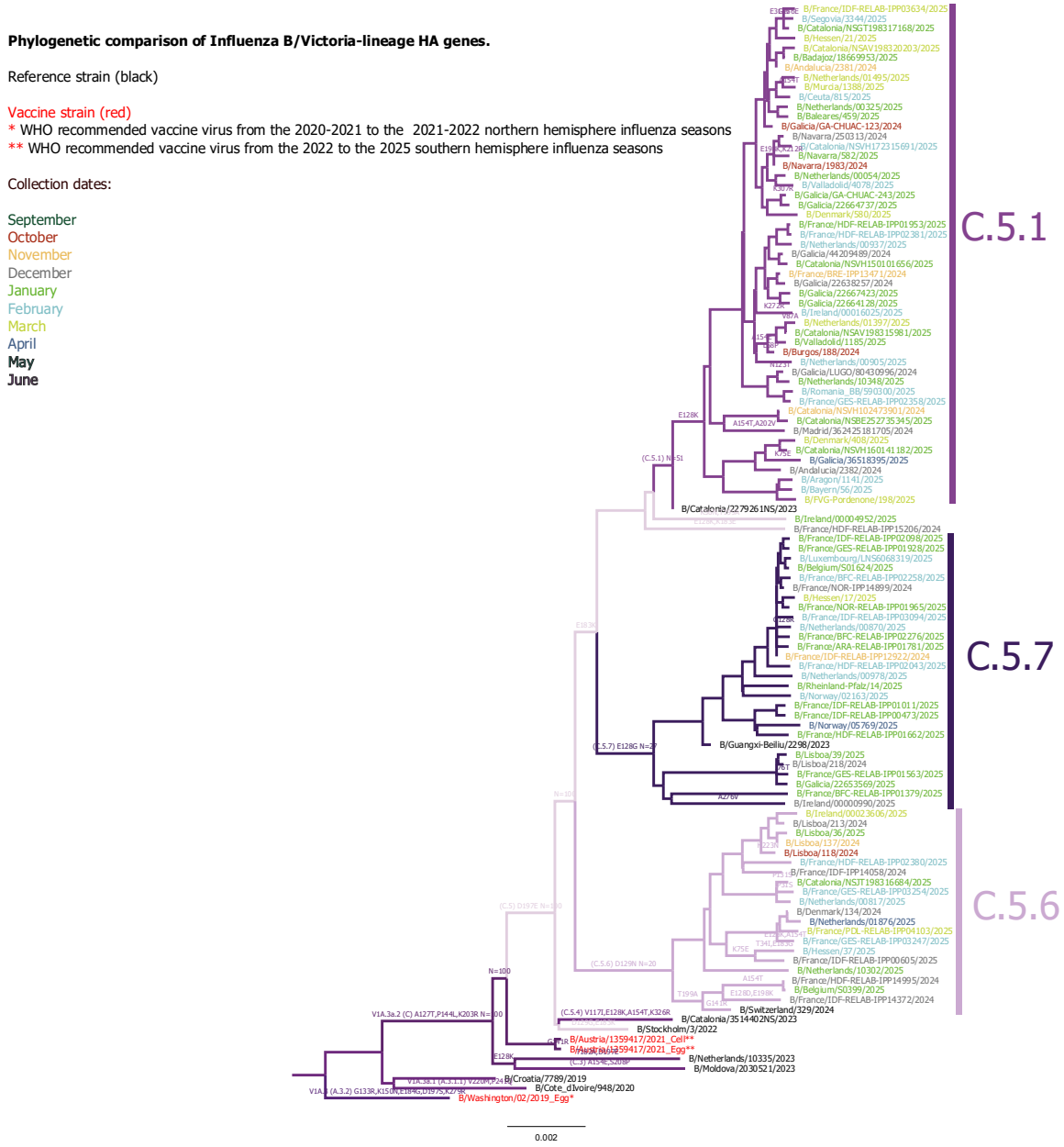
A majority (2 494; 58%) of the viruses within 3a.2 fell in a branch with E128K in subclade C.5.1. This was followed by 943 (22%) in C.5.7 defined by E128G amino acid substitution and 806 (19%) in C.5.6. All viruses within C.5.1 also carried E128K compared with the representative strain B/Catalonia/2279261NS/2023.

Nineteen viruses represented the subclade C.5, characterised by the amino acid substitution D197E shared with reference strain B/Stockholm/3/2022. Thirteen viruses represented the subclade C.3, characterised by the combination of E128K, A154E and S208P, similar to B/Moldova/2030521/2023. All subclades represented in this analysis contained a reference sequence. Overall, the V1A.3a.2 clade was characterised by multiple evolving branches absent from defining HA1 amino-acid substitutions.

No viruses fell in clade V1A.3 (e.g. former vaccine strain B/Washington/02/2019).

The concordance between assigned clade and subclade was high for B/Victoria, where all (4 251) viruses with a reported clade matched at clade level and 4 224 (99%) matched at subclade level.

Figure 24. 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 https://www.ecdc.europa.eu/en/publications-data/influenza-virus-characteristics-week-40-2024-week-33-2025).

Match between antigenic and genetic characterisations

Of the 441 B/Victoria viruses that had genetic and antigenic data reported, the majority (422; 96%) were reported antigenically as V1A.3a.2 B/Austria/1359417/2021-like, the vaccine component of this season (Annex 1, Table 4A). HA sequences that were reported for B/Victoria viruses fell in six reporting categories within V1A.3a.2: 197 (47%) viruses as B/Catalonia/2279261NS/2023, 107 (25%) as B/Switzerland/329/2024, 101 (24%) as B/Guangxi-Beiliu/2298/2023, 11 (4%) as homologous B/Austria/1359417/2021, four (0.9%) as B/Stockholm/3/2022 and two that could not be assigned to any of the predefined subclades.

Two B/Victoria viruses were antigenically reported without category but were genetically assigned to C.5.6 B/Switzerland/329/2024 and C.5.7 B/Guangxi-Beiliu/2298/2023.

Antiviral susceptibility

From week 40 2024 to week 33 2025, with latest data reported for week 23 2025, 4 063 B(Victoria) influenza viruses were assessed genotypically and/or phenotypically for susceptibility to at least one drug (oseltamivir, zanamivir or baloxavir marboxil) by 17 countries. The three main countries that contributed were: Spain (36.1%), France (21.4%) and Germany (11.4%).

Eight countries performed a phenotypic assessment of susceptibility to neuraminidase inhibitors: France, Germany, Italy, the Netherlands, Poland, Portugal, Romania and Spain. Reduced inhibition by oseltamivir and zanamivir was observed for eight (3.6%) of the 223 and six (2.8%) of the 215 tested B(Victoria) viruses, respectively (Table 20). These viruses could not be assessed genetically or associated with any particular amino acid substitution.

The susceptibility of the remaining viruses was assessed genetically based on the presence of substitutions in the neuraminidase known to be associated with reduced inhibition. Substitutions associated with reduced inhibition by oseltamivir were observed for six (0.2%; associated with NA_H273Y or NA_D197N) of the 3 473 viruses that could be assessed. For zanamivir, substitutions associated with reduced and highly reduced inhibition were observed for four (0.1%; associated with NA_D197N) and one (<0.1%; NA_H134N) of the 3 480 assessed viruses.

