

Seasonal influenza 2018–2019

Annual Epidemiological Report

Key facts

- Influenza activity started in week 49/2018, peaked in week 7/2019 and returned to baseline levels in week 17/2019.
- Influenza viruses circulated at high levels between weeks 52/2018 and 12/2019.
- The vast majority of influenza viruses detected were type A.
- Both influenza A subtypes, A(H1N1)pdm09 and A(H3N2), co-circulated and different distributions of A subtypes were observed among countries.
- Very low numbers of type B viruses and both influenza B lineages, B/Yamagata and B/Victoria, were detected.
- ICU cases were mainly aged 65 years and older, but there was a substantial number of hospitalisations in persons aged 40–64 years. Most hospitalisations were due to influenza A infections.
- Excess mortality from all causes was reported by the majority of 22 reporting countries and was mainly observed in people aged 65 years and older but also in the 15–64 year age group.
- The vast majority of influenza viruses tested were susceptible to neuraminidase inhibitors.

Methods

For a detailed description of methods used to produce this report, please refer to the [Methods chapter](#).

An overview of the national surveillance systems is available [online](#) [1,2].

Corrigendum: On 2 December 2019, the following corrections were made: country suggestions were incorporated in the text (p. 1, bullet point 6 now reads: 'ICU cases were mainly aged 65 years and older, but there was a substantial number of hospitalisations in persons aged 40–64 years. Most hospitalisations were due to influenza A infections.'). p. 6: the sections on vaccine effectiveness and antiviral susceptibility were restructured; p. 7, the final bullet point now includes the phrase: '... may have implications to the VE during 2019–2020 influenza season'; Figure 2 was changed (country data were corrected upon request, 'baseline' intensity is shown in beige, and 'very high' is now indicated by dark red); additional references were added).

Suggested citation: European Centre for Disease Prevention and Control. Seasonal influenza 2018–2019. In: ECDC. Annual epidemiological report for 2018. Stockholm: ECDC; 2019.

Stockholm, October 2019

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Additional data on influenza are accessible from the European Centre for Disease Prevention and Control (ECDC) online *Surveillance Atlas of Infectious Diseases* [3].

ECDC published an early season rapid communication with the European Influenza Surveillance Network (EISN) in February 2019 [4].

The surveillance of influenza in EU/EEA countries is carried out by the EISN, coordinated by the ECDC.

This report of EU/EEA influenza surveillance data is based on weekly data reported to national public health authorities from week 40 to week 20 of the following year. Seasonal influenza surveillance in the EU/EEA also draws on sentinel data reported by national influenza reference laboratories and general practitioners and, in some countries, other physicians, non-sentinel and severe disease data.

Surveillance data include:

- Qualitative indicators of influenza activity, namely intensity, geographic spread and trend. Intensity may range from baseline or below epidemic threshold (i.e. influenza-like illness (ILI) or acute respiratory infection (ARI) rates at levels usually seen between seasons) to very high and is an indicator of the level of influenza activity.
- Geographical spread, ranging from no activity to widespread, is a measure of the geographic distribution of reported detections of influenza viruses in specimens from sentinel or non-sentinel sources.
- Trend – increasing, stable or decreasing – compares the level of ILI and ARI sentinel consultations with the previous week(s).
- The aggregate number of ILI and/or ARI cases seen by sentinel physicians¹ [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 sample of ILI/ARI patients that tested 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 at European level.
- Antigenic and genetic characterisation and strain-based antiviral susceptibility data for a subset of influenza viruses detected in sentinel and non-sentinel specimens [2].
- Case-based data on patients admitted to intensive care units and/or hospitalised influenza patients; data were reported by a subset of countries² and included demographic, clinical and virological data [2].

Since the 2014–2015 season, influenza surveillance in the 53 countries of the WHO European Region has been jointly coordinated by ECDC and the WHO Regional Office for Europe. Results are disseminated through a joint weekly bulletin (available from: <https://flunewseurope.org/>) [5]. Archived weekly data from October 2014 onwards are available from: <http://www.flunewseurope.org/Archives> [5].

This report presents data from EU/EEA countries and the [EuroMOMO](#) project, which monitors weekly all-cause excess mortality in Europe [6].

Seasonal data in this report, covering the period from week 40/2018 to week 20/2019, were extracted from the database during week 39/2019.

