SURVEILLANCE REPORT

Seasonal influenza, 2023–2024

Annual Epidemiological Report for 2023

Key facts

- The 2023–2024 influenza season was a short flu season compared with the previous seasons, with sentinel positivity above the 10% threshold for 15 weeks compared with 25 weeks in 2022–2023.
- The 2023–2024 season saw influenza activity return to patterns observed before the COVID-19 pandemic, although there were variations in timing and intensity across different countries.
- The percentage of positive specimens peaked at 39% in week 52, 2023. This was followed by a decrease until week 2, 2024, when it reached 29% positivity, before rising again to fluctuate around 35% positivity between weeks 3 and 6, 2024.
- The threshold of <10% positivity was passed in week 12, indicating the end of the seasonal influenza epidemic.
- In all surveillance systems, influenza A(H1N1)pdm09 viruses predominated during the season, followed by A(H3N2). Type B viruses were more prevalent from week 13 onward.
- Most genetically characterised influenza viruses fell within clades of the recommended vaccine components, but some A(H3N2) viruses were antigenically distinct from the vaccine viruses.
- Interim vaccine effectiveness estimations for the 2023–2024 season have been reported by the ECDC Vaccine Effectiveness, Burden and Impact Studies (VEBIS) multi-country network, with data collected from 15 European countries submitted from multi-country primary care and hospital study sites between September 2023 and January 2024. These data indicated that up to 51% (95% CI:41–59) and 38% (95% CI: 27 to 48) of vaccinated individuals in primary care and hospital settings, respectively, were protected against influenza.
- During 2023–2024, there was an increase in the influenza viruses with antiviral resistance against oseltamivir compared with the 2022–2023 season. Thirty-four influenza A(H1N1)pdm09 viruses and one influenza type B/Victoria virus were reported with reduced susceptibility against oseltamivir, compared with five A(H1N1)pdm09, one A(H3N2), and one B/Victoria virus in 2022–2023.

Methods

For a detailed description of methods used to produce this report, please refer to the 'Methods' chapter of the 'Introduction to the Annual Epidemiological Report' [1].

An overview of the national surveillance systems is available online [2].

Additional data on influenza are available from ECDC's online 'Surveillance atlas of infectious diseases' [3].

Surveillance of influenza in EU/EEA countries is carried out by the EU Respiratory Virus network, coordinated by the European Centre for Disease Prevention and Control (ECDC).

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Stockholm, November 2024

EU/EEA influenza surveillance is based on weekly data reported to ECDC by sentinel general practitioners (in some countries also by other physicians, such as paediatricians) and national influenza reference laboratories of the following year. Surveillance data include:

- The aggregate number of ILI and/or ARI cases reported by sentinel physicians[1] [2]. Each country also reports denominator data (population covered by sentinel surveillance) to enable the calculation of weekly ILI and ARI consultation rates.
- The aggregate number of sentinel specimens obtained from a systematic sample of ILI/ARI patients testing positive for influenza, by type, A subtype and B lineage [2]. Overall positivity rates of sentinel specimens are used to estimate the start, duration, and end of influenza activity; a 10% threshold is used to indicate the start of the seasonal epidemic.
- Genetic characterisation and strain-based antiviral susceptibility data for a subset of influenza viruses detected in sentinel and non-sentinel specimens [2].
- Case-based and aggregated hospital data reported by a subset of countries on a voluntary basis[2], including demographic, clinical and virological data [2].

Severe acute respiratory infection (SARI)-based surveillance systems used the SARI case definition, and most SARI data were reported from sentinel SARI sites. However, some countries used universal reporting systems.

Since the 2014–2015 season, influenza surveillance in the 53 countries of the World Health Organization (WHO) European Region has been jointly coordinated by ECDC and WHO's Regional Office for Europe. Starting in 2023–2024, the results are disseminated through a joint weekly summary, The European Respiratory Virus Surveillance Summary (ERVISS) (erviss.org) [4,5]. ERVISS describes the epidemiological and virological situation for influenza, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and respiratory syncytial virus (RSV) across the EU/EEA and the WHO European Region and follows the principles of integrated respiratory virus surveillance outlined in Operational considerations for respiratory virus surveillance in Europe [5].

Archived weekly summaries for the EU/EEA drafted by ECDC weekly are available in the Communicable Disease Threats Report (website).[4]

This report presents data from EU/EEA countries. Seasonal data in this report, covering the period from week 40, 2023 to week 20, 2024, were extracted from the database during week 21, 2024. Throughout the document, COVID-19 pandemic seasons (2020–2021) were excluded in all comparisons with standard flu seasons from the past. If not specified separately, the comparisons are to all other seasons (2014–2015 to 2022–2023).

Primary care sentinel surveillance

During the 2023–2024 season, in the EU/EEA, 89 343 specimens from sentinel primary care providers were tested for influenza virus and 15 028 (17%) of the specimens tested positive. The number of influenza virus detections from sentinel sources for this past season (n=15 028 out of 89 343 tests) decreased by 23% compared with 2022–2023 (n=19 488 out of 81 926 tests) but represented a 37% increase from the pre-pandemic season (e.g. in the pre-pandemic season 2019–2020, n=10 955 specimens tested positive; in 2018–2019, n=11 255; 2017–2018, n=16 265; and 2016–2017, n=10 879) [6-12].

The test positivity crossed the 10% threshold in week 49, 2023, indicating the start of the influenza seasonal activity. The activity started later than the previous season (week 50 in 2023–2024 season versus week 45 in 2022–2023 season). The 2023–2024 season was the shortest flu season compared with previous seasons: 15 weeks sentinel positivity above the 10% threshold in the 2023–2024 season compared with 25 weeks in the 2022–2023 and 2021–2022 seasons and 19 weeks in 2019–2020.