Table 20. Number of B(Victoria) viruses by reporting categories for neuraminidase inhibitor susceptibility, EU/EEA, week 40 2024 to week 33 2025

Antiviral	Phenotypic		Genotypic			Total
	NI	RI	AANI	AARI	AAHRI	
Oseltamivir	215	8	3 467	6[a]	0	3 696
Zanamivir[b]	209	6	3 475	4[c]	1[d]	3 695

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 to oseltamivir were NA_H273Y or NA_D197N.*
[b] *For viruses undergoing phenotypic assessment of zanamivir, no substitution was found.*
[c] *The substitution related to reduced susceptibility to zanamivir was NA_D197N.*
[d] *The substitution related to highly reduced susceptibility to zanamivir was NA_H134N.*

The susceptibility to polymerase inhibitors were assessed genetically based on the presence of substitutions in the PA polymerase subunit that are known to confer reduced susceptibility. Fourteen countries reported sequencing data; the three main contributors were France, Germany and Spain. Substitutions associated with reduced susceptibility were observed for one (<0.1%; associated with PA_I38T) of the 2 699 assessed B(Victoria) viruses (Table 21).

Table 21. Number of B(Victoria) viruses by reporting categories for baloxavir marboxil susceptibility, EU/EEA, week 40 2024 to week 33 2025

Antiviral	Genotypic		Total
	AANS	AARS[b]	
Baloxavir	2 698	1	2 699

[a] *The substitution related to reduced susceptibility was PA_I38T.*

B/Yamagata lineage viruses

Although one B/Yamagata RNA was detected, no characterisation of B/Yamagata virus was available during the 2024–25 season.

4 Discussion

Influenza virus detection and virus characterisation data from the EU/EEA remain crucial for the genetic monitoring of influenza virus evolution, for the assessment of antiviral susceptibility in the circulating seasonal influenza viruses and for the selection of viruses to be sent to a WHO CC for more detailed analyses that inform the decision-making process of recommending influenza viruses for inclusion in vaccines at biannual WHO vaccine composition meetings.

From week 40 2024 to week 33 2025, EU/EEA countries reported 354 455 influenza virus detections to TESSy, as well as 1 991 antigenic and 14 126 genetic characterisations. This influenza season was characterised by co-circulation of influenza type A subtype A(H1)pdm09 and A(H3) and type B/Victoria lineage. Among the 61 721 (sub)typed or lineage-defined viruses, 31 638 A(H1)pdm09 (51%), 20 804 A(H3) (34%), 9 278 B/Victoria (15%) viruses and one (<0.1%) B/Yamagata viral RNA were reported from sentinel and non-sentinel surveillance specimens.[1]

For the single detection of B/Yamagata virus RNA found in a sentinel specimen, there was no indication that this could have resulted from inactivated vaccine contamination or live-attenuated vaccine-derived virus, while proof of wildtype virus could not be obtained by virus isolation and sequencing due to very low viral load.

NRLs have been encouraged to characterise as many of their sentinel influenza viruses as possible, with both ECDC and WHO/Europe recommending that all sentinel influenza viruses be sequenced [16]. Although this has not been implemented, clear efforts towards characterisation of influenza viruses have been made across Europe. In total, 14 935 (4.2%) of 354 455 influenza virus detections were entered into TESSy as characterised during the reporting period. For the sentinel specimens, 5 013 (20%) of 25 557 were characterised; this is very similar to August 2024, when 5 443 of 25 434 (21%) sentinel specimens were characterised.

Of the 30 EU/EEA countries, 17 reported virus characterisation data along with influenza detection data, to varying extents (Figures 2, 8 and 9). Eight countries reported antigenic data, compared with nine in August 2024. Sixteen countries reported genetic data, the same as in the previous season. Over several years, the trend for antigenic reporting has been decreasing. Keeping with this decreasing trend, during this reporting period there were 1 991 antigenic reports compared with 2 479 in August 2024.

The overall number of genetic clade data reports made by EU/EEA countries in the 2024–25 season almost doubled, even though seven countries reported fewer genetic reports. During this season (up to week 33 2025), individual countries reported 5–70% more genetic clade reports compared with the full season data for 2023–24 (up to week 39). France performed 11.7 times more influenza virus sequencing compared with last season, Spain 3.1 times more and multiple countries approximately 1.1–2.0 times more (Denmark, Germany, Ireland, Luxembourg, the Netherlands and Portugal). For the genetic clade reports, 95% contained SequenceID or HA sequence ID number (only 787 viruses did not). Furthermore, the country-reported genetic clade categories aligned well with our phylogenetic analysis and assignment of clades.

The distribution of type A and B viruses that had antigenic analyses differed from the overall virus distribution: 73% influenza A and 26% influenza B viruses detected vs 66% and 34% antigenically characterised, respectively. It is possible that a higher proportion of B viruses were characterised because some countries had a B virus dominated start of the season or because countries tried to characterise as many B viruses as possible to exclude circulation of B Yamagata viruses. Among the A viruses, the proportion of antigenically characterised A(H3) viruses was 37%, compared with 63% for A(H1)pdm09 viruses. The detection rates were similarly distributed, with 40% for A(H3) and 60% for A(H1)pdm09.

Around half of the A(H1N1)pdm09 and A(H3) viruses that were detected were characterised genetically. Among the subtyped A viruses, A(H1N1)pdm09 accounted for 60% of the detected viruses, 57% of which were genetically characterised; A(H3N2) accounted for 40% of the detected viruses, 43% of which were genetically characterised. B viruses represented 15% of all the detected influenza viruses; of the characterised viruses, 30% were B viruses.

Three recombinants were genetically characterised – one A(H1N2) and two A(H3N2) viruses – which demonstrates the network's ability to detect atypical influenza viruses. No substitution associated with reduced antiviral susceptibility was observed for those three recombinant viruses (data not shown).

Minority influenza virus types and A subtypes are more likely to cause an epidemic next year compared with the majority strains. Therefore, it is useful if these types and A subtypes are selectively sampled for sequencing. Sequencing strategies should prioritise these minority types and A subtypes rather than adhering strictly to proportional sampling.

When comparing the antigenic similarity of circulating A(H1)pdm09 viruses to the 2024–25 NH vaccine strains, 48% of circulating viruses were similar to the NH 2024–25 vaccine strains A/Victoria/4897/2022 or A/Wisconsin/67/2022-like, when characterised with ferret antisera. However, the majority (51%) of

[1] Further surveillance data, maps and country-specific tables are available at: www.erviss.org.

A(H1N1)pdm09 viruses circulating in Europe were similar to A/Sydney/5/2021, which was the SH 2023 vaccine strain. Furthermore, genetically, 84% of A(H1)pdm09 viruses fell to the 5a.2a C.1.9 subclade represented by A/Lisboa/188/2023, which is within subclade C.1 represented by A/Sydney/5/2021. Similar dominance of the C.1.9 subclade was presented earlier in the Vaccine Effectiveness, Burden and Impact Studies (VEBIS) [17]. Based on clade, subclade and mutations retrieved from the phylogenetic analysis, all 5a.2a viruses fell into subclade C.1.9 defined by T120A and K169Q substitutions with a majority (87%) further assigned to subclade C.1.9.3 defined by S83P. There was also some genetic diversity observed in the 5a.2a.1 viruses, with 69% belonging to D.3 and 19% carrying R113K that defines subclade D.2. Few viruses (0.2–3.5%) represented D.1, D.4 and D.5.

Even if the majority of A(H1)pdm09 viruses were antigenically similar to A/Sydney/5/2021, the antigenic group results supported that ferret antisera raised against A/Victoria/4897/2022 from the 5a.2a.1 clade recognised viruses of the C.1, C.1.9 and D subclades well, as observed previously [18]. It is noteworthy that the joint ECDC and WHO/Europe virus characterisation guidance instructs NRLs to preferentially categorise viruses as the current vaccine strain when the titre-differences between a vaccine strain and another reference strain are the same.