Sentinel surveillance

During the 2018–2019 season, 36 289 specimens from sentinel primary care providers were tested for influenza, 14% less than in the previous season; 45% of the specimens were positive for influenza virus.

In week 49/2019, the weekly percentage of sentinel specimens positive for influenza crossed the 10% threshold, signalling the beginning of the seasonal epidemic in the EU/EEA countries. Influenza viruses circulated at high levels between weeks 52/2018 and 12/2019 (based on proportions of 40% and above of sentinel specimens testing positive for influenza virus). The percentage of positive specimens peaked at 62% in week 7/2019 and influenza activity returned to baseline levels in week 17/2019 (Figures 1 and 2).

¹ ILI and a denominator were reported by Austria, Belgium, Croatia, Cyprus, the Czech Republic, Denmark, Estonia, Finland, France, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain and the United Kingdom.

ARI and a denominator were reported by Belgium, Bulgaria, Cyprus, the Czech Republic, Estonia, Finland, Germany, Latvia, Lithuania, Luxembourg, the Netherlands, Romania, Slovakia, Slovenia and the United Kingdom.

² Laboratory confirmed influenza hospitalised case data were reported by Belgium, the Czech Republic, Denmark, Estonia, Finland, France, Ireland, the Netherlands, Romania, Slovakia, Spain, Sweden and the United Kingdom.

Of 16 472 positive sentinel specimens, 99% were type A, and 1% were type B. The level of circulation of influenza B viruses was lower than in recent seasons. Of 11 890 A viruses subtyped, 55% were A(H1N1)pdm09 and 45% were A(H3N2) viruses. Of 62 influenza B viruses ascribed to a lineage, 79% were B/Yamagata, and 21% were B/Victoria viruses. Different distributions of A subtypes were observed between countries.

Figure 1. Weekly proportion of sentinel specimens positive for influenza virus and number of detections by type and subtype, EU/EEA, 2018–2019