The percentage of positive specimens peaked at 39% in week 52, 2023, followed by a decrease until week 2, 2024, when it reached 29% positivity before rising again to fluctuate around 35% positivity between weeks 3 and 6, 2024. The positivity went back below the threshold of 10% positivity in week 12, indicating the end of the seasonal activity. The pooled test positivity for the EU/EEA did not go above 40%, which marks the 'high virus circulation' threshold, in any of the weeks in the 2023–2024 season (Figure 1).

Comparison between the pre- and post-pandemic seasons show that the mean positivity rate in the EU/EEA has decreased in the post-pandemic period (post-pandemic: mean positivity 13.8% in 2023–2024, 20.3% in 2022–2023, 14.5% in 2021–2022 versus pre-pandemic: 23.9% in 2019–2020, 25.2% in 2018–2019, 32.7% in 2017–2018, 25.6% in 2016–2017, 28.1% in 2015–2016, and 30.5% in 2014–2015). However, in half of EU/EEA countries (Belgium, Czechia, Estonia, France, Germany, Hungary, Italy, Lithuania, Luxembourg, the Netherlands,

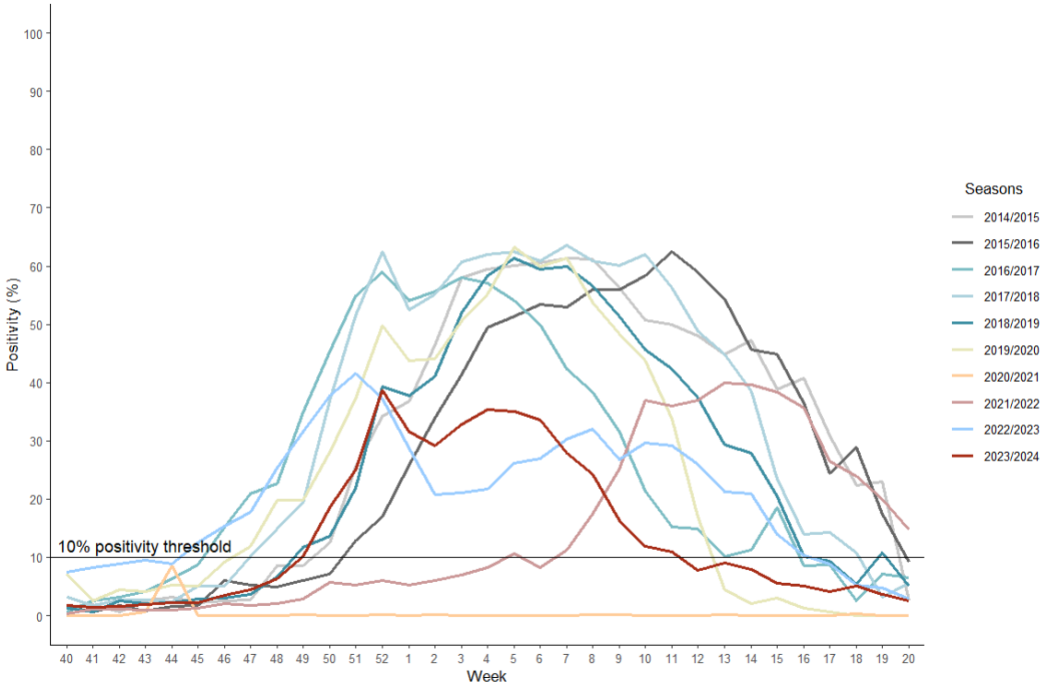
[1] ILI and a denominator were reported by Austria, Belgium, Croatia, Czechia, Denmark, Estonia, Finland, France, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Poland, Romania, and Slovenia.

ARI and a denominator were reported by Belgium, Bulgaria, Czechia, Estonia, Finland, France, Germany, Hungary, Latvia, Lithuania, Luxembourg, Romania, Slovenia, and Spain.

Poland, Portugal, Romania, Slovakia, Slovenia, Spain, and Sweden), the high virus circulation threshold in positivity (>40% threshold) was passed at some point during the 2023–2024 season (Annex, Figure A).

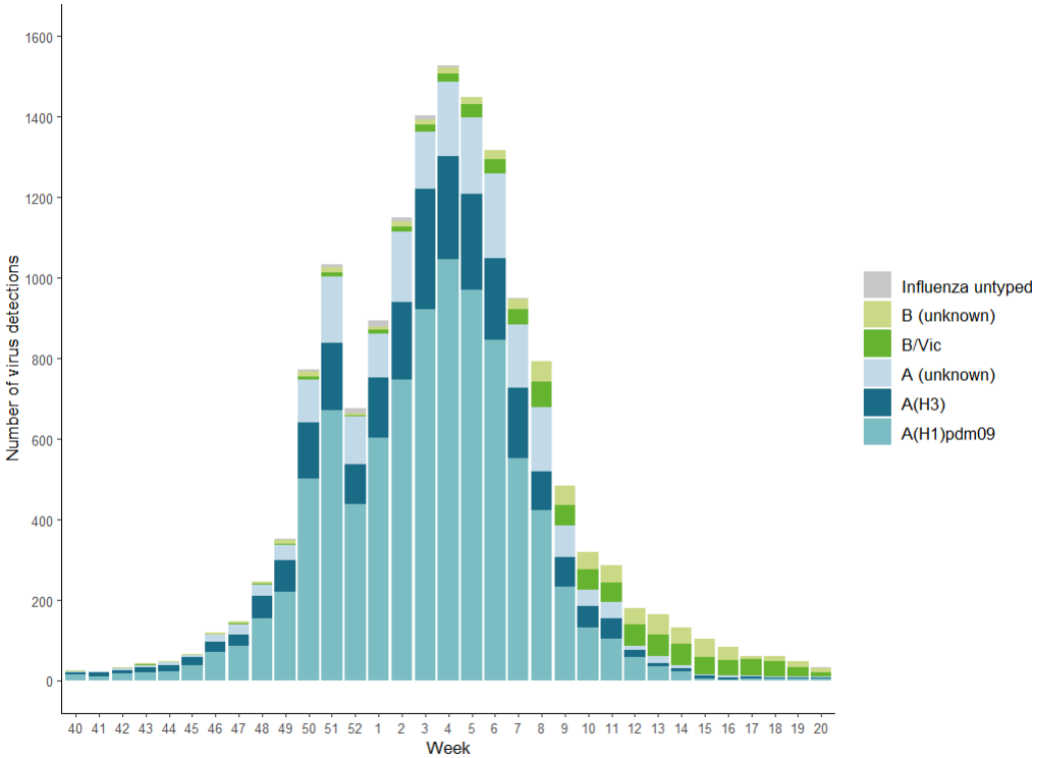
Of 15 028 positive sentinel specimens, 90% were influenza type A virus, 9.2% were type B virus and 0.6% were untyped (Figure 2). Of 13 562 influenza A viruses, 11 498 were subtyped. Of these, 8 986 (78%) resulted as A(H1N1)pdm09 viruses and 2 512 (23%) as A(H3N2) viruses. All the 1 383 influenza type B viruses reported that were ascribed to a lineage (n=767,) were B/Victoria. Virus (sub)type distribution by country varied throughout the season (Annex, Figure 1B).

