

Summary

Week 17/2023 (24 April-30 April 2023)

- The percentage of all sentinel primary care specimens from patients presenting with ILI or ARI symptoms that tested positive for an influenza virus decreased to 7% from 9% in the previous week, which is below the epidemic threshold set at 10%.
- Only one country or area reported medium and 23 of 42 countries or areas reported low intensity. Nine of 41 countries across the Region reported widespread activity.
- Ten countries and areas with more than ten specimens tested reported sentinel primary care specimen influenza virus positivity at or above the 10% epidemic threshold.
- Influenza type A and type B viruses were detected in sentinel and non-sentinel surveillance, with type B predominating in both systems.
- Hospitalized patients with confirmed influenza virus infection were reported from ICU (both type A and type B viruses), other wards (only type A viruses) and SARI surveillance (with higher proportions of type B viruses). No countries or areas reported influenza virus positivity rates above 10% in SARI surveillance.

2022-2023 season overview

- The seasonal epidemic activity threshold of 10% positivity in sentinel specimens was first crossed in week 45/2022.
- Following a peak at week 51/2022 with 39% positivity, influenza activity had been decreasing across the Region until week 4/2023 when it reached 21% positivity before rising again to fluctuate around 25% positivity between weeks 6 and 11/2023 before decreasing below 10% positivity in week 16/2023.
- Overall this season, influenza A(H3) viruses have dominated in sentinel primary care specimens, however higher circulation of A(H1)pdm09 and type B viruses was observed starting from week 50/2022 and week 2/2023, respectively. In non-sentinel specimens, higher circulation of A(H1)pdm09 (55%) than A(H3) viruses (45%) was detected.
- Both influenza type A and type B viruses have been detected in hospitalized patients in ICU and other wards and influenza A(H1)pdm09 viruses have dominated among SARI patients.
- Virus type and subtype prevalence by country and surveillance system has been variable across the season.
- The B/Yamagata viruses sporadically detected and reported by different countries have been further investigated and were proven to be LAIV related detections.

Other news

- RSV is another respiratory virus that causes acute respiratory disease, mainly among young infants and the elderly, often mild but frequently severe among children less than 1 year of age and frail elderly. High levels of RSV have been circulating across the Region since week 40/2022, with overall positivity amongst patients in primary care with acute respiratory illness decreasing after a peak at 18% positivity in week 47/2022 to <1% for week 17/2023. More information on the risk of RSV infections can be found [here](#).

For more information about the SARS-CoV-2 situation in the WHO European Region visit:

- WHO website: <https://www.who.int/emergencies/diseases/novel-coronavirus-2019>
- ECDC website: <https://www.ecdc.europa.eu/en/novel-coronavirus-china>

Qualitative indicators

For week 17/2023, of 42 countries and areas reporting on intensity of influenza activity, 18 reported baseline-intensity (across the Region), 23 reported low-intensity (across the Region) and 1 reported medium-intensity (Poland) (Fig. 1).

Of 41 countries and areas reporting on geographic spread of influenza viruses, 4 reported no activity (Azerbaijan, Kazakhstan, Kyrgyzstan and Uzbekistan), 15 reported sporadic spread (across the Region), 5 reported local spread (Bosnia and Herzegovina, Czechia, Estonia, Georgia and Romania), 8 reported regional spread (Albania, Bulgaria, Croatia, Hungary, Latvia, Lithuania, Russian Federation and Ukraine) and 9 reported widespread activity (across the Region) (Fig. 2).

