Seasonal influenza 2022–2023

Annual Epidemiological Report for 2023

Key facts

- The 2022/2023 influenza season marked the return of influenza virus activity at almost pre-pandemic levels in the EU/EEA countries. This season was characterised by an earlier start of the seasonal epidemic and an earlier peak in positivity compared to the four previous seasons.
- The percentage of positive specimens peaked at 42% in week 51/2022, followed by a decrease until week 4/2023 when it reached 22% positivity before rising again to fluctuate around 28% positivity between week 5–12/2023.
- The threshold of <10% positivity was passed in week 17, indicating the end of the seasonal influenza epidemic.
- Overall, influenza A(H3N2) viruses dominated in sentinel primary care specimens, however higher circulations of A(H1N1)pdm09 (from week 50/2022) and type B viruses (from week 2/2023) were observed.
- In non-sentinel specimens, A(H3N2) dominated over A(H1N1)pdm09 viruses.
- Both influenza type A and type B viruses have been detected in hospitalised patients in ICUs and other wards, with influenza type A the dominant type. Similarly, influenza type A viruses have been dominant among SARI patients.
- The majority of genetically characterised influenza viruses fell within clades of the recommended vaccine components.
- Interim vaccine effectiveness estimations for the 2022−2023 season have been reported by the ECDC Vaccine Effectiveness, Burden and Impact Studies (VEBIS) multi-country network, with data collected from 16 European countries from 3 October 2022 to 31 January 2023. These interim results indicate a ≥27% and a ≥50% reduction in disease occurrence among all-age influenza vaccine recipients for influenza A and B, respectively during the 2022−2023 influenza season.
- Very few influenza viruses with antiviral resistance were reported.

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 European Influenza Surveillance Network (EISN), coordinated by the European Centre for Disease Prevention and Control (ECDC).

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 from week 40 to week 20 of the following year.

Surveillance data include:

- Qualitative indicators of influenza activity, namely intensity, geographical spread and trend. Intensity – ranging from low activity (i.e. no activity or activity at baseline level) to very high – is an indicator of the level of influenza activity. Geographical spread – ranging from no activity to widespread – refers to the number of affected areas in a given country. Trend – increasing, stable or decreasing – compares the level of sentinel consultations for influenza-like illness (ILI)/ acute respiratory infection (ARI) against the previous week.
- 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 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 hospital data reported by a subset of countries on a voluntary basis[2], including demographic, clinical and virological data [2].

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. Results are disseminated through a joint weekly bulletin (www.FlunewsEurope.org) [4].

This report presents data from EU/EEA countries. Archived weekly data from October 2014 onwards are available from: http://www.flunewseurope.org/Archives [4].

Seasonal data in this report, covering the period from week 40/2022 to 20/2023, were extracted from the database during week 21/2023.
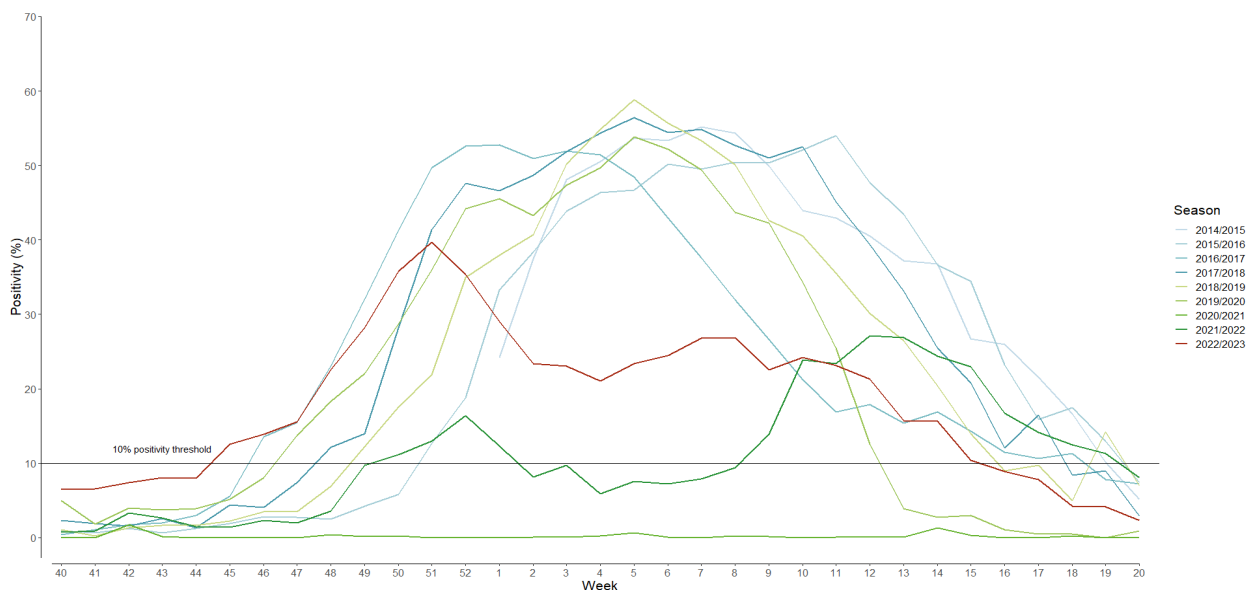
Sentinel surveillance