Only about 0.7% of the A(H1N1)pdm09 viruses tested were found to have reduced susceptibility to any antiviral by either phenotypic or genotypic testing. Most viruses that showed reduced or highly reduced inhibition by oseltamivir carried amino acid substitution NA_D199Y/E, NA_I223T/K or NA_H275Y, which are amino acid substitutions that are well known to confer reduced or highly reduced susceptibility to oseltamivir [19]. The double substitution of NA_I223V+NA_S247N, also known to confer reduced susceptibility to oseltamivir, was not detected this season, although it was present in the majority of A(H1N1)pdm09 viruses characterised in the 2023–24 season.

For A(H3N2), based on genetic clade reporting, the majority (78%) of circulating viruses fell in clade 2a.3a.1 subclade J.2 represented by next winter's NH 2025–26 vaccine strain A/Croatia/10136RV/2023. Available antigenic data indicate that half (50%) of circulating viruses were antigenically similar to the A/Croatia/10136RV/2023-like viruses and 44% were similar to the NH 2024–2025 season vaccine strain A/Thailand/8/2022.

Furthermore, global data analysis from the NH vaccine composition meeting (VCM) revealed reduced reactivity of A/Thailand/8/2022-like viruses against many recent strains [20]. This reduced reactivity was more pronounced in viruses with either the N158K or K189R HA substitutions, or both [20]. In the current EU/EEA dataset, 115 A(H3N2) viruses with both these mutations were reported. Strains tested with these mutations have shown an eight-fold reduction of reactivity against antisera compared with the vaccine strain for NH 2024–25 [21]. The VCM concluded to recommend a change to the A(H3) vaccine for the 2025–26 season to A/Croatia/10136RV/2023-like viruses [20].

In keeping with the global analysis, 50% of the viruses reported to TESSy were similar to next winter's suggested vaccine component. However, it should be noted that the NRLs did not have many types of ferret antisera available to test for more detailed antigenic characteristics. It is noteworthy that within clade 2a.3a.1, 4 120 (97%) viruses fell into the subclade J.2 defining branch with N122D, which confers loss of a potential glycosylation site that may influence antigenicity [22], and amino acid substitution K276E; additionally, 208 (4.9%) fell into J.2.1 (F79L) and 591 (14%) into J.2.2 (S124N).

Only 33 (<0.8%) A(H3N2) viruses had reduced susceptibility to antivirals. All viruses with the neuraminidase sequence available carried substitutions known to reduce susceptibility. The NA_S331R substitution is, however, listed by WHO as 'normal inhibition/reduced inhibition' (NI/RI) for both oseltamivir and zanamivir. The 22 viruses reported this season carrying the NA_S331R substitution were categorised as 'amino acid mutations associated with reduced inhibition' (AARI) in this report to highlight the substitution's presence in circulating strains. However, instructions on how to report genetically assessed antiviral susceptibility based on this substitution needs further clarification, as some countries reported it as 'interpretation not possible' (AAINP).

For the B/Victoria lineage, 92% of antigenically characterised viruses were V1A.3a.2 B/Austria/1359417/2021-like, which is the current vaccine strain in tri- and quadrivalent vaccines in the NH 2024–2025 season [18]. However, the B/Victoria lineage viruses have genetically diversified and, within the V1A.3a.2 (C.5), 58% fell into subclade C.5.1, 22% into C.5.7, 19% into C.5.6 and <1% as parent C.5.

Only 25 (about 0.6%) B/Victoria viruses were reported to have reduced susceptibility to antivirals. All viruses with the neuraminidase sequence available carried substitutions well known to reduce inhibition by oseltamivir and/or zanamivir. One virus exhibited reduced inhibition by zanamivir in phenotypic testing, but no substitution listed in the WHO table was found in the sequence; further investigation of this virus is recommended. Substitution associated with reduced susceptibility to baloxavir marboxil was detected in the PA polymerase subunit sequence of one B/Victoria virus.

Interim European vaccine effectiveness data showed a varied vaccine effectiveness (VE) that ranged from 30–72% protection against influenza A(H1N1)pdm09 in all ages in primary care [22]. The same study showed moderate protection against currently circulating A(H3N2) viruses (29–47% among all ages in primary care; 31–49% among all ages in hospital). This may indicate that many of the circulating A(H3N2) 2a.3a.1 subclade strains in the EU/EEA diversified antigenically from the NH 2024–25 vaccine strain A/Thailand/8/2022 [20], as shown for approximately one third of the viruses in our data. Early influenza VE results from Canadian sentinel practitioner surveillance against infection showed similar estimates as the European study, with 53% (95% confidence interval (CI): 36–65) against influenza A(H1N1)pdm09 and 54% (95% CI: 29–70) against influenza A(H3N2) [23].

It is challenging to understand why countries are reporting less antigenic data. This could be due to a sequencing-first approach, i.e. selecting viruses for antigenic characterisation based on initial sequence screening. The decline in antigenic and genetic reports could also be simply due to a change in the timing of this end-of-season reporting from August to June and countries not yet being ready with their seasonal virus characterisation at the time of the data snapshot. Further discussion with the laboratory network is needed to understand the reasons behind the declining trends of antigenic and genetic reporting.

Given the ongoing question of whether B/Yamagata lineage viruses have become extinct, all B viruses detected by NRLs or submitted from clinical diagnostic laboratories should be tested with B/Victoria-specific RT-PCR. Viruses that test negative should be further characterised to exclude the presence of B/Yamagata viruses. Alternatively, a triplex test for B, B/Victoria and B/Yamagata could be used. In the sentinel source data for this reporting period, the lineage was determined for about 84% of the B viruses, which is an improvement from August 2024 when only one third were determined. In the virus characterisation data, all of the B viruses were reported as belonging to B/Victoria lineage.

There are limitations to the data presented in this report. The specimen sources (sentinel general practitioners, hospitals, intensive care units, outbreak investigations) and selection processes for the viruses that undergo characterisation vary from country to country. Only a small percentage of total influenza detections were characterised: 0.4% antigenically and 3.2% genetically (3.1% and 16% were from sentinel sources, respectively). These are low numbers, especially for the specimens from sentinel sources.

This suggests that the network characterises less than 10% of detected viruses from sentinel specimens – and mainly through genetic characterisation – despite ECDC and WHO/Europe's recommendations to sequence all influenza viruses detected from sentinel sources [16]. 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 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.

5 Conclusions

The following conclusions are drawn from this 2024–2025 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.
- Influenza virus characterisation specimens originate from both sentinel and non-sentinel surveillance systems, with approximately two-thirds (66%) 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.
- Only eight EU/EEA countries provided antigenic characterisation data, for fewer viruses than in the previous season, which indicates decreasing capacity or efforts for influenza virus antigenic characterisation that may be related to increased focus on sequencing in the region.
- Seventeen countries provided genetic characterisation data for more viruses than the previous year, showing increasing sequencing efforts at least in selected countries.
- Characterisation data showed that the genetic diversification of influenza viruses has continued. Antigenically, approximately half of the A(H3N2) viruses in the EU/EEA became distinct from the 2024–25 vaccine component. Similar observations in other parts of the world prompted WHO to recommend a new A(H3N2) vaccine component for the 2025–26 season.
- Phylogenetic analysis showed diversification within influenza A subtypes and B/Victoria viruses circulating in the EU/EEA. Several subclades – such as C.1.9.3 of A(H1)pdm09 clade 5a.2a and J.3 of A(H3N2) clade 2a.3a.1 – display an expansion but are not represented by reference strains. Within subclade J.2, the branch of strains with the amino-acid substitutions N158K and K189R merit further attention due to antigenic characteristics. Additional subclade designation may also be needed for an expanding branch carrying the amino-acid substitution N8D, involving loss of a potential N-glycosylation site. Despite a higher proportion of B/Victoria viruses and sequences compared with previous seasons, the multiple evolving branches of the V1A.3a.2 clade were not characterised by defining HA1 amino-acid substitutions.
- Overall, only a few (57/13 626 analysed viruses; 0.4%) influenza viruses with reduced susceptibility to antiviral drugs were detected this season.