Figure 1. Intensity of influenza activity in the European Region, week 17/2023

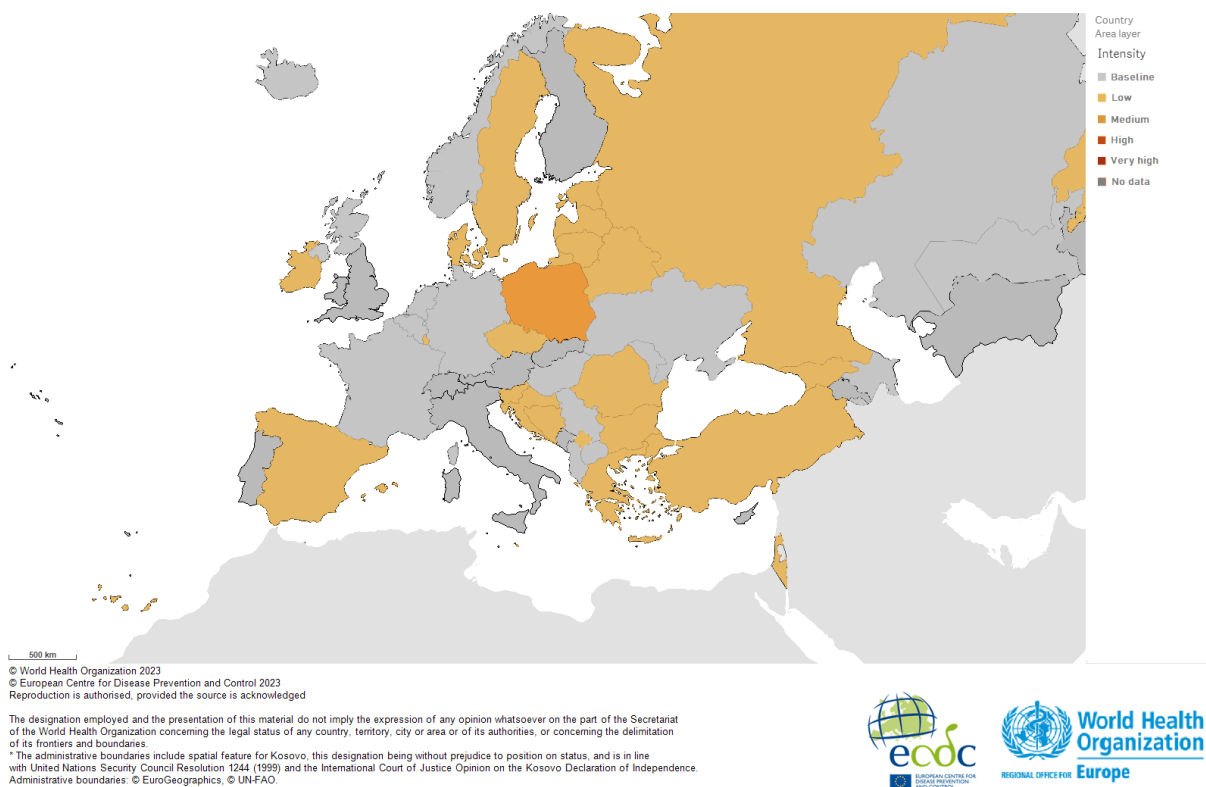
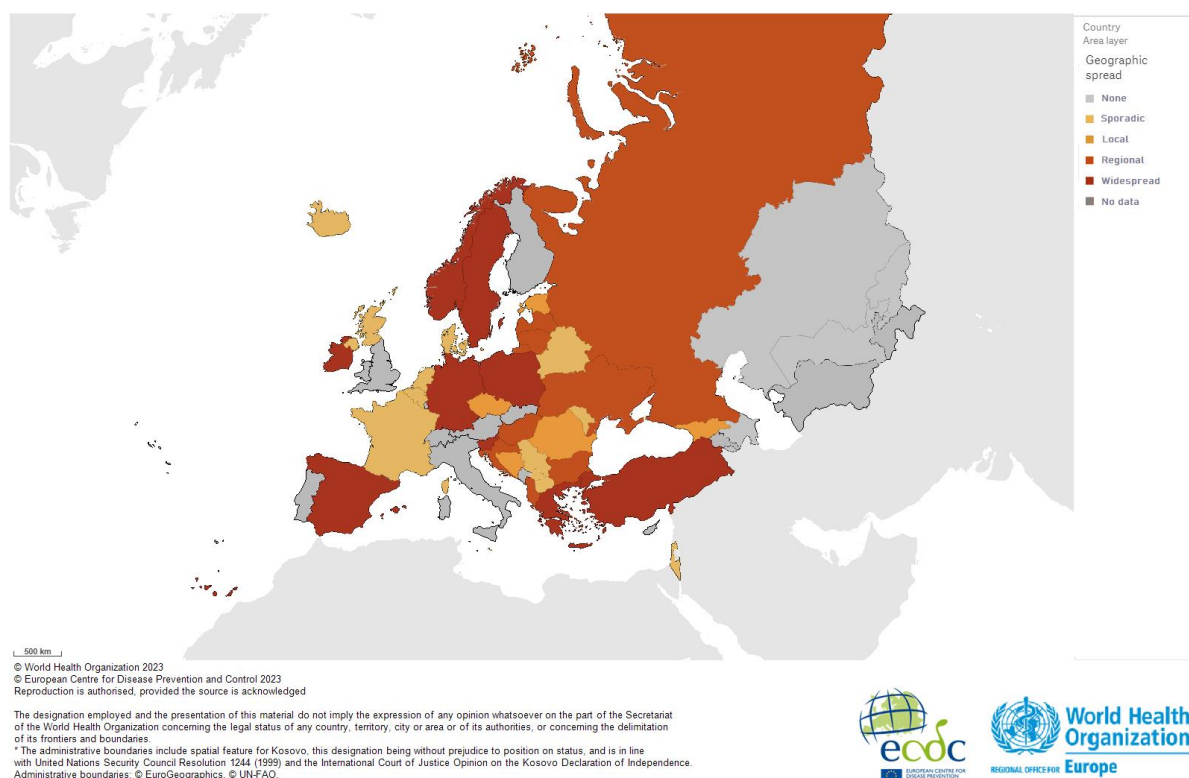


Figure 2. Geographic spread of influenza viruses in the European Region, week 17/2023



For interactive maps of influenza intensity and geographic spread, see the [Flu News Europe website](#).

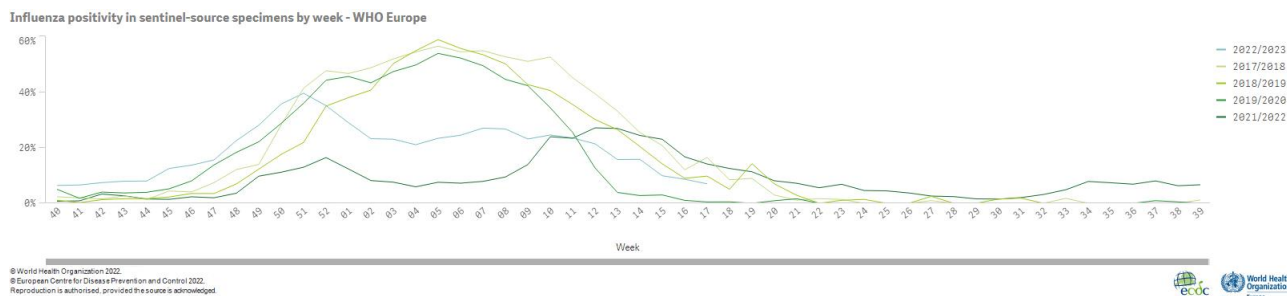
Please note:

- Assessment of the intensity of activity indicator includes consideration of ILI or ARI rates. These ILI or ARI rates might be driven by respiratory infections other than influenza virus, including SARS-CoV-2, leading to observed increases in the absence of influenza virus detections.
- Assessment of intensity and geographic spread indicators includes consideration of sentinel and non-sentinel influenza virus detection data. Non-sentinel influenza virus detections, often higher, might translate into reporting of elevated geographic spread even in the absence of sentinel detections and/or low intensity of activity measured by ILI and ARI incidence.

Influenza positivity

For the European Region, influenza virus positivity in sentinel primary care specimens decreased from 9% in the previous week to 7% in week 17/2023, falling below the epidemic threshold of 10%. Seasonal activity started in week 45/2022 when positivity crossed above the epidemic threshold. The current seasonal influenza epidemic started earlier than in the four previous seasons, ranging from week 47 (2019/20 season) to 49 (2021/22 season). Positivity reached a peak in week 51/2022 at 40% which was earlier than in the four previous seasons, ranging from week 52 (2021/22 season) to 5 (2018/19 and 2019/20). Across the Region, influenza activity decreased to 21% up to week 4/2023, then fluctuated around 25% between weeks 6 and 11/2023 and decreased to 7% in week 17/2023 (Fig. 3).

Figure 3. Influenza virus positivity in sentinel-source specimens by week, WHO European Region, seasons 2017/2018, 2018/2019, 2019/2020, 2021/2022 and 2022/2023



External data sources

Mortality monitoring:

The EuroMOMO report can be found here: <https://www.euromomo.eu/>

Please refer to the EuroMOMO website for a cautionary note relating to interpretation of these data.

Primary care data

Syndromic surveillance data

Of the countries and areas in which thresholds for ILI activity are defined, countries in eastern (n=4; Azerbaijan, Georgia, Kazakhstan and Kyrgyzstan), northern (n=3; Denmark, Estonia and Latvia), southern (n=4; Croatia, Greece, Slovenia and Türkiye) and western (n=1; Luxembourg) areas of the European Region reported activity above baseline levels.

Of the countries and areas in which thresholds for ARI activity are defined, countries in eastern (n=3; Kazakhstan, Kyrgyzstan and Uzbekistan) and northern (n=1; Latvia) areas of the European Region reported activity above baseline levels.

Please note:

- Assessment of the syndromic surveillance data of ILI or ARI rates might be driven by respiratory infections other than influenza virus, including SARS-CoV-2, leading to observed increases in the absence of influenza virus detections. The thresholds mentioned are related to the Moving Epidemic Method (MEM) method and based on historic ILI/ARI data.

Viruses detected in sentinel-source specimens (ILI and ARI)

For week 17/2023, 133 (7%) of 1 909 sentinel specimens tested positive for an influenza virus; 75% were type B and 25% were type A. Of 13 subtyped A viruses, 92% were A(H1)pdm09 and 8% A(H3). All 33 type B viruses ascribed to a lineage were B/Victoria (Fig. 4 and Table 1). Of 27 countries and areas across the Region that each tested at least 10 sentinel specimens in week 17/2023, 10 reported a rate of influenza virus detections at or above 10% (median 17%; range 10% - 35%): Estonia (35%), Slovenia (29%), Hungary

(22%), Norway (19%), Kosovo (in accordance with Security Council resolution 1244 (1999)) (18%), Ukraine (15%), Slovakia (12%), Germany (12%), Italy (10%) and Denmark (10%).

For the season to date, 27 815 (22%) of 124 669 sentinel specimens tested positive for an influenza virus. More influenza type A (n=19 492, 70%) than type B (n=8 323, 30%) viruses have been detected. Of 15 758 subtyped A viruses, 10 068 (64%) were A(H3) and 5 690 (36%) were A(H1)pdm09. All 2 534 influenza type B viruses ascribed to a lineage were B/Victoria (70% of type B viruses were reported without a lineage). All detected B/Yamagata viruses were confirmed as LAIV related detections and are not included in the season's count (Fig. 4 and Table 1).

Details of the distribution of viruses detected in non-sentinel-source specimens are presented in the **virus characteristics** section.

Figure 4. Influenza virus positivity and detections by type, subtype/lineage – sentinel sources, WHO European Region, season 2022/2023