During the 2022−2023 season, 81 800 specimens from sentinel primary care providers were tested for influenza virus and 19 538 (24%) of the specimens tested positive in the EU/EEA. The number of influenza virus detections from sentinel sources for this season (n=19 538) increased more than four-fold compared to 2021−2022 (n=4 609) and represented the highest number of detections for the previous four seasons (e.g. in the pre-pandemic season 2019−2020 a total of 11 978 specimens tested positive) [5-8].

The positivity crossed the 10% threshold in week 45/2022, indicating the start of seasonal activity. The activity started earlier than in the four previous seasons, ranging from week 47 (2019/2020 season) to week 8 (2021/2022 season). The 2022−2023 season was much longer than the previous season − 24 weeks sentinel positivity above the 10% threshold compared to 13 weeks in 2021−2022. The percentage of positive specimens peaked at 42% in week 51/2022, followed by a decrease until week 4/2023, when it reached 22% positivity before rising again to fluctuate around 28% positivity between weeks 5 and 12/2023. The positivity crossed the threshold with values of <10% in week 17, indicating the end of the seasonal activity. Only week 51, with 42% positivity, was marked as 'high virus circulation with a level above 40%' (Figure 1).

Of 19 538 positive sentinel specimens, 67% were type A and 33% were type B virus. Of 13 126 influenza A viruses, 11 257 were sub-typed as 3 405 (30%) A(H1N1)pdm09 and 7 852 (70%) as A(H3N2). Of 6 412 influenza type B viruses reported, 1 968 were ascribed to a lineage, all as B/Victoria. One B/Yamagata virus was detected and confirmed as a live attenuated virus vaccination (LAIV) - related detection (Figure 2). Virus type and subtype prevalence by country varied throughout the season.

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[1] ILI and a denominator were reported by Austria, Belgium, Croatia, Cyprus, Czechia, Denmark, Estonia, Finland, France, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxemburg, Malta, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain and United Kingdom. ARI and a denominator were reported by Belgium, Bulgaria, Cyprus, Czechia, Estonia, Finland, Germany, Latvia, Lithuania, Luxemburg, the Netherlands, Romania, Slovakia and Slovenia.

Figure 1. **Weekly proportion of sentinel specimens positive for influenza virus by season and week of reporting, EU/EEA, 2010−11 to 2021−22**