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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 2024 to week 33 2025

Antigenic Group	Denmark	France	Germany	Italy	Portugal	Romania	Slovenia	Belgium	Total
agAH1/Lisboa/188/2023	13	0	0	0	0	0	1	0	14
agAH1/Sydney/5/2021	0	17	374	0	0	25	0	0	416
agAH1/Victoria/4897/2022	21	248	71	7	17	5	9	0	378
agAH1/Wisconsin/67/2022	10	0	0	0	0	0	3	0	13
agAH3/Croatia/10136RV/2023	25	156	0	0	24	3	23	11	242
agAH3/Darwin/9/202	0	2	19	0	0	0	0	0	21
agAH3/France/IDF-IPP29542/2023	2	0	0	0	0	0	0	0	2
agAH3/Thailand/8/2022	23	27	157	0	0	8	0	0	215
agAH3NOCAT	0	6	0	0	0	0	0	0	6
agBVicB/Austria/1359417/2021	38	180	430	2		13	0	0	663
agBVicB/Stockholm/3/2022	4	0	0	0	15	0	0	0	19
agBVicNOCAT	0	2	0	0	0	0	0	0	2
Total	**136**	**638**	**1 051**	**9**	**56**	**54**	**36**	**11**	**1 991**

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=16), EU/EEA, week 40 2024 to week 33 2025

GeneticClade	Belgium	Denmark	Finland	France	Germany	Greece	Ireland	Italy	Luxembourg	Netherlands	Norway	Portugal	Romania	Slovenia	Spain	Sweden	Total
genAH1/Hungary/286/2024	0	0	0	578	0	0	0	9	0	1	108	0	0	0	0	0	**696**
genAH1/Lisboa/188/2023	34	186	38	201	418	2	358	9	84	534	36	211	0	0	1524	127	**3 762**
genAH1/Norway/00926/2025	0	0	0	63	0	0	0	1	0	16	97	0	0	0	0	0	**177**
genAH1/Sydney/5/2021	1	0	0	0	0	0	0	0	0	18	0	0	138	0	0	0	**157**
genAH1/Victoria/4897/2022	8	68	10	30	50	0	55	0	11	99	6	18	0	5	340	34	**734**
genAH1SubgroupNotListed	0	0	0	38	0	0	0	0	0	0	0	0	0	0	0	0	**38**
genAH3/Croatia/10136RV/2023	27	145	26	691	72	0	35	11	118	553	111	250	4	10	1243	47	**3 343**
genAH3/France/IDF-IPP29542/2023	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0	**3**
genAH3/Lisboa/216/2023	1	23	8	66	35	0	0	0	4	103	63	24	0	0	229	20	**576**
genAH3/Netherlands/10685/2024	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	**2**
genAH3/Sydney/856/2023	0	8	1	2	2	4	0	2	0	7	6	0	0	0	7	0	**39**
genAH3/Thailand/8/2022	0	0	1	0	0	0	0	0	0	14	0	0	28	0	0	0	**43**
genAH3/West Virginia/51/2024	1	75	0	34	1	0	4	1	6	24	6	21	0	0	67	7	**247**
genAH3SubgroupNotListed	0	0	0	2	0	0	0	0	0	5	2	0	0	0	10	0	**19**
genBVicB/Austria/1359417/2021	0	0	0	0	1	0	0	0	0	0	9	1	58	9	0	0	**798**
genBVicB/Catalonia/2279261NS/2023	11	58	8	299	329	3	40	7	39	215	81	67	0	0	1303	13	**2 473**
genBVicB/Guangxi-Beiliu/2298/2023	12	34	4	391	73	0	26	2	42	69	31	100	0	0	115	22	**921**
genBVicB/Stockholm/3/2022	2	5	0	4	1	0	2	0	0	1	0	0	0	0	0	2	**17**
genBVicB/Switzerland/329/2024	8	47	13	175	166	0	47	2	26	59	22	87	0	0	110	17	**779**
genBVicSubgroupNotListed	0	0	0	2	0	0	16	0	0	0	0	0	0	0	1	0	**19**
Total	**105**	**649**	**109**	**2 578**	**1 148**	**9**	**583**	**44**	**330**	**1 719**	**578**	**779**	**228**	**24**	**4 951**	**289**	**14 123**

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 2024 to week 33 2025

A. Antigenic

Year-Week no.	agAH1/Lisboa/188/2023	agAH1/Sydney/5/2021	agAH1/Victoria/4897/2022	agAH1/Wisconsin/67/2022	agAH3/Croatia/10136RV/2023	agAH3/Darwin/9/2021	agAH3/France/IDF-IPP29542/2023	agAH3/Thailand/8/2022	agAH3NOCAT	agBVicB/Austria/1359417/2021	agBVicB/Stockholm/3/2022	agBVicNOCAT	Total
2024-40	0	0	1	0	3	0	0	1	0	0	0	0	**5**
2024-41	0	1	1	0	1	0	0	0	0	1	1	0	**5**
2024-42	0	3	2	0	6	0	0	2	1	1	0	0	**15**
2024-43	0	2	2	1	3	0	0	0	0	2	1	0	**11**
2024-44	0	2	6	0	4	0	0	0	0	3	2	0	**17**
2024-45	0	2	3	0	0	0	0	2	0	1	2	0	**10**
2024-46	0	0	3	1	5	0	0	2	0	2	2	0	**15**
2024-47	0	4	5	0	1	0	0	1	0	4	0	0	**15**
2024-48	0	6	10	0	3	0	0	0	0	6	3	0	**28**
2024-49	0	13	26	0	8	0	0	3	0	14	4	2	**70**
2024-50	0	12	18	0	11	0	0	3	0	18	0	0	**62**
2024-51	0	17	32	0	14	0	0	6	1	21	1	0	**92**
2024-52	0	7	17	1	9	1	0	4	0	13	0	0	**52**
2025-01	1	17	24	2	18	0	0	3	0	15	1	0	**81**
2025-02	0	25	37	0	20	0	0	9	0	34	0	0	**125**
2025-03	0	28	41	2	18	0	0	24	0	73	0	0	**186**
2025-04	2	39	32	0	20	0	0	33	1	74	1	0	**202**
2025-05	2	41	21	0	13	0	0	22	2	51	0	0	**152**
2025-06	3	47	9	3	21	0	2	13	0	50	0	0	**148**
2025-07	2	24	18	1	7	3	0	20	1	52	0	0	**128**
2025-08	0	24	16	0	10	0	0	16	0	28	0	0	**94**
2025-09	2	20	11	1	17	1	0	18	0	45	1	0	**116**
2025-10	1	29	8	0	6	1	0	11	0	34	0	0	**90**
2025-11	0	17	3	0	10	1	0	5	0	39	0	0	**75**
2025-12	1	13	8	1	7	10	0	3	0	32	0	0	**75**