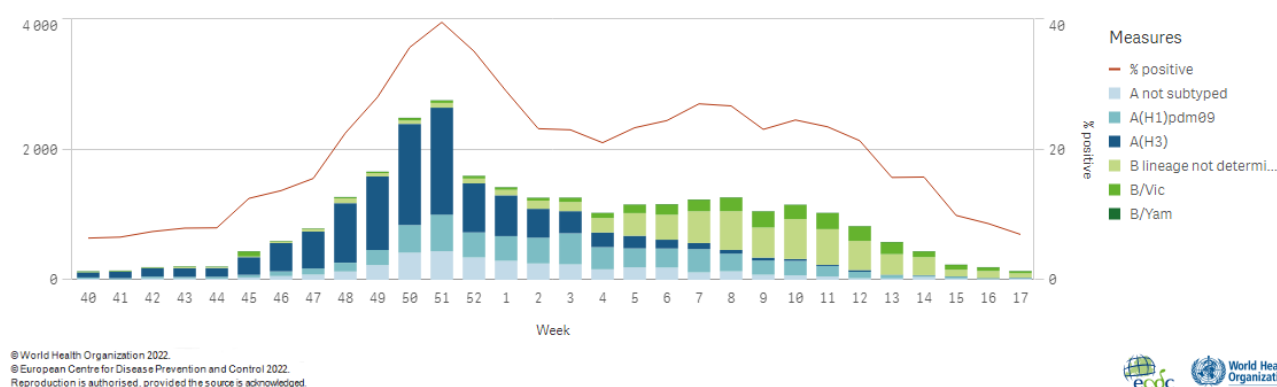


Table 1. Influenza virus detections in sentinel source specimens by type and subtype for week 17/2023 and cumulatively for the season

Sentinel	Current Week (17)		Season 2022-2023	
Virus type and subtype	Number	% ^a	Number	% ^a
Influenza A	33	24.8	19 492	70.1
A(H1)pdm09	12	92	5 690	36
A(H3)	1	8	10 068	64
A not subtyped	20	-	3 734	-
Influenza B	100	75.2	8 323	29.9
B/Victoria lineage	33	100	2 534	100
B/Yamagata lineage	0	0	0	0
Unknown lineage	67	-	5 789	-
Total detections (total tested)	133 (1 909)	7.0	27 815 (124 669)	22.3

^a For influenza type percentage calculations, the denominator is total detections; for subtype and lineage, it is total influenza A subtyped and total influenza B lineage determined, respectively; for total detections, it is total tested.

External data sources

Influenzanet collects weekly data on symptoms in the general community from different participating countries across the EU/EEA. Please refer to the website for information for this week.

Hospital surveillance

A subset of Member States and areas monitors severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in ICUs, or other wards, or 2) severe acute respiratory infections (SARI).

Laboratory-confirmed hospitalized cases

1.1) Hospitalized laboratory-confirmed influenza cases - Intensive care units (ICUs)

For week 17/2023, 2 laboratory-confirmed influenza cases were reported from ICU wards (in Sweden). One influenza type A virus and one type B virus were detected. No viruses were ascribed to a subtype or lineage (Fig. 5 and 6).

Since week 40/2022, 2 723 influenza type A (89%) and 320 type B (11%) viruses were detected (in Czechia (n=142), France (n=952), Ireland (n=151), Sweden (n=294) and United Kingdom (England) (n=1 504)). Of 491 subtyped influenza A viruses, 53% were A(H3) and 47% were A(H1)pdm09. No influenza B viruses were ascribed to a lineage. Of 1 529 cases with known age, 732 were 15-64 years old, 602 were 65 years and older, 119 were 0-4 years old and 76 were 5-14 years old.

Figure 5. Number of laboratory-confirmed hospitalized influenza cases in intensive care units (ICU) by week of reporting, WHO European Region, season 2022/2023

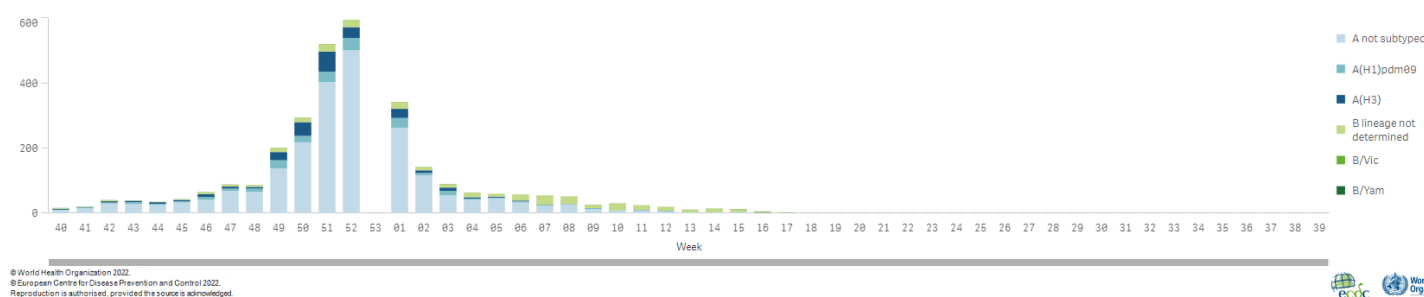
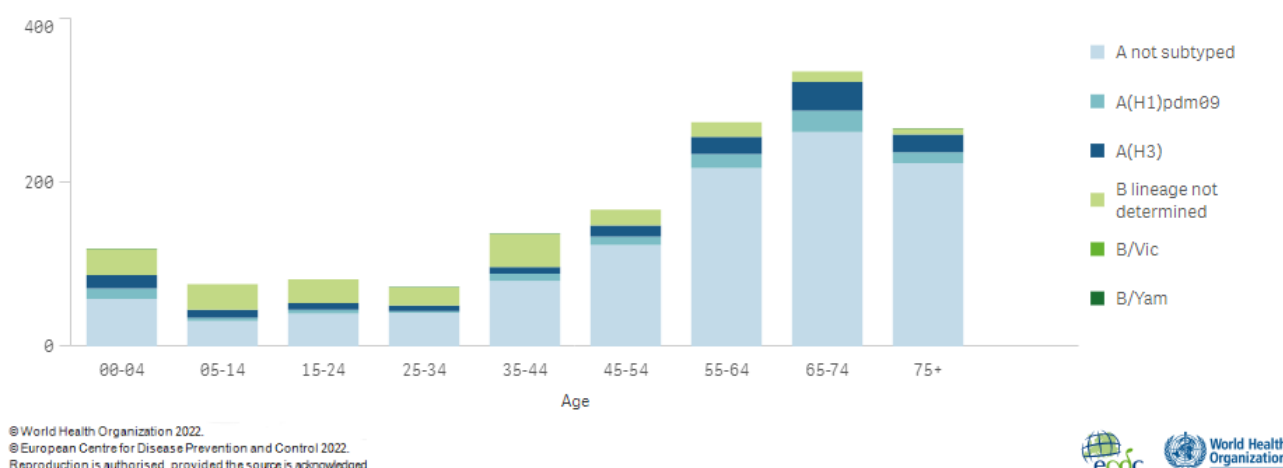