Figure 1. Weekly proportion of sentinel specimens positive for influenza virus by season and week of reporting, EU/EEA, 2014–2015 to 2023–2024



** Seasons 2015–2016 and 2020–21 have 53 weeks of reporting and week 53 has been excluded in this display.*

Figure 2. Influenza virus detections from sentinel surveillance by virus (sub)type and lineage and week of reporting, week 40, 2023 to week 20, 2024, EU/EEA

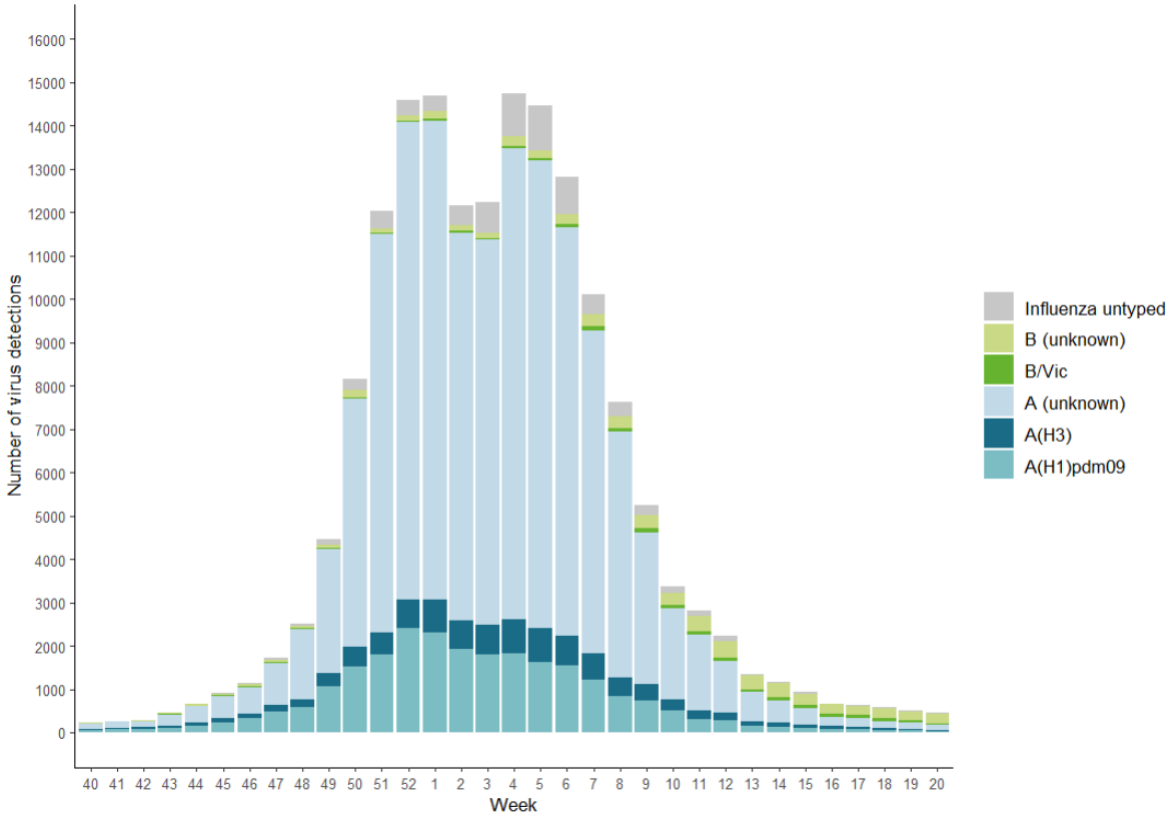


Non-sentinel surveillance

During the 2023–2024 season, 1 558 368 specimens from non-sentinel sources (hospitals, non-sentinel physicians, nursing/care homes, clinics, etc.) were tested for influenza in EU/EEA countries, and 166 150 (10%) of the specimens tested positive. The highest number of virus detections (14 732) was observed in week 4, 2024 (Figure 3).

Of 166 150 positive non-sentinel specimens, 15 1543 (91%) were influenza type A viruses, 7 333 (4%) were type B viruses, and 7 274 (4%) were untyped. Of 151 543 influenza type A viruses, 34 004 (22%) were subtyped: 24 449 (72%) were A(H1)pdm09, and 9 555 (28%) were A(H3). Of 7 333 influenza type B viruses, 1 475 (20%) were assigned as B/Victoria, and the lineage was not determined for the remainder (Figure 3).