Year-Week no.	agAH1/Lisboa/188/2023	agAH1/Sydney/5/2021	agAH1/Victoria/4897/2022	agAH1/Wisconsin/67/2022	agAH3/Croatia/10136RV/2023	agAH3/Darwin/9/2021	agAH3/France/IDF-IPP29542/2023	agAH3/Thailand/8/2022	agAH3NOCAT	agBVicB/Austria/1359417/2021	agBVicB/Stockholm/3/2022	agBVicNOCAT	Total
2025-13	0	8	4	0	1	1	0	3	0	22	0	0	**39**
2025-14	0	3	6	0	4	0	0	3	0	17	0	0	**33**
2025-15	0	2	6	0	0	2	0	2	0	6	0	0	**18**
2025-16	0	2	8	0	1	1	0	4	0	5	0	0	**21**
2025-17	0	1	0	0	0	0	0	0	0	0	0	0	**1**
2025-19	0	2	0	0	1	0	0	0	0	0	0	0	**3**
2025-20	0	2	0	0	0	0	0	0	0	0	0	0	**2**
2025-21	0	1	0	0	0	0	0	0	0	0	0	0	**1**
2025-22	0	2	0	0	0	0	0	0	0	0	0	0	**2**
2025-31	0	0	0	0	0	0	0	2	0	0	0	0	**2**
Total	**14**	**416**	**378**	**13**	**242**	**21**	**2**	**215**	**6**	**663**	**19**	**2**	**1 989**

B. Genetic

Year-Week no.	genAH1/Hungary/286/2024	genAH1/Lisboa/188/2023	genAH1/Norway/00926/2025	genAH1/Sydney/5/2021	genAH1/Victoria/4897/2022	genAH1SubgroupNotListed	genAH3/Croatia/10136RV/2023	genAH3/France/IDF-IPP29542/2023	genAH3/Lisboa/216/2023	genAH3/Netherlands/10685/2024	genAH3/Sydney/856/2023	genAH3/Thailand/8/2022	genAH3/West Virginia/51/2024	genAH3SubgroupNotListed	genBVicB/Austria/13594417/2021	genBVicB/Catalonia/2279261NS/2023	genBVicB/Guangxi-Beiliu/2298/2023	genBVicB/Stockholm/3/2022	genBVicB/Switzerland/329/2024	genBVicSubgroupNotListed	Total
2024-40	0	15	0	0	1	2	20	0	0	0	0	4	6	0	0	13	7	0	3	0	71
2024-41	6	15	0	2	6	0	16	1	1	0	0	2	6	0	1	15	5	0	5	0	81
2024-42	8	25	0	3	2	1	27	1	3	0	0	2	10	0	0	16	5	0	5	0	108
2024-43	9	35	0	7	6	1	13	1	1	0	0	0	9	0	1	26	10	0	2	1	122
2024-44	13	39	0	6	7	2	17	0	3	0	0	4	7	0	2	18	7	1	4	0	130
2024-45	19	48	2	–	5	2	10	0	2	0	0	2	2	0	4	25	12	0	8	0	141
2024-46	19	38	0	1	3	2	17	0	4	0	0	1	9	1	2	22	13	0	8	1	141
2024-47	16	49	2	2	7	1	14	0	7	0	0	0	5	0	1	43	10	0	18	4	179
2024-48	25	79	0	1	7	1	39	0	6	0	1	0	10	0	0	54	14	0	13	1	251
2024-49	46	110	1	3	20	2	43	0	5	0	1	0	15	0	1	65	25	1	28	6	372
2024-50	41	167	2	2	17	2	72	0	14	0	2	2	14	0	2	91	33	0	35	1	497
2024-51	48	200	2	1	25	0	64	0	14	0	0	0	19	3	3	129	34	0	31	0	573
2024-52	34	150	2	7	20	1	61	0	3	0	3	1	9	2	7	97	31	0	24	0	452
2025-01	43	280	0	20	17	2	119	0	14	0	1	2	13	1	1	117	51	1	32	1	715
2025-02	57	373	3	5	22	3	178	0	21	0	1	0	12	4	2	148	57	1	51	1	939
2025-03	71	391	4	32	18	5	221	0	35	0	3	3	10	0	3	200	60	0	51	0	1 107
2025-04	64	389	5	13	43	3	247	0	33	0	0	4	12	3	1	216	88	1	69	1	1 192
2025-05	54	365	11	17	48	1	293	0	47	0	5	3	20	1	5	207	85	2	62	1	1 227
2025-06	24	259	2	14	25	1	243	0	42	0	3	0	15	0	6	169	69	1	47	0	920
2025-07	29	218	3	7	40	0	269	0	39	0	2	5	4	1	7	155	57	1	55	0	892
2025-08	27	167	11	4	32	2	244	0	49	0	2	2	7	0	9	113	64	2	33	1	769
2025-09	10	124	6	5	27	0	217	0	25	0	3	1	7	2	3	123	47	0	50	0	650
2025-10	12	77	3	4	27	1	200	0	39	0	2	3	6	0	9	90	34	0	37	0	544
2025-11	8	50	11	1	55	0	174	0	40	0	3	2	4	0	6	94	19	2	34	0	503
2025-12	6	39	8	0	52	1	165	0	27	0	1	0	4	0	2	56	24	1	25	0	411
2025-13	2	26	8	0	40	2	107	0	24	1	2	0	3	0	0	60	27	0	14	0	316
2025-14	4	16	8	0	42	0	81	0	23	0	2	0	3	1	0	40	11	2	14	0	247

Year-Week no.	genAH1/Hungary/286/2024	genAH1/Lisboa/188/2023	genAH1/Norway/00926/2025	genAH1/Sydney/5/2021	genAH1/Victoria/4897/2022	genAH1SubgroupNotListed	genAH3/Croatia/10136RV/2023	genAH3/France/IDF-IPP29542/2023	genAH3/Lisboa/216/2023	genAH3/Netherlands/10685/2024	genAH3/Sydney/856/2023	genAH3/Thailand/8/2022	genAH3/West Virginia/51/2024	genAH3SubgroupNotListed	genBVicB/Austria/13594417/2021	genBVicB/Catalonia/2279261NS/2023	genBVicB/Guangxi-Beiliu/2298/2023	genBVicB/Stockholm/3/2022	genBVicB/Switzerland/329/2024	genBVicSubgroupNotListed	Total
2025-15	1	6	23	0	32	0	64	0	16	0	1	0	1	0	0	28	9	0	8	0	189
2025-16	0	1	12	0	26	0	26	0	13	0	1	0	2	0	0	14	3	0	5	0	103
2025-17	0	5	1	0	15	0	41	0	7	0	0	0	1	0	0	11	7	1	2	0	91
2025-18	0	3	14	0	12	0	13	0	7	0	0	0	1	0	0	4	1	0	1	0	56
2025-19	0	1	16	0	6	0	13	0	2	0	0	0	0	0	0	8	2	0	1	0	49
2025-20	0	1	8	0	3	0	8	0	2	0	0	0	1	0	0	4	0	0	4	0	31
2025-21	0	1	3	0	6	0	5	0	5	0	0	0	0	0	0	1	0	0	0	0	21
2025-22	0	0	2	0	6	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	10
2025-23	0	0	2	0	6	0	1	0	2	0	0	0	0	0	0	1	0	0	0	0	12
2025-24	0	0	1	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6
2025-25	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
2025-26	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
2025-29	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Total	696	3 762	177	157	734	38	3 343	3	576	2	39	43	247	19	78	2 473	921	17	779	19	14 123

Table 4A. Antigenic and genetic characterisation data where both types of data were available in TESSy by categories of reporting, EU/EEA, week 40 2024 to week 33 2025