Figure 6. Distribution of influenza virus types, subtypes/lineages by age group in intensive care units (ICU), WHO European Region, season 2022/2023



1.2) Hospitalized laboratory-confirmed influenza cases – other wards

For week 17/2023, 2 laboratory-confirmed influenza cases were reported from other wards (in Czechia). Only influenza type A viruses were detected. No viruses were ascribed to a subtype or lineage (Fig. 7 and 8).

Since week 40/2022, 3 810 influenza type A viruses and 179 influenza type B viruses were detected from Czechia (n=172) and Ireland (n=3 817). Of 399 subtyped influenza A viruses, 63% (n=251) were A(H1)pdm09 and 37% (n=148) A(H3). The 3 989 cases with known age fell in 4 age groups: 1 714 were 65 years and older, 1 374 were 15-64 years old, 500 were 0-4 years old and 401 were 5-14 years old.

Figure 7. Number of laboratory-confirmed hospitalized influenza cases in wards other than intensive care units (non-ICU) by week of reporting, WHO European Region, season 2022/2023

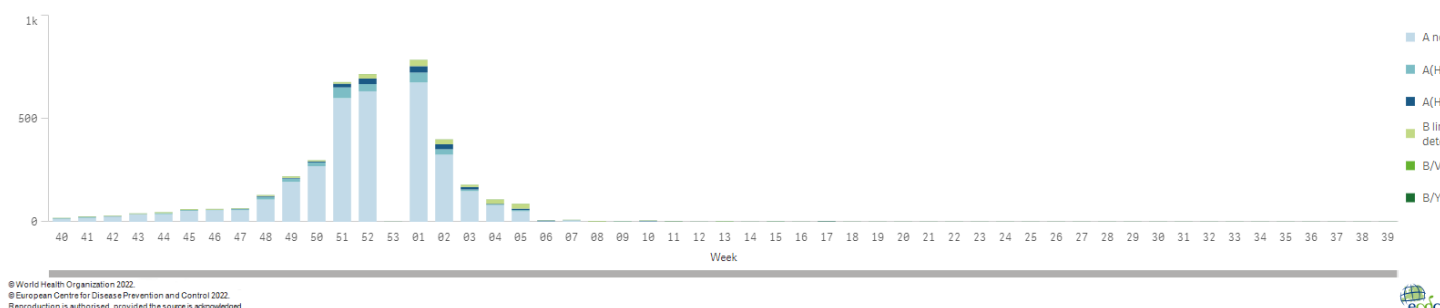
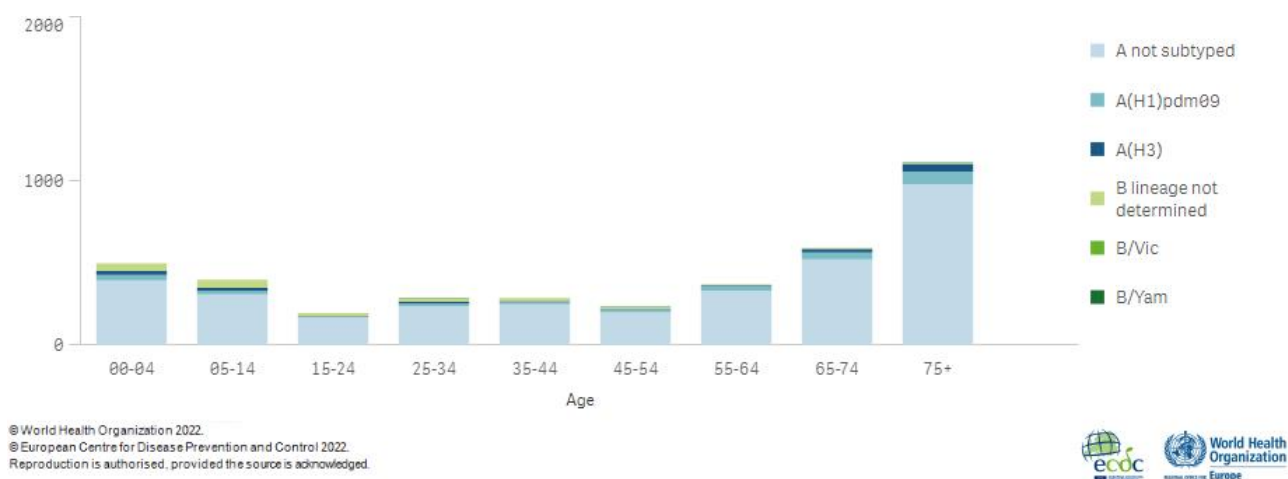