Figure 3. Influenza virus detections from non-sentinel surveillance by virus (sub)type and lineage and week of reporting, week 40, 2023 to week 20, 2024, EU/EEA

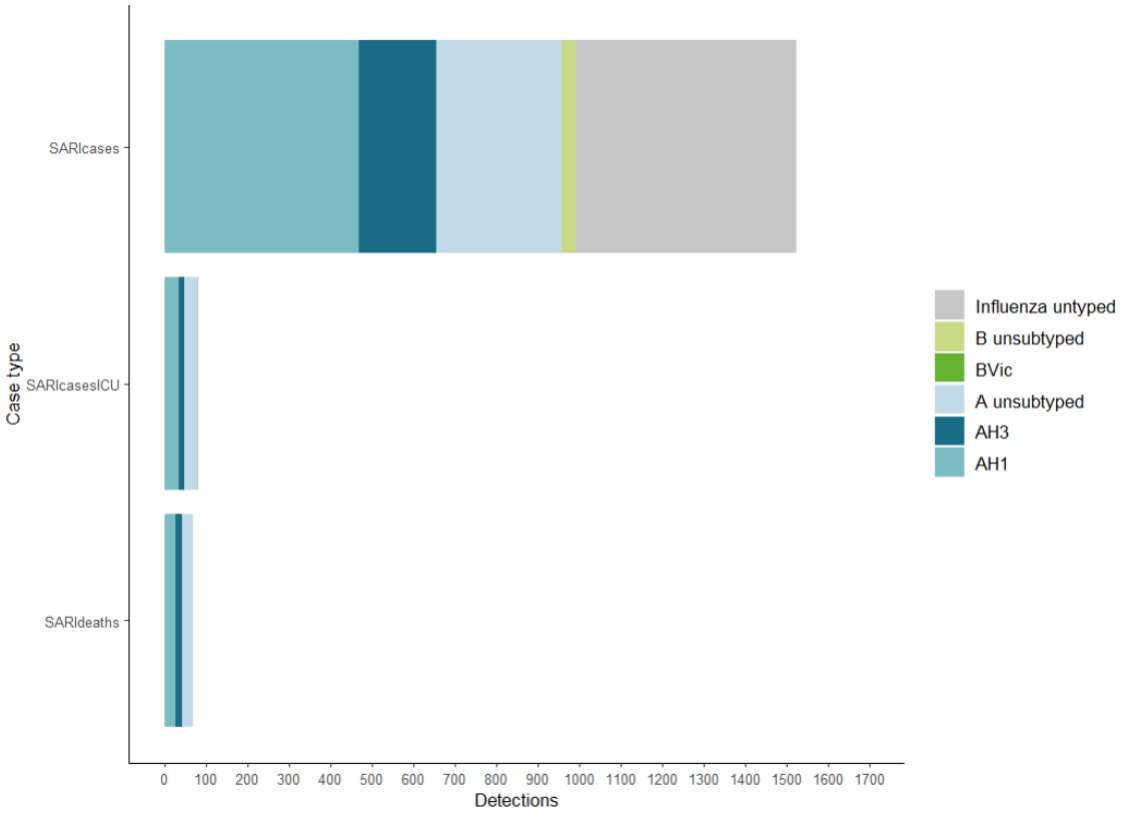


Severe acute respiratory infection-based surveillance

Ten countries (Belgium, Croatia, Germany, Greece, Ireland, Lithuania, Malta, Romania, Slovakia, and Spain) reported a total of 73 645 SARI patients from hospital settings, 2 847 (4%) of whom died.

Of 59 082 SARI cases tested for influenza, 5 042 were positive (9%). The highest number of virus detections was observed during week 5, 2024. Among the SARI cases with confirmed influenza infection, type A viruses were the most common type (n=958; 28%), followed by type B viruses (n=35; 1%) and influenza untyped (n=2 431; 70%). A total of 657 A viruses were subtyped: 470 (72%) were A(H1)pdm09 viruses and 187 (28%) were A(H3) viruses. The two influenza B viruses ascribed to a lineage were B/Victoria.

Figure 6. Distribution of virus types, subtypes and lineages by type of ward and fatal cases, based on SARI surveillance, week 40, 2023 to week 20, 2024, EU/EEA



Hospitalisations due to influenza

Laboratory-based surveillance from intensive care units (ICU) and other wards (non-ICU)

Seven countries (Czechia, Finland, France, Ireland, Malta, Slovakia, and Sweden) reported a total of 8 209 laboratory-confirmed hospitalised influenza cases during the 2023–2024 influenza season. All countries reported intensive care unit (ICU) cases, except Finland. All countries except Finland, France, and Sweden reported cases that were not from ICUs. Overall, most cases (n=6 300, 77%) were due to influenza type A viruses and 459 (6% of the cases) were reported as type B viruses, while 1 450 (18%) were untyped (Figure 5).

In laboratory-confirmed influenza cases reported from ICUs (n=1 604), influenza virus types A, B and untyped viruses were detected in 1 444 (90%), 38 (2%) and 122 (7%) people, respectively. France reported the highest number of ICU cases with 897 (56%), followed by Sweden with 338 (21%), Czechia with 188 (12%), and Ireland with 123 (8%). The most affected age groups were people aged 65–79 years (25%) and 30–64 years (25%), followed by people aged 80 years and older (17%), 0–4 years (16%), 5–14 years (12%), 15–29 years (5%), and of unknown age (0.06%) (Figure 4). Across all age groups, influenza A viruses without subtype constituted most of the virus detections (n=5 065). Of the subtyped viruses (n=1 235), more influenza A(H1)pdm09 (n=783, 63%) than A(H3) (n=452, 36%) infections were detected. None of the influenza type B viruses (n=459) were ascribed to a lineage (Figure 4).