Genetic clade	Antigenic group												Total
	agAH1/Lisboa/188/2023	agAH1/Sydney/5/2021	agAH1/Victoria/4897/2022	agAH1/Wisconsin/67/2022	agAH3/Croatia/10136RV/2023	agAH3/Darwin/9/2021	agAH3/France/IDF-IPP29542/2023	agAH3/Thailand/8/2022	agAH3NOCAT	agBVicB/Austria/1359417/2021	agBVicB/Stockholm/3/2022	agBVicNOCAT	
genAH1/Hungary/286/2024	0	11	148	0	0	0	0	0	0	0	0	0	**159**
genAH1/Lisboa/188/2023	9	141	129	8	0	0	0	0	0	0	0	0	**287**
genAH1/Norway/00926/2025	0	2	29	0	0	0	0	0	0	0	0	0	**31**
genAH1/Sydney/5/2021	0	20	3	0	0	0	0	0	0	0	0	0	**23**
genAH1/Victoria/4897/2022	4	15	15	3	0	0	0	0	0	0	0	0	**37**
genAH1SubgroupNotListed	0	1	8	0	0	0	0	0	0	0	0	0	**9**
genAH3/Croatia/10136RV/2023	0	0	0	0	171	8	2	86	6	0	0	0	**273**
genAH3/France/IDF-IPP29542/2023	0	0	0	0	1	0	0	0	0	0	0	0	**1**
genAH3/Lisboa/216/2023	0	0	0	0	22	1	0	31	0	0	0	0	**54**
genAH3/Sydney/856/2023	0	0	0	0	0	0	0	2	0	0	0	0	**2**
genAH3/Thailand/8/2022	0	0	0	0	0	0	0	6	0	0	0	0	**6**
genAH3/West Virginia/51/2024	0	0	0	0	19	0	0	8	0	0	0	0	**27**
genAH3SubgroupNotListed	0	0	0	0	1	0	0	0	0	0	0	0	**1**
genBVicB/Austria/1359417/2021	0	0	0	0	0	0	0	0	0	11	0	0	**11**
genBVicB/Catalonia/2279261NS/2023	0	0	0	0	0	0	0	0	0	197	5	0	**202**
genBVicB/Guangxi-Beiliu/2298/2023	0	0	0	0	0	0	0	0	0	101	6	1	**108**
genBVicB/Stockholm/3/2022	0	0	0	0	0	0	0	0	0	4	0	0	**4**
genBVicB/Switzerland/329/2024	0	0	0	0	0	0	0	0	0	107	6	1	**114**
genBVicSubgroupNotListed	0	0	0	0	0	0	0	0	0	2	0	0	**2**
Total	**13**	**190**	**332**	**11**	**214**	**9**	**2**	**133**	**6**	**422**	**17**	**2**	**1 351**

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 2024 to week 33 2025

Antiviral	Virus	Subtype	Assessment	Interpretation	GISAID	Substitution
Baloxavir	A/Goteborg/SE24-14949/2024	A(H1)pdm09	Genotypic	AARS	EPI3669559	PA_E199G
	A/Lisboa/8/2025	A(H1)pdm09	Genotypic	AARS	EPI4157264	PA_A37T
	A/Luxembourg/LNS3193181/2024	A(H3)	Genotypic	AARS	EPI3842253	PA_I38M
	A/Luxembourg/LNS3307598/2025	A(H3)	Genotypic	AARS	EPI4086013	PA_I38M
	A/Aragon/1612/2025	A(H3)	Genotypic	AARS	EPI4394138	PA_I38T
	B/France/IDF-IPP02399/2025	B(Vic)	Genotypic	AARS	EPI4039928	PA_I38T
Oseltamivir	A/Norway/07557/2024	A(H1)pdm09	Genotypic	AAHRI	EPI3628213	NA_H275Y
	A/Finland/621/2024	A(H1)pdm09	Genotypic	AAHRI	EPI3914540	NA_H275Y
	A/Murcia/2159/2024	A(H1)pdm09	Genotypic	AAHRI	EPI3687260	NA_H275Y
	A/Netherlands/01983/2024	A(H1)pdm09	Genotypic	AAHRI	EPI3756317	NA_H275Y
	A/Catalonia/NSVH172314890/2024	A(H1)pdm09	Genotypic	AAHRI	EPI3769257	NA_H275Y
	A/France/IDF-RELAB-IPP14966/2024	A(H1)pdm09	Genotypic	AARI	EPI3804312	NA_I223T
	A/Madrid/302425181704/2024	A(H1)pdm09	Genotypic	AARI	EPI4038586	NA_D199Y
	A/Bialystok/137/2024	A(H1)pdm09	Phenotypic	RI	Unknown	Unknown
	A/Cantabria/1657/2025	A(H1)pdm09	Genotypic	AARI	EPI4555529	NA_I223K
	A/Catalonia/NSVH102507276/2025	A(H1)pdm09	Genotypic	AAHRI	EPI3884388	NA_H275Y
	A/Catalonia/NSVH111879905/2025	A(H1)pdm09	Genotypic	AAHRI	EPI3890035	NA_H275Y
	A/FVG-Pordenone/24/2025	A(H1)pdm09	Genotypic	AAHRI	EPI3864303	NA_H275Y
	A/Berlin/9/2025	A(H1)pdm09	Phenotypic	HRI	EPI3976573	NA_H275Y
	A/FVG-Pordenone/62/2025	A(H1)pdm09	Phenotypic	HRI	EPI4023211	NA_H275Y
	A/Athens.GR/21/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4224792	NA_H275Y
	A/Torino/98/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4019501	NA_H275Y
	A/Netherlands/00390/2025	A(H1)pdm09	Phenotypic	HRI	EPI4120657	NA_H275Y
	A/Catalonia/NSJO510842505/2025	A(H1)pdm09	Genotypic	AAHRI	EPI3883960	NA_H275Y
	A/Lisboa/208/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4279643	NA_H275Y
	A/Catalonia/NSAV198317353/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4005531	NA_H275Y
	A/Denmark/780/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4049753	NA_H275Y
	A/Galicia/GA-CHUAC-240/2025	A(H1)pdm09	Genotypic	AAHRI	EPI3988847	NA_H275Y
	A/FVG-Pordenone/134/2025	A(H1)pdm09	Phenotypic	HRI	EPI4147994	NA_H275Y
	A/France/IDF-RELAB-IPP02921/2025	A(H1)pdm09	Genotypic	AARI	EPI4088058	NA_D199E
	A/Romania_HD/590296/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4118811	NA_H275Y
	A/France/NOR-IPP04188/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4291693	NA_H275Y
	A/France/PDL-IPP03396/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4217592	NA_H275Y
	A/Netherlands/01548/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4120806	NA_H275Y