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, weeks 40/2021 to 20/2022, EU/EEA
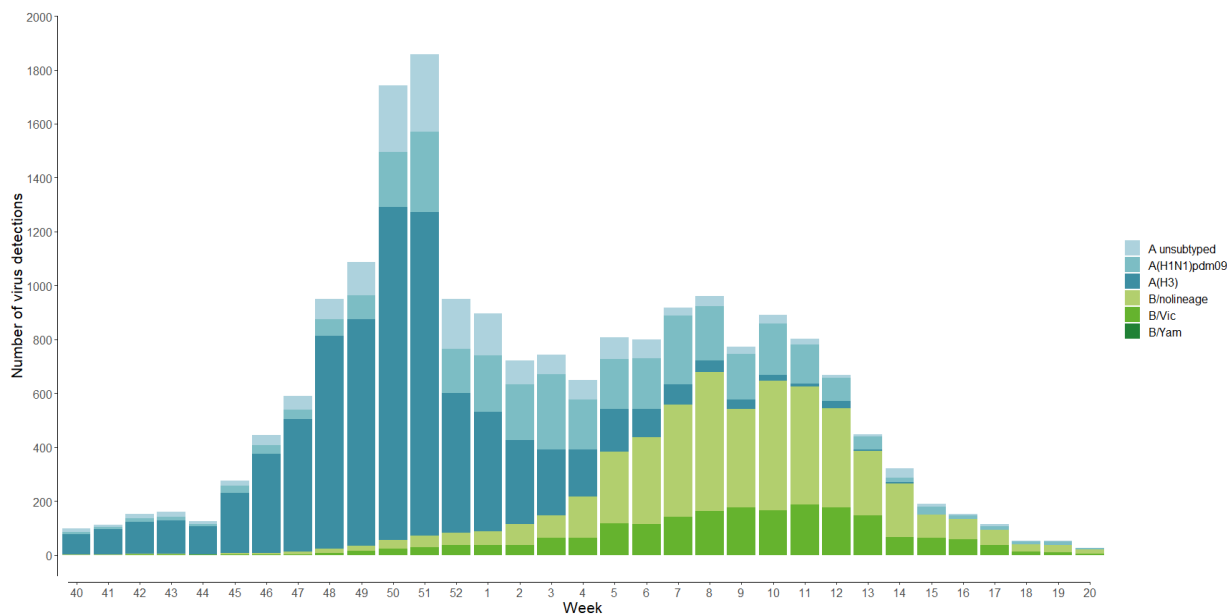

Non-sentinel surveillance

During the 2022−2023 season, 1 702 059 specimens from non-sentinel sources were tested for influenza in EU/EEA countries and 176 358 of the specimens tested positive. The highest number of virus detections was observed for week 51/2022 (Figure 3).

Of 176 358 positive non-sentinel specimens, 129 482 (73%) were type A and 46 876 (27%) were type B viruses; comparable proportions were seen in sentinel surveillance data. Of 129 482 influenza type A viruses, 30 050 (23%) were subtyped: 18 604 (62%) as influenza A(H3N2) and 11 446 (38%) as A(H1N1)pdm09. Of 46 876 influenza type B viruses, all 4 925 (12%) were assigned B/Victoria (Figure 3). One B/Yamagata virus was detected and confirmed as a live attenuated virus vaccination (LAIV)-related detection [9].

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Figure 3. Influenza virus detections from non-sentinel surveillance by virus (sub)type and lineage and week of reporting, weeks 40/2021 to 20/2022, EU/EEA
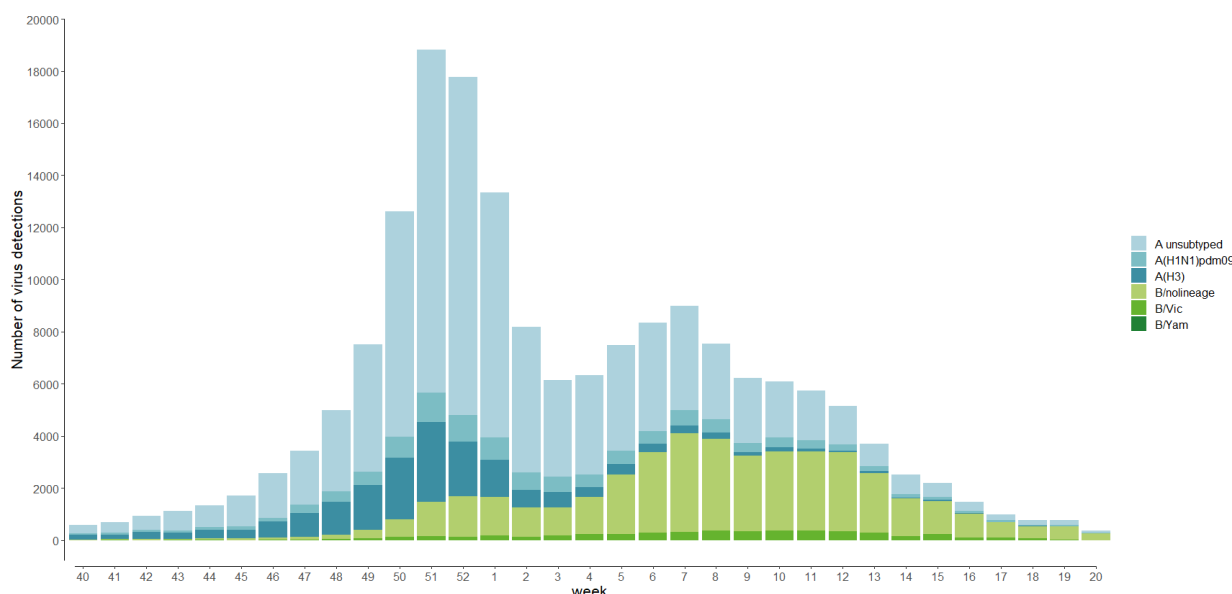
Hospitalisations due to influenza