For laboratory-confirmed influenza cases reported from non-ICU wards (n=6 100), 4 404 of the viruses detected were type A viruses (72%) and 410 (7%) were type B viruses. Of the subtyped influenza A viruses, 58% (n=471) were A(H1N1)pdm09 and 42% (n=345) were A(H3). The laboratory-confirmed influenza cases with known age reported from non-ICU wards were distributed as follows: 1 132 (19%) were 80 years and older, 1 324 (22%) were 65–79 years, 1 237 (20%) were 30–64 years, 327 (5%) were 15–29 years, 895 (14%) were 5–14 years, and 1 185 (19%) were 0–4 years.

Of 8 214 hospitalised patients with laboratory-confirmed influenza, 505 were reported to have died. Of the typed viruses (n=463) most deaths were detected with influenza type A (unsubtyped) virus (n=341; 73%), followed by A(H1)pdm09 (94; 20%), A(H3) (17; 3%) and influenza type B viruses (11; 2%). Overall, most deaths occurred in individuals aged 60–79 years (195; 39%) followed by 80 years and above (162; 32%), 3–64 years (132; 26%), 0–4 years (7; 1.4%), 5–14 years (5; 0.9%), and 15–29 years (4; 0.8%).

Figure 4. Distribution of virus types, subtypes and lineages by age group in people warded in intensive care units, week 40, 2023 to week 20, 2024, EU/EEA

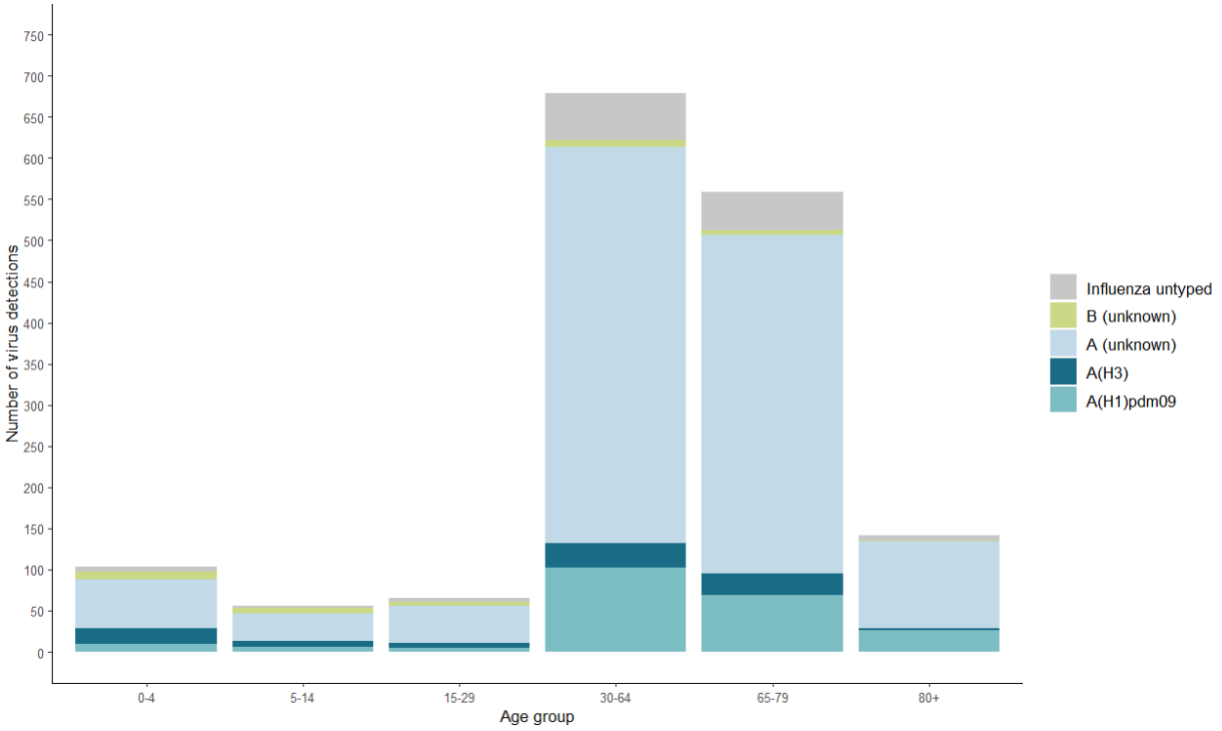
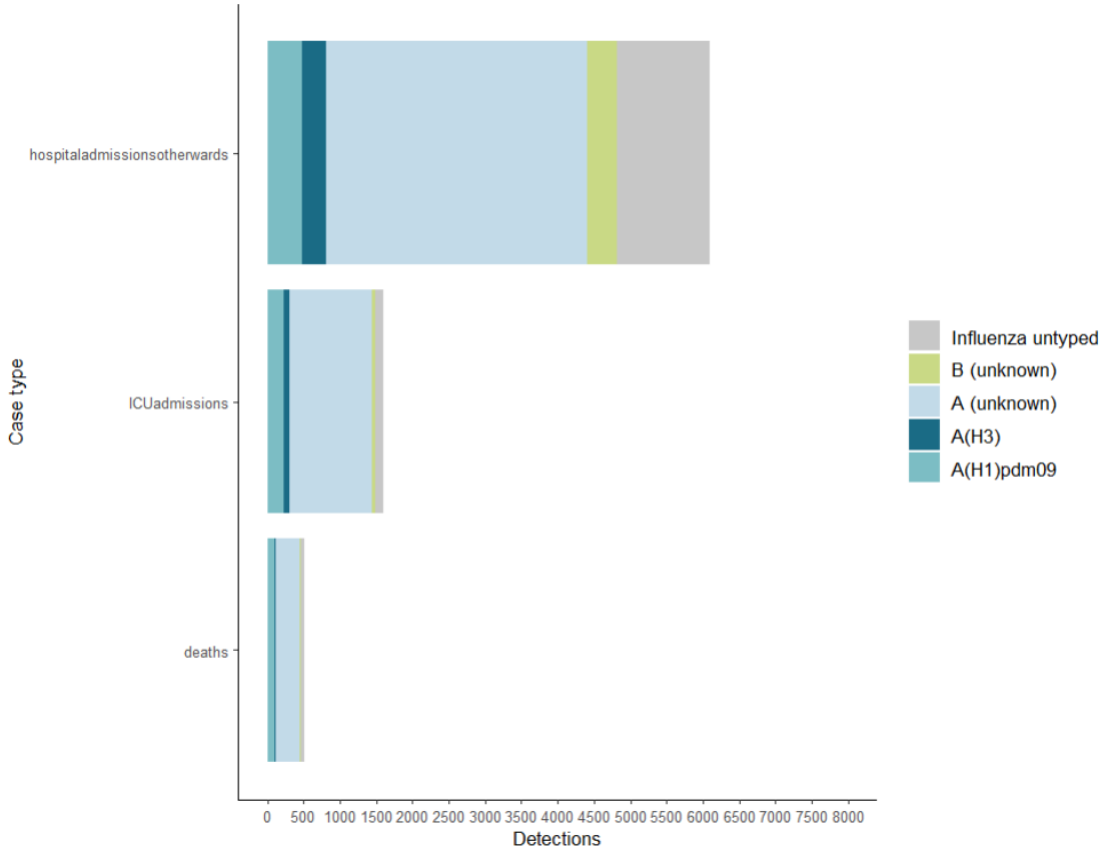