Antiviral	Virus	Subtype	Assessment	Interpretation	GISAID	Substitution
Oseltamivir	A/Athens.GR/63/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4224795	NA_H275Y
	A/Netherlands/01482/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4120766	NA_H275Y
	A/Denmark/2233/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4373538	NA_H275Y
	A/France/NOR-IPP04189/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4291701	NA_H275Y
	A/Denmark/2483/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4374046	NA_H275Y
	A/Denmark/2479/2025	A(H1)pdm09	Genotypic	AAHRI	EPI4433890	NA_H275Y
	A/France/NOR-IPP04190/2025	A(H1)pdm09	Phenotypic	RI	EPI4291709	Unknown
	A/Bialystok/136/2024	A(H3)	Phenotypic	RI	Unknown	Unknown
	A/Bialystok/139/2024	A(H3)	Phenotypic	RI	Unknown	Unknown
	A/Bialystok/138/2024	A(H3)	Phenotypic	RI	Unknown	Unknown
	A/Bialystok/141/2024	A(H3)	Phenotypic	RI	Unknown	Unknown
	A/CastillaLaMancha/FLUCEN24-14/2025	A(H3)	Genotypic	AARI	EPI4372395	NA_S331R
	A/France/HDF-RELAB-IPP01089/2025	A(H3)	Genotypic	AARI	EPI3976430	NA_S331R
	A/France/HDF-RELAB-IPP01463/2025	A(H3)	Genotypic	AARI	EPI4003793	NA_S331R
	A/France/IDF-IPP01396/2025	A(H3)	Genotypic	AAHRI	EPI3907180	NA_E119V
	A/Lisboa/57/2025	A(H3)	Genotypic	AARI	EPI4231790	NA_S331R
	A/France/HDF-IPP01887/2025	A(H3)	Genotypic	AARI	EPI3961963	NA_S331R
	A/France/PDL-IPP02124/2025	A(H3)	Genotypic	AAHRI	EPI3977725	NA_E119V
	A/France/PDL-IPP03381/2025	A(H3)	Genotypic	AAHRI	EPI4160017	NA_E119V
	A/France/HDF-RELAB-IPP02744/2025	A(H3)	Genotypic	AARI	EPI4087290	NA_S331R
	A/France/HDF-RELAB-IPP02747/2025	A(H3)	Genotypic	AARI	EPI4087312	NA_S331R
	A/Catalonia/NSAV198319727/2025	A(H3)	Genotypic	AARI	EPI4079170	NA_K249E
	A/Catalonia/NSVH172316135/2025	A(H3)	Genotypic	AARI	EPI4147249	NA_S331R
	A/Galicia/52497561/2025	A(H3)	Genotypic	AARI	EPI4321932	NA_K249E
	A/CastillaLaMancha/FLUCEN24-160/2025	A(H3)	Genotypic	AARI	EPI4372495	NA_S331R
	A/France/IDF-RELAB-IPP04777/2025	A(H3)	Genotypic	AARI	EPI4449830	NA_S331R
	B/Lisboa/133/2024	B(Vic)	Genotypic	AARI	EPI3831033	NA_D197N
	B/France/IDF-RELAB-IPP14156/2024	B(Vic)	Phenotypic	RI	EPI3776962	Unknown
	B/Poland/20/2024	B(Vic)	Phenotypic	RI	Unknown	Unknown
	B/Poland/21/2024	B(Vic)	Phenotypic	RI	Unknown	Unknown
	B/Poland/22/2024	B(Vic)	Phenotypic	RI	Unknown	Unknown
	B/Poland/23/2024	B(Vic)	Phenotypic	RI	Unknown	Unknown
	B/Bialystok/135/2024	B(Vic)	Phenotypic	RI	Unknown	Unknown
	B/Szczecin/157/2024	B(Vic)	Phenotypic	RI	Unknown	Unknown
	B/Poland/61/2025	B(Vic)	Phenotypic	RI	Unknown	Unknown
	B/Andalucia/PMC-00647/2025	B(Vic)	Genotypic	AARI	EPI3904037	NA_H273Y
	B/Andalucia/PMC-00680/2025	B(Vic)	Genotypic	AARI	EPI3976207	NA_H273Y
	B/Andalucia/PMC-00791/2025	B(Vic)	Genotypic	AARI	EPI4210475	NA_D197N
	B/France/GES-RELAB-IPP04077/2025	B(Vic)	Genotypic	AARI	EPI4245473	NA_D197N
	B/France/GES-RELAB-IPP04358/2025	B(Vic)	Genotypic	AARI	EPI4292090	NA_D197N

Antiviral	Virus	Subtype	Assessment	Interpretation	GISAID	Substitution
Zanamivir	A/Madrid/302425181704/2024	A(H1)pdm09	Genotypic	AARI	EPI4038586	NA_D199Y
	A/Poland/35/2024	A(H3)	Phenotypic	RI	Unknown	Unknown
	A/CastillaLaMancha/FLUCEN24-14/2025	A(H3)	Genotypic	AARI	EPI4372395	NA_S331R
	A/France/HDF-RELAB-IPP01089/2025	A(H3)	Genotypic	AARI	EPI3976430	NA_S331R
	A/France/HDF-RELAB-IPP01463/2025	A(H3)	Genotypic	AARI	EPI4003793	NA_S331R
	A/Lisboa/57/2025	A(H3)	Genotypic	AARI	EPI4231790	NA_S331R
	A/France/HDF-IPP01887/2025	A(H3)	Genotypic	AARI	EPI3961963	NA_S331R
	A/France/HDF-RELAB-IPP02744/2025	A(H3)	Genotypic	AARI	EPI4087290	NA_S331R
	A/France/HDF-RELAB-IPP02747/2025	A(H3)	Genotypic	AARI	EPI4087312	NA_S331R
	A/Catalonia/NSVH172316135/2025	A(H3)	Genotypic	AARI	EPI4147249	NA_S331R
	A/CastillaLaMancha/FLUCEN24-160/2025	A(H3)	Genotypic	AARI	EPI4372495	NA_S331R
	A/France/IDF-RELAB-IPP04777/2025	A(H3)	Genotypic	AARI	EPI4449830	NA_S331R
	B/Lisboa/133/2024	B(Vic)	Genotypic	AARI	EPI3831033	NA_D197N
	B/France/IDF-RELAB-IPP14156/2024	B(Vic)	Phenotypic	RI	EPI3776962	Unknown
	B/Poland/20/2024	B(Vic)	Phenotypic	RI	Unknown	Unknown
	B/Poland/21/2024	B(Vic)	Phenotypic	RI	Unknown	Unknown
	B/Poland/22/2024	B(Vic)	Phenotypic	RI	Unknown	Unknown
	B/Bialystok/135/2024	B(Vic)	Phenotypic	RI	Unknown	Unknown
	B/Andalucia/PMC-00791/2025	B(Vic)	Genotypic	AARI	EPI4210475	NA_D197N
	B/Netherlands/10658/2025	B(Vic)	Phenotypic	RI	EPI4079711	NA_M464T
	B/France/GES-RELAB-IPP04077/2025	B(Vic)	Genotypic	AARI	EPI4245473	NA_D197N
	B/France/GES-RELAB-IPP04358/2025	B(Vic)	Genotypic	AARI	EPI4292090	NA_D197N
	B/Denmark/743/2025	B(Vic)	Genotypic	AAHRI	EPI4434322	NA_H134N

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.
[a] As defined in the WHO documentation [12-14].

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 = 17), EU/EEA, weeks 40 2024 to week 33 2025

Country	HA sequences				
	A(H1N1)pdm09	A(H3N2)	B/Victoria	Total	% of total sequences
Belgium	43	29	33	105	0.7%
Denmark	254	251	144	649	4.6%
Finland	47	36	25	108	0.8%
France	905	796	871	2 572	18.2%
Germany	477	117	573	1 167	8.3%
Greece	2	4	3	9	0.1%
Ireland	413	39	131	583	4.1%
Italy	19	14	11	44	0.3%
Luxembourg	94	126	107	327	2.3%
Netherlands	666	708	344	1 718	12.1%
Norway	247	188	143	578	4.1%
Poland	1	2	1	4	0.0%
Portugal	234	295	256	785	5.6%
Romania	140	32	59	231	1.6%
Slovenia	5	10	9	24	0.2%
Spain	1 863	1 558	1 528	4 949	35.0%
Sweden	162	74	54	290	2.1%
Total number of HA sequences	**5 572**	**4 279**	**4 292**	**14 143**	—

HA: haemagglutinin.