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

Four countries (Czechia, France, Ireland and Sweden) reported a total of 5 587 laboratory-confirmed hospitalised influenza cases during the 2022−2023 influenza season. All four countries reported intensive care unit (ICU) cases, while only Czechia and Ireland reported cases in non-ICU. Most cases (93%) were due to influenza type A viruses and 7% of the cases were reported as type B.

In laboratory-confirmed influenza cases reported from ICUs (n=1 596), influenza virus type A and type B viruses were detected in 1 117 (86%) and 479 (14%), respectively. France reported 957 (60%) of the cases, followed by Sweden (345; 22%), Ireland (151; 9%) and Czechia (143; 9%). No influenza type B virus was ascribed to a lineage. Most affected age-groups were people aged 60−79 years (42%) followed by 40−59 years (23%), 0−19 years (16%), 20−39 years (11%) and 80+ years (8%) (Figure 4). Across all age groups, influenza A viruses without subtype constituted most of the virus detections (n=1 117); of the subtyped viruses (n=253), more influenza A(H3N2) (59%) than A(H1N1)pdm09 (41%) infections were detected. None of the influenza type B viruses (n=226) were ascribed to a lineage (Figure 4).

For laboratory-confirmed influenza cases reported from non-ICU wards (n=3 991), most of the viruses detected were type A viruses (3 811; 96%) and (180; 4%) type B viruses. Of the subtyped influenza A viruses, 63% (n=251) were A(H1N1)pdm09 and 37% (n=148) A(H3N2). Only one influenza type B virus was ascribed to a lineage as B/Victoria. The laboratory-confirmed influenza cases with known age reported from non-ICU wards fell in four age groups: 1 714 (43%) were 65 years and older, 1 376 (34%) were 15−64 years, 500 (13%) were 0−4 years and 401 (10%) were 5−14 years.

Of 5 587 hospitalised patients with laboratory-confirmed influenza, 367 were reported to have died; 246 and 121 fatal cases occurred in ICU and non-ICU wards, respectively. Of the typed viruses (n=361) most deaths were attributed to unsubtyped influenza type A virus (n=280; 78%), followed by A(H3N2) (40; 11%), A(H1N1)pdm09 (23; 6%) and influenza type B viruses (18; 5%). Similarly, of 240 typed viruses from fatal cases in ICUs, 179 (74%) were reported as unsubtyped influenza type A virus, 25 (10%) as A(H3N2), 18 (8%) as A(H1N1)pdm09 and 18 (8%) as influenza type B viruses. Overall, the majority of deaths occurred in individuals aged 60−79 years (177; 49%) followed by 80+ years (100; 28%), 40−59 (49; 14%), 20−39 years (19; 5%) and 0−19 (16; 4%).