Figure 5. Distribution of virus types, subtypes and lineages by type of ward and fatal cases, week 40, 2023 to week 20, 2024, EU/EEA



Virus characterisations

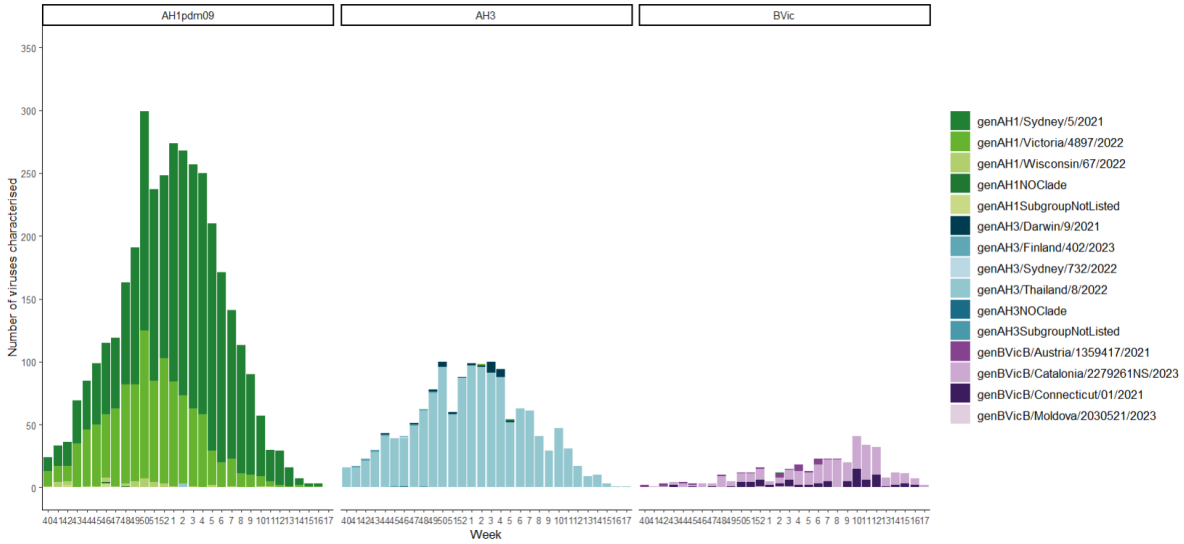
For specimens collected since week 40, 2023, genetic characterisation data were reported to TESSy for 5 420 viruses (Figure 7). Among these, 5 043 (93%) were influenza A and 377 (6%) were influenza B.

Of the 3 630 characterised A(H1N1)pdm09 viruses (72% of all influenza A viruses), 2471 (68%) were assigned to the genetic group A/Sydney/5/2021 (clade 5a.2a), 43 (1.2%) to A/Wisconsin/67/2022 (clade 5a.2a.1) and 1116 (31%) A/Victoria/4897/2022 (clade 5a.2a.1). They all belonged to the genetic clade 5a.2, which is the virus component for the 2023–2024 northern hemisphere vaccine. In addition, 7 (0.2%) viruses could not be attributed to a pre-defined subgroup in the guidance.

For the 1 403 genetically characterised A(H3N2) viruses (28% of influenza A viruses), 1 363 (97%) belonged to clade 2a.3a.1, represented by A/Thailand/8/2022, which has antigenically moved away from the recommended clade for the vaccine virus strain for the 2023–2024 northern hemisphere influenza season A/Darwin/9/2021. In our data, only 30 (2.1%) of the A(H3N2) viruses were assigned to the genetic group A/Darwin/9/2021 (clade 2a), 10 (0.7%) to the genetic group A/Finland/402/2023 (clade 2a.3a) and 1 (0.07%) to the genetic group A/Sydney/732/2022 (clade 2a.3b). In addition, three (<1%) viruses could not be attributed to a pre-defined subgroup in the guidance.

The B/Victoria lineage constituted all 376 characterised viruses. All the viruses belonged to clade V1A.3a.2, the recommended vaccine virus strain for the 2023–2024 northern hemisphere influenza season. Of these, 263 (70%) belonged to B/Catalonia/227926INS/2023, 83 (22%) belonged to B/Connecticut/01/2021, 27 (7%) were represented by B/Austria/1359417/2021, the vaccine component, and 3 (0.8%) to the reference virus B/Moldova/2030521/2023. There were no reports of B/Yamagata lineage.