Figure 8. Distribution of influenza virus types, subtypes/lineages by age group in wards other than intensive care units (non-ICU), WHO European Region, season 2022/2023



Severe acute respiratory infection (SARI)-based hospital surveillance

For week 17/2023, 1 669 SARI cases were reported by 16 countries or areas (Albania, Belarus, Bosnia and Herzegovina, Germany, Ireland, Kazakhstan, Lithuania, Malta, Republic of Moldova, Romania, Russian Federation, Serbia, Spain, Ukraine, Uzbekistan and Kosovo (in accordance with Security Council resolution 1244 (1999))). Of 864 specimens tested for influenza viruses, 3% (n=22) were positive (Fig. 9). Of these, influenza type B viruses (n=19, 86%) were detected more frequently than influenza type A viruses (n=3, 14%). Only one influenza type A virus was assigned to a subtype, and it was A(H1)pdm09. Of 10 countries and areas across the Region that each tested at least 10 specimens, none reported positivity rates above 10%.

For the season, 108 957 SARI cases were reported by 26 countries or areas (Albania, Armenia, Belarus, Belgium, Bosnia and Herzegovina, Croatia, Georgia, Germany, Ireland, Kazakhstan, Kyrgyzstan, Lithuania, Malta, Montenegro, North Macedonia, Republic of Moldova, Romania, Russian Federation, Serbia, Slovakia, Spain, Türkiye, Turkmenistan, Ukraine, Uzbekistan and Kosovo (in accordance with Security Council resolution 1244 (1999))). For SARI cases testing positive for influenza virus since week 40/2022, type A viruses have been the most common (n=4 100, 70%) and of these 3 131 were subtyped: 2 184 (70%) were infected by A(H1)pdm09 viruses and 947 (30%) were infected by A(H3) viruses. Of those influenza B viruses that have been ascribed to a lineage (n=409, 30%), all were B/Victoria (Fig. 10).

Figure 9. Number of severe acute respiratory infection (SARI) cases (bar) and positivity for influenza virus and SARS-CoV-2 (line) by week, WHO European Region, season 2022/2023

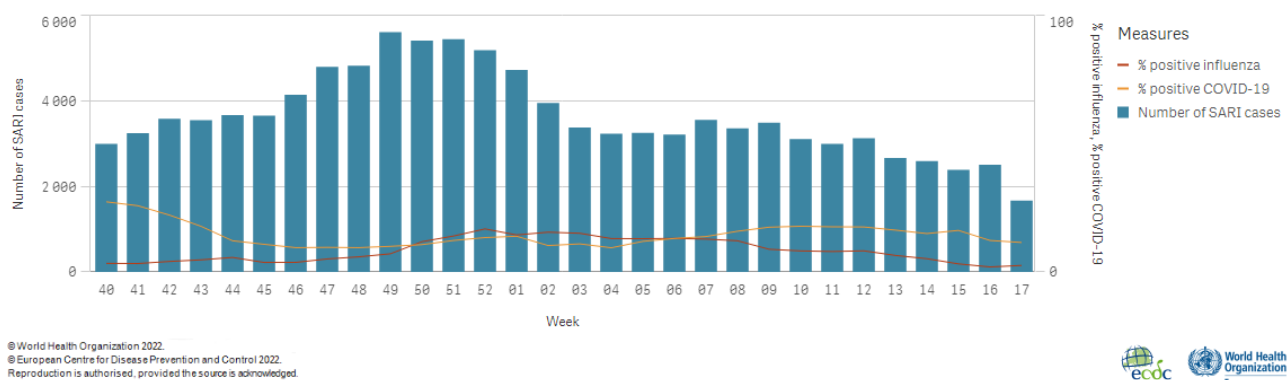
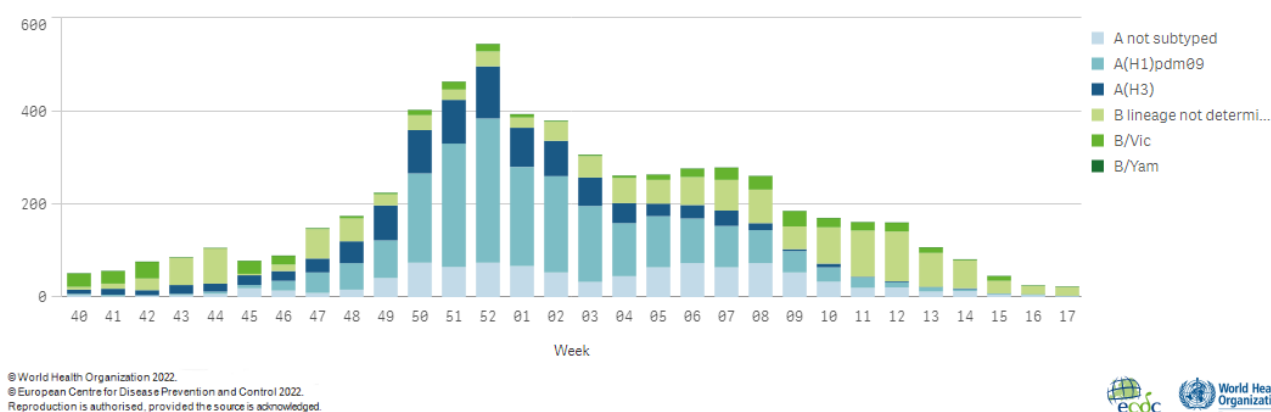


Figure 10. Influenza virus detections by type, subtype/lineage from severe acute respiratory infection (SARI), WHO European Region, season 2022/2023



Virus characteristics

Details of the distribution of viruses detected in sentinel-source specimens can be found in the **Primary care data** section.