Figure 4. Distribution of virus types, subtypes and lineages by age group in ICU, weeks 40/2021 to 20/2022, EU/EEA
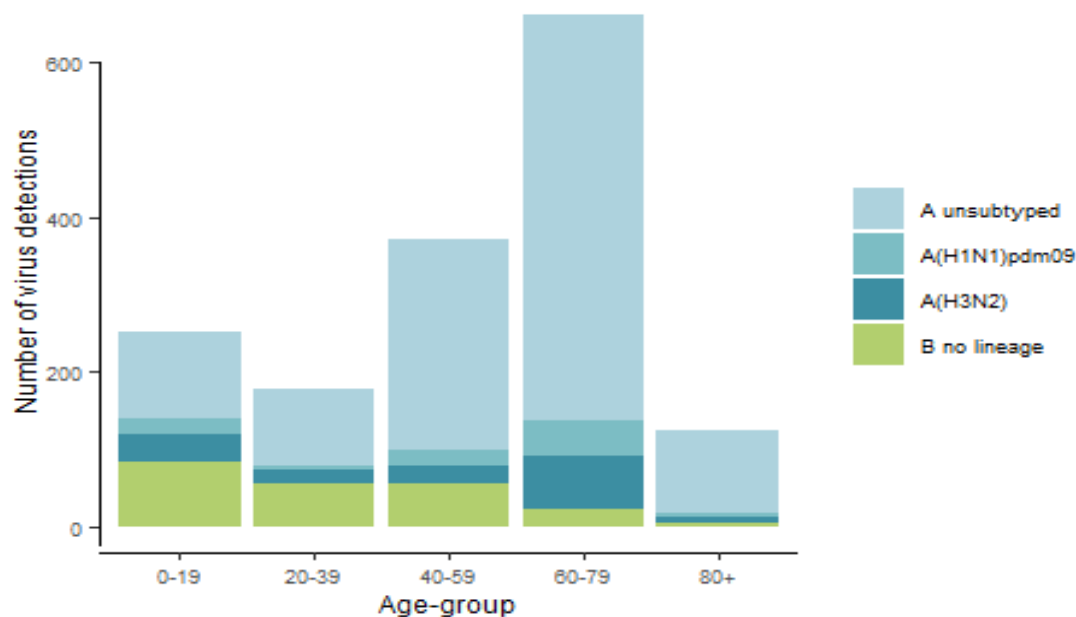
Severe acute respiratory infection (SARI)-based surveillance

Nine countries (Belgium, Croatia, Germany, Ireland, Lithuania, Malta, Romania, Slovakia and Spain) reported a total of 41 097 SARI patients from hospital settings, 3 857 of whom died in the hospital.

Of 39 438 SARI cases tested for influenza, 1 733 were positive (4%). The highest number of virus detections was observed during week 52/2022. Among the SARI cases with confirmed influenza infection, type A viruses were the most common type (n=1 269; 73%) and 913 were subtyped: 476 (52%) were A(H3N2) viruses and 437 (48%) were A(H1N1)pdm09 viruses. All influenza B viruses ascribed to a lineage were B/Victoria (n=76).

Virus characterisations

For specimens collected since week 40/2022, genetic characterisation data were reported to TESSy for 5 176 viruses. Among the genetically characterised viruses, 4 085 (79%) were influenza A and 1 091 (21%) were influenza B. Of the 1 661 characterised A(H1N1)pdm09 viruses (41% of all influenza A viruses), 770 (46%) were assigned to the genetic group A/Sydney/5/2021 and 621 (37%) to A/Norway/25089/2022 and 12 (<1%) A/Victoria/2570/2019, which all belong to genetic group 6B.1A.5a.2, the virus component for the 2022−2023 northern hemisphere vaccine. The remaining five (<1%) belonged to the 6B.1A.5a.1 group, represented by A/Guangdong-Maonan/SWL1536/2019. In addition, 253 (15%) viruses could not be attributed to a pre-defined subgroup in the guidance.

For the 2 424 genetically characterised A(H3N2) viruses (59% of influenza A viruses), the majority, 1 374 (57%), belonged to clade 3C.2a1b.2a.2, represented by A/Bangladesh/4005/2020. In addition, 806 (33%) viruses were assigned to the genetic group A/Slovenia/8720/2022 and 154 (6%) viruses to the genetic group A/Darwin/9/2021, both in the clade 3C.2a1b.2a.2, which was the recommended clade for the vaccine virus strain for the 2022−2023 northern hemisphere influenza season. Of the remainder, three (<1%) belonged to the subclade 3C.2a1b.1a, represented by A/Denmark/3264/2019. Of all the reported A(H3N2) viruses characterised, 87 (4%) viruses could not be attributed to a pre-defined subgroup in the guidance.

The B/Victoria lineage constituted 1 091 characterised viruses. Most of these, 796 (73%) viruses belonged to clade V1A.3a.2, represented by B/Austria/1359417/2021, the recommended vaccine virus strain for the 2022−2023 northern hemisphere influenza season. The remaining 295 (27%) viruses could not be attributed to a pre-defined subgroup in the guidance.

There were no reports of B/Yamagata lineage virus characterisations.