Figure 7. Distribution of influenza virus genetic clades, by (sub)type, week 40, 2023 to week 20, 2024, EU/EEA



Antiviral susceptibility

Since week 40, 2023, 4 379 viruses were assessed genotypically and/or phenotypically for susceptibility to oseltamivir (2 852 A(H1N1)pdm09, 1 209 A(H3), and 318 type B viruses), 4 263 viruses for susceptibility to zanamivir (2 768 A(H1N1)pdm09, 1 177 A(H3), and 318 type B viruses) and 1 420 viruses for susceptibility to M2 blockers (1 051 A(H1N1)pdm09, 327 A(H3), and 42 type B viruses). During this period, 3 006 viruses were assessed genotypically for susceptibility to baloxavir marboxil (1 991 A(H1N1)pdm09, 891 A(H3), and 124 type B viruses).

Thirty-four (1%) influenza A(H1N1)pdm09 viruses and one influenza (0.3%) type B/Victoria virus were reported with reduced susceptibility against oseltamivir. Two A(H1N1)pdm09 (0.07%) viruses and one B/Victoria virus (0.3%) were reported with reduced susceptibility against zanamivir. All (1 420) viruses were reported with reduced susceptibility against M2 blockers. Two A(H1N1)pdm09 viruses (0.1%) and two A(H3) viruses (0.2%) were associated with reduced susceptibility to baloxavir marboxil.

Genotypically, five A(H1N1)pdm09 viruses were identified as carrying the mutation H275Y in the neuraminidase gene (NA) that is associated with highly-reduced inhibition by oseltamivir. One A(H1N1)pdm09 virus was identified as carrying the mutation I223T, and 26 carrying the combination of I223T and S247N, which are associated with reduced inhibition by oseltamivir.

Phenotypically, four A(H1N1)pdm09 viruses were identified with reduced susceptibility to oseltamivir and one B/Victoria virus to Zanamivir.

Vaccine effectiveness

On 24 February 2023, WHO published recommendations for the components of influenza vaccines for use in the 2023–2024 northern hemisphere influenza season [13]. One change in the vaccine virus components was recommended compared with the northern hemisphere 2022–2023 vaccines: the A(H1N1)pdm09 component was replaced by A/Victoria/4897/2022 (H1N1)pdm09-like virus in the egg-based vaccines [14]. The recommended vaccine composition for the 2023–2024 influenza season in the northern hemisphere contained the following (egg-based and cell culture or recombinant-based vaccines respectively): an A/Victoria/4897/2022 or A/Wisconsin/67/2022 (H1N1)pdm09-like virus (subclade 5a.2a.1); an A/Darwin/9/2021 or A/Darwin/6/2021 (H3N2)-like virus (clade 2a); and a B/Austria/1359417/2021 (B/Victoria lineage)-like virus (subclade V1A.3a.2) [13].

Interim vaccine effectiveness (VE) estimations for the 2023–2024 season have been reported by the ECDC Vaccine Effectiveness, Burden and Impact Studies (VEBIS) multi-country network, with data collected from 15 European countries (across two studies between September 2023 and January 2024) assessing patients recruited in primary care and hospital settings [15]. Interim VE against influenza A (all subtypes) was 51% (95% confidence interval (CI): 41 to 59) among primary care patients and 38% (95% CI: 27 to 48) among hospitalised patients.

Against influenza A(H1N1)pdm09, VE point estimates were 53% (95% CI: 41 to 63) in primary care and 44% (95% CI: 30 to 55) in hospitals. The point estimates for VE against A(H1N1)pdm09 viruses were also higher among children (85%; 95% CI: 71 to 93), compared with all ages 53% (95% CI: 41 to 63). VE clade-specific results in primary care and for all ages were 52% (95% CI: −7 to 78) against clade 5a.2a and 39% (95% CI: −44 to 74) against clade 5a.2a.1.

Against influenza A(H3N2), VE point estimates among all ages were 30% (95% CI: −3 to 54) in primary care and 14% (95% CI: −32 to 43) in hospitals [16]. According to the study, the 2023/24 interim VE point estimates against influenza A(H3N2) (30–35%) in the primary care setting were similar to the estimate against A(H3N2) in 2022/23 but for the hospital setting, the interim 2023/24 point estimates (13–14%) against influenza A(H3N2) were lower than the estimates of 20–25% in the 2022/23 season. This might have been due to the small sample size for the interim vaccine effectiveness against A(H3N2), as influenza A(H1N1)pdm09 circulation has dominated the season thus far, resulting in low precision and some stratified estimates not being calculated [15,16].

These interim results indicate that during the 2023–2024 influenza season, up to 51% (95% CI:41 to 59) and 38% (95% CI: 27 to 48) of vaccinated individuals in primary care or hospital settings, respectively, were protected against influenza. However, these results should be interpreted with caution pending end-of-season influenza VE estimates and further genetic characterisation data.

Discussion

The 2023–2024 influenza season was a short flu season, with 15 weeks of sentinel positivity above the 10% threshold compared with 25 weeks in the 2022–2023 and 2021–2022 seasons and 19 weeks in 2019–2020.

The 2023–2024 season saw influenza activity return to temporal patterns of the start of the season observed before the COVID-19 pandemic, although there were variations in timing and intensity among different countries. Virus type and subtype distribution by country and surveillance system varied across the season (Annex figures B and C). Overall, influenza A(H1N1)pdm09 viruses were dominant in specimens from both sentinel and non-sentinel sources, both from primary and secondary care. Hospitalisations due to influenza and SARI cases were mainly due to influenza type A viruses and were mostly reported among people aged 60 years and older. Similar observations were made in previous seasons.

With more than threefold increase in testing in the past three (post-pandemic) seasons (n=89 343 in 2023–2024 versus n=28 062 in the 2019–2020 season), the number of influenza virus detections from sentinel sources show that the mean positivity has remained between 15 to 20 percent in the post-pandemic seasons compared with 25 to 32 percent mean positivity rates during the pre-pandemic seasons.