Non-sentinel virologic data

For week 17/2023, 988 of 33 537 specimens from non-sentinel sources (such as hospitals, schools, primary care facilities not involved in sentinel surveillance, or nursing homes and other institutions) tested positive for an influenza virus; 738 (75%) were type B and 250 (25%) were type A. Of 30 subtyped A viruses, 24 (80%) were A(H1)pdm09 and 6 (20%) A(H3). All 20 type B viruses ascribed to a lineage were B/Victoria (Fig. 11 and Table 2).

For the season to date, more influenza type A (n=193 356, 76%) than type B (n=63 665, 25%) viruses have been detected. Of 56 335 subtyped A viruses, 31 193 (55%) were A(H1)pdm09 and 25 142 (45%) were A(H3). All 5 089 influenza type B viruses ascribed to a lineage were B/Victoria (92% of type B viruses were reported without a lineage). All detected B/Yamagata viruses were confirmed as LAIV related detections and are not included in the season's count (Fig. 11 and Table 2).

Figure 11. Influenza detections by type, subtype/lineage and week, non-sentinel sources, WHO European Region, season 2022/2023

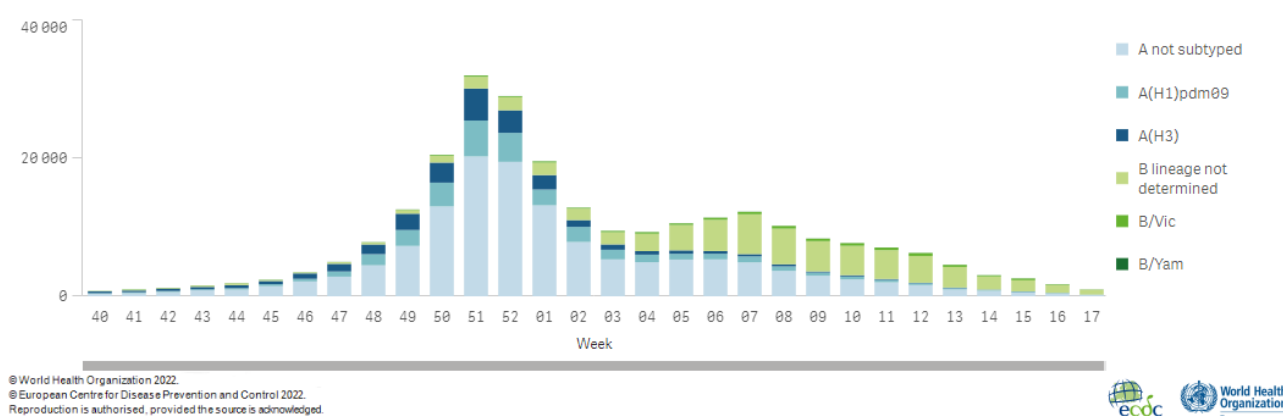


Table 2. Influenza virus detections in non-sentinel-source specimens by type and subtype, week 17/2023 and cumulatively for the season

Non-sentinel	Current Week (17)		Season 2022-2023	
Virus type and subtype	Number	% ^a	Number	% ^a
Influenza A	250	25.3	193 356	75.2
A(H1)pdm09	24	80	31 193	55
A(H3)	6	20	25 142	45
A not subtyped	220	-	137 021	-
Influenza B	738	74.7	63 665	24.8
B/Victoria lineage	20	100	5 089	100
B/Yamagata lineage	0	0	0	0
Unknown lineage	718	-	58 576	-
Total detections (total tested)	988 (33 537)	-	257 021 (2 094 445)	-

^a For type percentage calculations, the denominator is total detections; for subtype and lineage, it is total influenza A subtyped and total influenza B lineage determined, respectively; as not all countries have a true non-sentinel testing denominator, no percentage calculations for total tested are shown.

Genetic characterization

Of the 2 487 genetically characterized A(H1)pdm09 viruses up to week 17/2023, 1 468 were attributed to clade 6B.1A.5a.2, of which 737 (50%) were represented by A/Sydney/5/2021, 698 (47%) by A/Norway/25089/2022 and 33 (2%) by A/Victoria/2570/2019. 5 (<1%) were attributed to clade 6B.1A.5a.1 represented by A/Guangdong-Maonan/SWL1536/2019. 1 014 (41%) viruses could not be attributed to a pre-defined subgroup in the guidance.

Among the 2 497 A(H3) viruses characterized up to week 17/2023, 2 377 were attributed to clade 3C.2a1b.2a.2, of which 1 449 (61%) were represented by A/Bangladesh/4005/2020, 773 (32%) by A/Slovenia/8720/2022, 155 (7%) by A/Darwin/9/2021. 3 (<1%) were attributed to clade 3C.2a1b.1a represented by A/Denmark/3264/2019. 117 (5%) viruses could not be attributed to a pre-defined subgroup in the guidance.

Up to week 17/2023, 1 041 B/Victoria viruses were characterized, 722 (69%) of which were attributed to clade V1A.3a.2 represented by B/Austria/1359417/2021. 319 (31%) viruses could not be attributed to a pre-defined subgroup in the guidance.