Antiviral susceptibility

Since week 40/2022, 4 299 viruses were assessed genotypically and/or phenotypically for susceptibility to oseltamivir (1 640 A(H1N1)pdm09, 1 566 A(H3N2) and 1 093 type B viruses) and 3 156 viruses for susceptibility to zanamivir (982 A(H1N1)pdm09, 1 286 A(H3N2) and 888 type B viruses). During this period, 3 248 viruses were assessed genotypically for susceptibility to baloxavir marboxil (906 A(H1N1)pdm09, 1 616 A(H3N2) and 726 type B viruses). In total, five A(H1N1)pdm09, one A(H3N2) and one B/Victoria virus were reported with reduced susceptibility, all seven against oseltamivir and one additional A(H1N1)pdm09 virus against zanamivir. No viruses carried substitutions associated with reduced susceptibility to baloxavir marboxil. Genotypically, two 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. Moreover, one A(H1N1)pdm09 virus was found to be carrying I223R that is associated with reduced inhibition by oseltamivir. One B/Victoria virus was carrying H273Y that is associated with reduced inhibition by oseltamivir. Phenotypically, two A(H1N1)pdm09 viruses and one A(H3N2) virus were identified with reduced susceptibility to oseltamivir.

Vaccine effectiveness

On 25 February 2022, WHO published recommendations for the components of influenza vaccines for use in the 2022−2023 northern hemisphere influenza season [10]. Two changes in the vaccine virus components were recommended compared to the northern hemisphere 2021−2022 vaccines: the A(H3N2) component was replaced by A/Darwin/9/2021(H3N2)-like virus for egg-based vaccines, as well as A/Darwin/6/2021(H3N2)-like virus for cell- or recombinant-based vaccines, and the B/Victoria component was replaced with a B/Austria/1359417/2021-like virus [10,11]. The recommended vaccine composition for the 2023−2024 influenza season in the northern hemisphere is an A/Victoria/4897/2022 (H1N1)pdm09-like virus; an A/Darwin/9/2021 (H3N2)-like virus; a B/Austria/1359417/2021 (B/Victoria lineage)-like virus, and a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus [12].

Interim vaccine effectiveness (VE) estimations for the 2022−2023 season have been reported by the ECDC Vaccine Effectiveness, Burden and Impact Studies (VEBIS) multi-country network, with data collected from 16 European countries (across six studies between 3 October 2022 and 31 January 2023) assessing patients recruited in primary care, emergency and hospital settings. Interim VE against influenza A (all subtypes; all ages; primary care, emergency care and hospital settings) ranged from 27–44%. All interim VE against influenza B was ≥ 50%, among overall and age-stratified estimates. Against influenza A (all subtypes), VE point estimates were higher among children (50–90%), compared with adults (12–49%). Against influenza A(H1N1)pdm09, VE point estimates among all ages ranged from 28–46%. VE point estimates were higher among children (49–77%) than among those aged 18–64 years (21–56%). Against influenza A(H3N2), VE point estimates among all ages ranged from 2–44%. VE point estimates were higher among children (62–70%) than among those aged 18–64-years (36–42%). Against influenza B, VE in children < 18 years ranged from 88–90%, compared with 87–95% in those aged 2–6 years [13]. These interim results indicate that during the 2022−2023 influenza season a ≥ 27% and ≥ 50% reduction in disease occurrence was observed among all-age influenza vaccine recipients for influenza A and B, respectively. However, results should be interpreted with caution pending end-of-season influenza VE estimates and further genetic characterisation data.

Discussion

The 2022−2023 influenza season marked the return of influenza virus activity to almost pre-pandemic levels in the EU/EEA countries. This season was characterised by an earlier start of the seasonal epidemic and an earlier peak in positivity compared to the four previous seasons. The 2022−2023 season also had a longer period of widespread influenza activity than the previous 2021-2022 season.

Virus type and subtype prevalence by country and surveillance system varied across the season.
Overall, influenza A(H3N2) viruses were dominant in specimens from sentinel and non-sentinel sources.

ICU cases were mainly due to influenza type A viruses and were mostly reported among people aged 60 years and older.

The majority of genetically characterised influenza viruses fell into clades covered by the recommended vaccine components.

Whilst interim, mid-season data indicate vaccination has been protective in a European context, with a ≥ 27% and ≥ 50% reduction in disease occurrence among all-age influenza vaccine recipients for influenza A and B, respectively, end-of-season influenza VE 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 Member States are moving towards integrating surveillance of SARS-CoV-2, influenza and other relevant respiratory viruses, underlying systems might change and reported data might not be comparable to historical data [4]. Continued surveillance activities for respiratory viruses, including influenza, are crucial to understand the epidemiological situation and assess pressure and burden on healthcare and population groups. In particular, severe disease surveillance in hospitals should be further developed and strengthened.

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