The majority of genetically characterised A(H1N1)pdm09 and B/Victoria lineage viruses fell into clades covered by the recommended vaccine components. Antigenic characterisation data presented in the WHO 2024–2025 northern hemisphere vaccine composition report [17] indicated that current northern hemisphere vaccine components were well matched to circulating 5a.2a and 5a.2a.1 A(H1N1)pdm09 subclades and V1A.3a.2 B/Victoria subclades. While vaccine components appeared well matched for 2a.3a A(H3) clade viruses, 2a.3a.1 clade viruses appeared less well matched. Based on human post-vaccination serology studies, haemagglutination inhibition and virus neutralisation against some recent 2a.3a.1 viruses were significantly reduced for some serum panels [15] and this was reflected also in the interim vaccine effectiveness estimates.

While interim, mid-season data indicate vaccination has been protective against symptomatic influenza in a European context, with a up to 51% and 38% of vaccinated individuals in primary care or hospital settings, respectively, end-of-season influenza vaccine effectiveness estimates and further genetic characterisation data are awaited to better understand the level of protection conferred by influenza vaccines, as well as age-specific differences in protection.

Public health implications

As EU/EEA countries have moved towards integrating surveillance of SARS-CoV-2, influenza and RSV, underlying systems are changing and reported data might not be comparable with historical data [5]. Continued surveillance activities for respiratory viruses, including influenza, are crucial to understand the epidemiological situation and assess the burden on healthcare and population groups.

Primary care sentinel surveillance was disrupted in the EU/EEA countries during the COVID-19 pandemic and the 2023–2024 influenza season marks the first post-pandemic influenza season and re-establishment of the sentinel systems. Currently, 11 countries in the EU/EEA have established SARI monitoring systems, which represents one third of EU/EEA countries. Hospitalised case data and ICU cases were reported by fewer than 10 countries. Therefore, severe disease surveillance in hospitals should be further developed and strengthened in countries that do not have severe respiratory virus monitoring in place.

The analysis shows that the EU/EEA is reverting to pre-pandemic flu patterns in terms of the start time of the season indicating the need to continue the regular influenza vaccination campaigns in the autumn. People aged 65 years and above have been identified as the most affected age group for severe influenza infection in the EU/EEA for the past 10 years and deserve special attention as a risk group to be targeted by vaccination.

The increase in viruses with reduced susceptibility to oseltamivir this season underlines the continued need for virological monitoring. In a same way, the continued genetic and antigenic diversification of especially A(H3N2) viruses calls for detailed virus characterisation and reporting during the influenza season.

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Annex 1

Figure 1A. Test positivity by week and country, sentinel surveillance, week 40, 2023 to week 20, 2024, EU/EEA

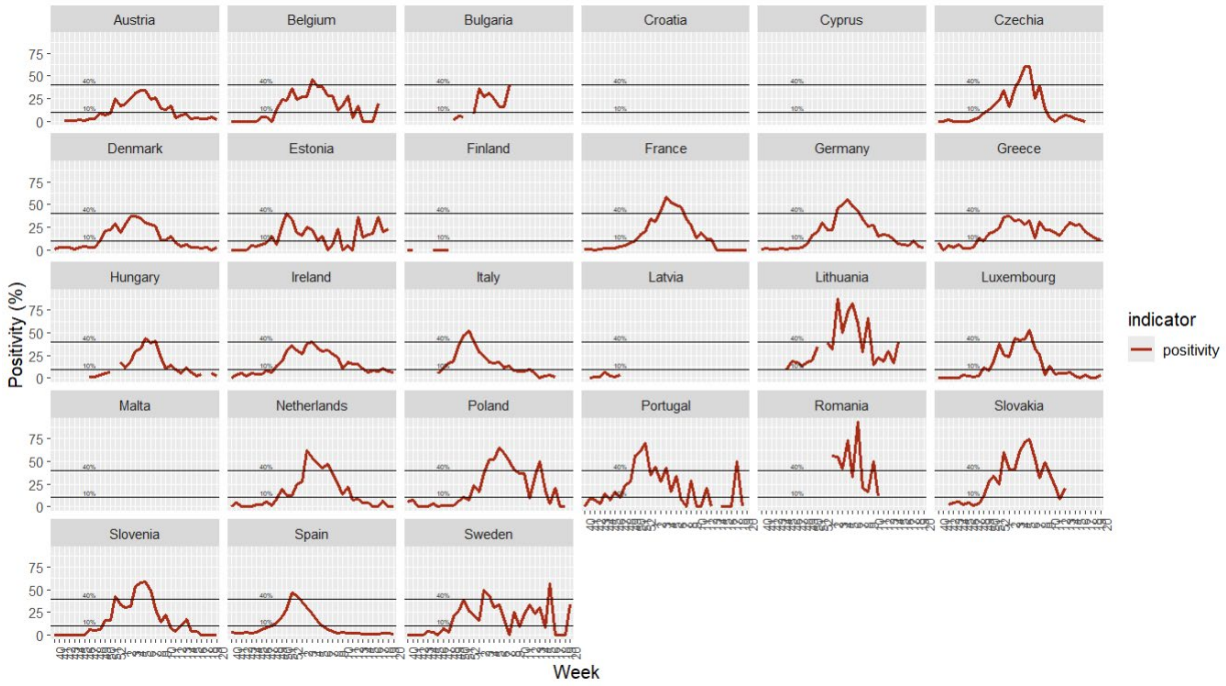

Figure 1B. Country panels for detections from sentinel sites by influenza (sub)types, week 40, 2023 to week 20, 2024, EU/EEA

Figure 1C. Variations in influenza (sub)types over the seasons, week 40, 2023 to week 20, 2024, EU/EEA