Table 3. Number of influenza viruses attributed to genetic groups, cumulative for the season, WHO European Region

	Number of influenza viruses attributed to genetic groups 2022/2023
Total	6 025
Influenza A	4 984
A(H1)pdm09	2 487
A(H1)pdm09_SubgroupNotListed *	1 014
A/Guangdong-Maonan/SWL1536/2019(H1N1)pdm09_6B.1A.5a.1	5
A/Norway/25089/2022(H1N1)pdm09_6B.1A.5a.2	698
A/Sydney/5/2021(H1N1)pdm09_6B.1A.5a.2	737
A/Victoria/2570/2019(H1N1)pdm09_6B.1A.5a.2	33
A(H3)	2 497
A(H3)_SubgroupNotListed *	117
A/Bangladesh/4005/2020(H3)_3C.2a1b.2a.2	1 449
A/Darwin/9/2021(H3)_3C.2a1b.2a.2	155
A/Denmark/3264/2019(H3N2)_3C.2a1b.1a	3
A/Slovenia/8720/2022(H3)_3C.2a1b.2a.2	773
Influenza B	1 041
B/Vic	1 041
B/Austria/1359417/2021(Victoria lineage_1A.3a.2)	722
BVic_SubgroupNotListed *	319

* No Clade: not attributed to a pre-defined clade and SubgroupNotListed: attributed to recognised group in current guidance but not listed here

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Currently, [WHO Europe and ECDC's February](#) virus characterization report is available and describes available data from circulating viruses for the early weeks of the 2022-2023 influenza season.

Antiviral susceptibility testing

Up to week 17/2023, 4 547 viruses were assessed for susceptibility to neuraminidase inhibitors (1 538 A(H1)pdm09, 1 344 A(H3) and 866 B viruses only genotypically and 335 A(H3), 257 A(H1)pdm09 and 207 B viruses phenotypically and some of these also genotypically), and 3 359 viruses were assessed for susceptibility to baloxavir marboxil (1 685 A(H3), 945 A(H1)pdm09 and 729 B viruses genotypically). Phenotypically and/or genotypically, seven A(H1)pdm09 viruses showed (highly) reduced inhibition by oseltamivir. Six of the viruses were reported to carry reduced inhibition markers, four with NA-H275Y (one confirmed phenotypically), one with NA-D199G (confirmed phenotypically), one with NA-I223R. One of those viruses showed reduced inhibition also

by zanamivir due to NA-I223R substitution. Phenotypically, one A(H3) virus showing highly reduced inhibition by oseltamivir was identified. Genotypically, one B/Victoria-lineage virus was showing reduced susceptibility by oseltamivir due to NA-H273Y substitution. Genotypically no markers associated with reduced susceptibility for baloxavir marboxil were identified.

Vaccine

Recently published results from a controlled, randomised trial in UK concluded that concomitant vaccination with one of two SARS-CoV-2 vaccines (ChAdOx1 or BNT162b2) plus an age-appropriate influenza vaccine raised no safety concerns and preserves **antibody responses** to both vaccines.

[https://www.thelancet.com/journals/lancet/article/PIIS0140-6736\(21\)02329-1/fulltext](https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(21)02329-1/fulltext)

Available vaccines in Europe <https://www.ecdc.europa.eu/en/seasonal-influenza/prevention-and-control/vaccines/types-of-seasonal-influenza-vaccine>

Vaccine composition

On 24 February 2023, WHO published recommendations for the components of influenza vaccines for use in the 2023-2024 northern hemisphere influenza season:

The WHO recommends that quadrivalent vaccines for use in the 2023-2024 influenza season in the northern hemisphere contain the following:

Egg-based Vaccines

- 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.

Cell culture- or recombinant-based Vaccines

- an A/Wisconsin/67/2022 (H1N1)pdm09-like virus;
- an A/Darwin/6/2021 (H3N2)-like virus;
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus; and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.

The WHO recommends that trivalent vaccines for use in the 2023-2024 influenza season in the northern hemisphere contain the following:

Egg-based vaccines

- an A/Victoria/4897/2022 (H1N1)pdm09-like virus;
- an A/Darwin/9/2021 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

Cell culture- or recombinant-based vaccines

- an A/Wisconsin/67/2022 (H1N1)pdm09-like virus;
- an A/Darwin/6/2021 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus

The full report is published [here](#).

On 23 September 2022, WHO published recommendations for the components of influenza vaccines for use in the 2023 southern hemisphere influenza season:

Egg-based Vaccines

- an A/Sydney/5/2021 (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.

Cell- or recombinant-based Vaccines

- an A/Sydney/5/2021 (H1N1)pdm09-like virus;
- an A/Darwin/6/2021 (H3N2)-like virus;
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus; and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.

It is recommended that **trivalent influenza vaccines** for use in the 2022 southern hemisphere influenza season contain the following:

Egg-based vaccines

- an A/Sydney/5/2021 (H1N1)pdm09-like virus;
- an A/Darwin/9/2021 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

Cell- or Recombinant-based vaccines

- an A/Sydney/5/2021 (H1N1)pdm09-like virus;
- an A/Darwin/6/2021 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus

The full report is published [here](#).

Acknowledgements

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Maps and commentary do not represent a statement on the legal or border status of the countries and territories shown.

All data are up to date on the day of publication. Past this date, however, published data should not be used for longitudinal comparisons, as countries retrospectively update their databases. The WHO Regional Office for Europe is responsible for the accuracy of the Russian translation.

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