Table 7A. Number and proportion of A(H1N1)pdm09 reported genetic clades by country and assigned clades based on phylogenetic analysis, EU/EEA, week 40 2024 to week 33 2025

Clade	*Reference virus*	*Reported clade*	*%*	*Assigned clade*	*%*
5a.2a.1 (D)	A/Victoria/4897/2022	735	13.2%	281[a]	5.0%
5a.2a.1 (D.3)	A/Norway/00926/2025	174	3.1%	631	11.3%
5a.2a (C.1.9)	A/Lisboa/188/2023	3 756	67.4%[b]	582[c]	10.4%[b]
5a.2a (C.1.9.3)	A/Hungary/286/2024	695	12.5%	4 062	72.9%
5a.2a (C.1)	A/Sydney/5/2021	157	2.8%	4[d]	0.1%
Undefined	–	55	1.0%	12	0.2%
Total		**5 572**		**5 572**	

[a] *Sum of 5a.2a.1 subclades: D.1, D.2, D.4, D.5.*
[b] *The large discrepancy is due to 5a.2a (C.1.9.3) not being available for reporting until May 2025.*
[c] *Sum of 5a.2a subclades: C.1.9.1, C.1.9.2, C.1.9.4.*
[d] *Sum of 5a.2a subclades: C, C.1.2, C.1.3, C.1.4, C.1.5, C.1.6, C.1.7.1, C.1.8.*

Table 8A. Number and proportion of A(H3N2) reported genetic clades by country and assigned clades based on phylogenetic analysis, EU/EEA, week 40 2024 to week 33 2025

Clade	Reference virus	Reported clade	%	Assigned clade	%
2a.3a.1 (J)	A/Thailand/8/2022	43	1.0%	94[a]	2.2%
2a.3a.1 (J.1)	A/Sydney/856/2023	39	0.9%	45[b]	1.1%
2a.3a.1 (J.2)	A/Croatia/10136RV/2023	3 341	78.1%	3 206	75.2%
2a.3a.1 (J.2.1)	A/West Virginia/51/2024	247	5.8%	208	4.9%
2a.3a.1 (J.2.2)	A/Lisboa/216/2023	576	13.5%	591	13.9%
2a.3a.1 (J.2)158K189R	A/Croatia/10136RV/2023	2	0.0%	115	2.7%
2a.3a.1 (J.4)	A/France/IDF-IPP29542/2023	3	0.1%	4	0.1%
Undefined	–	29	0.7%	2	0.0%
Total		**4 280**	–	**4 265**	–

[a] *Sum of 2a.3a.1 subclades: J.3.*
[b] *Sum of 2a.3a.1 subclades: J.1.1.*

Table 9A. Number and proportion of B/Victoria reported genetic clades by country and assigned clades based on phylogenetic analysis, EU/EEA, week 40 2024 to week 33 2025

Clade	Reference virus	Reported clade	%	Assigned clade	%
V1A.3a.2 (C)	B/Austria/1359417/2021	78	1.8%	13[a]	0.3%
V1A.3a.2 (C.5)	B/Connecticut/01/2021	17	0.4%	19[b]	0.4%
V1A.3a.2 (C.5.1)	B/Catalonia/2279261NS/2023	2 477	57.7%	2 494	58.1%
V1A.3a.2 (C.5.6)	B/Switzerland/329/2024	780	18.2%	806	18.8%
V1A.3a.2 (C.5.7)	B/Guangxi-Beiliu/2298/2023	915	21.3%	943	22.0%
Undefined	–	25	0.6%	17	0.4%
Total		**4 292**	–	**4 292**	–

[a] *Sum of V1A.3a.2 subclades: C.3.*
[b] *Sum of V1A.3a.2 subclades: 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/Wisconsin/588/2019_Cell	A(H1N1)pdm09	5a.2	C	2019-12-19	EPI1661231
A/Sydney/5/2021_Egg	A(H1N1)pdm09	5a.2a	C.1	2021-10-16	EPI2020645
A/Victoria/4897/2022_Egg	A(H1N1)pdm09	5a.2a.1	D	2022-10-02	EPI2437457
A/Wisconsin/67/2022_Cell	A(H1N1)pdm09	5a.2a.1	C.1.1	2022-10-25	EPI2224978
A/Maine/10/2022	A(H1N1)pdm09	5a.2a	C.1.2	2022-10-29	EPI2604143
A/Bulgaria/234/2023	A(H1N1)pdm09	5a.2a	C.1.5	2023-01-15	EPI2639660
A/Washington/22/2023	A(H1N1)pdm09	5a.2a	C.1.3	2023-02-14	EPI2499374
A/Netherlands/10468/2023	A(H1N1)pdm09	5a.2a	C.1	2023-03-13	EPI2660407
A/South_Dakota/31/2023	A(H1N1)pdm09	5a.2a	C.1.6	2023-04-05	EPI2544350
A/Maldives/936/2023	A(H1N1)pdm09	5a.2a	C.1.4	2023-06-14	EPI2690628
A/Michigan/62/2023	A(H1N1)pdm09	5a.2a	C.1	2023-10-16	EPI3351800
A/Darwin/422/2023	A(H1N1)pdm09	5a.2a	C.1.7.1	2023-11-04	EPI2804451
A/Lisboa/188/2023	A(H1N1)pdm09	5a.2a	C.1.9	2023-11-22	EPI3506999
A/Netherlands/10481/2024	A(H1N1)pdm09	5a.2a.1	D.1	2024-02-12	EPI3425497
A/Poland/28/2024	A(H1N1)pdm09	5a.2a.1	D.4	2024-03-04	EPI3379561
A/Bretagne/05126/2024	A(H1N1)pdm09	5a.2a.1	D	2024-03-29	EPI3551548
A/Darwin/6/2021_Cell	A(H3N2)	2a	G.1	2021-03-16	EPI1885402
A/Stockholm/5/2021	A(H3N2)	2a	G.1	2021-04-16	EPI1884889
A/Darwin/9/2021_Egg	A(H3N2)	2a	G.1	2021-04-17	EPI1888006
A/Norway/24873/2021	A(H3N2)	2a.3	G.1.3	2021-10-24	EPI2024234
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/Finland/402/2023	A(H3N2)	2a.3	G.1.3.1	2023-08-01	EPI2736719
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
B/Washington/02/2019_Egg	B/Victoria	V1A.3	A.3.2	2019-01-19	EPI1482046
B/Croatia/7789/2019	B/Victoria	V1A.3a	A.3.1	2019-11-11	EPI1670646
B/Cote_dIvoire/948/2020	B/Victoria	V1A.3a.1	A.3.1.1	2020-05-28	EPI1843721
B/Austria/1359417/2021_Cell	B/Victoria	V1A.3a.2	C	2021-01-09	EPI1845793
B/Austria/1359417/2021_Egg	B/Victoria	V1A.3a.2	C	2021-01-09	EPI1987381
B/Stockholm/3/2022	B/Victoria	V1A.3a.2	C.5	2022-03-22	EPI2100743
B/Catalonia/2279261NS/2023	B/Victoria	V1A.3a.2	C.5.1	2023-01-03	EPI2690180
B/Catalonia/3514402NS/2023	B/Victoria	V1A.3a.2	C.5.4	2023-01-03	EPI2690374
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/Guangxi-Beiliu/2298/2023	B/Victoria	V1A.3a.2	C.5.7	2023-09-05	EPI3017633

HA: haemagglutinin.

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