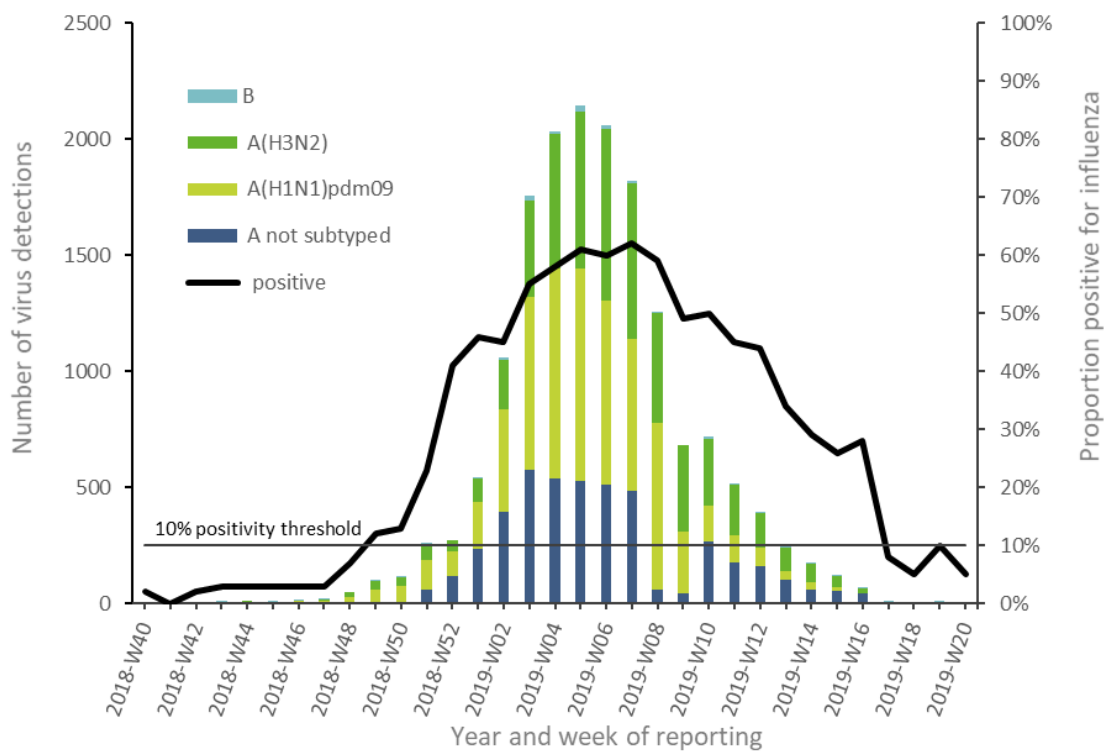
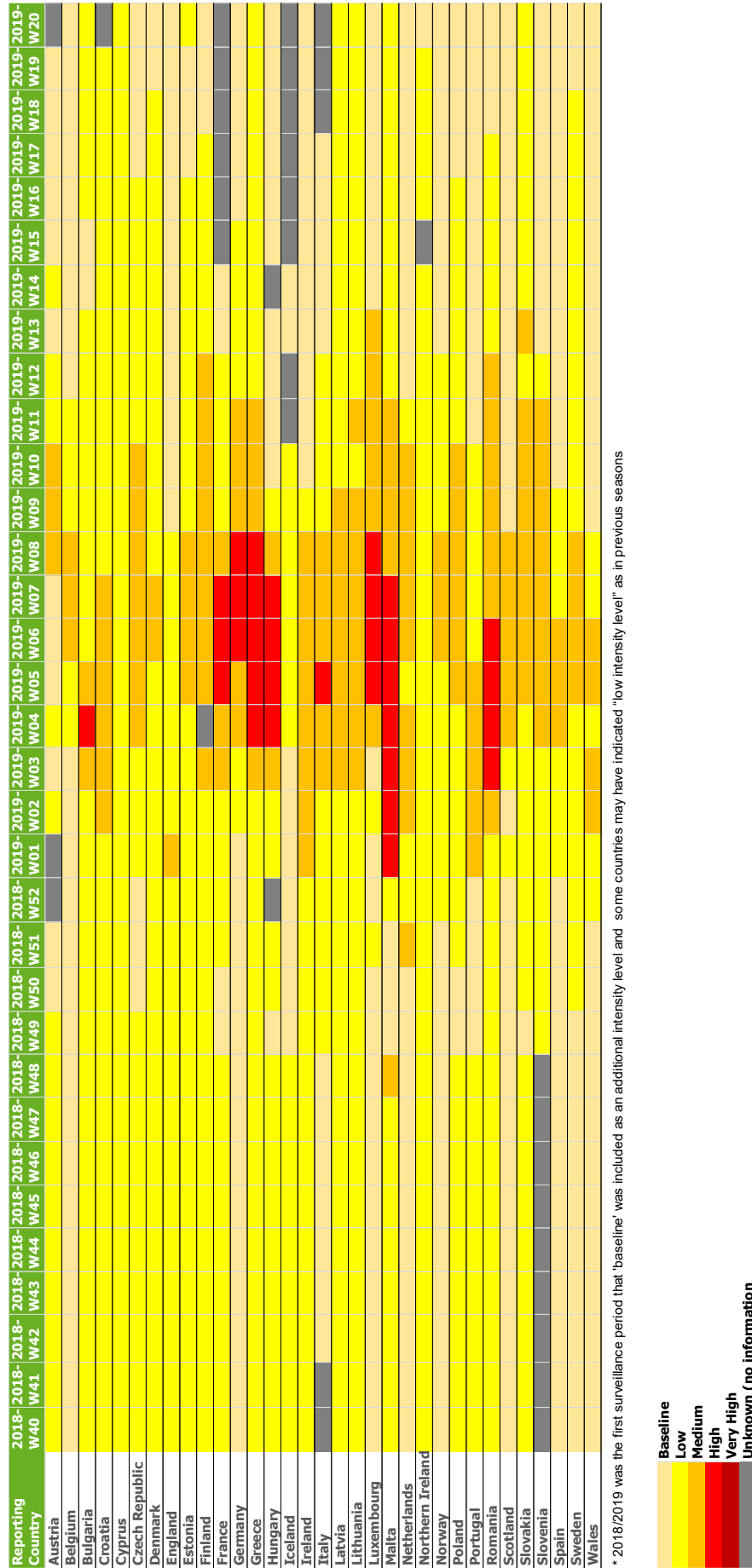
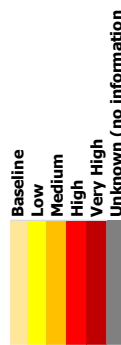


Figure 2. Influenza intensity by country and week, 2018–2019



* 2018/2019 was the first surveillance period that 'baseline' was included as an additional intensity level and some countries may have indicated "low intensity level" as in previous seasons



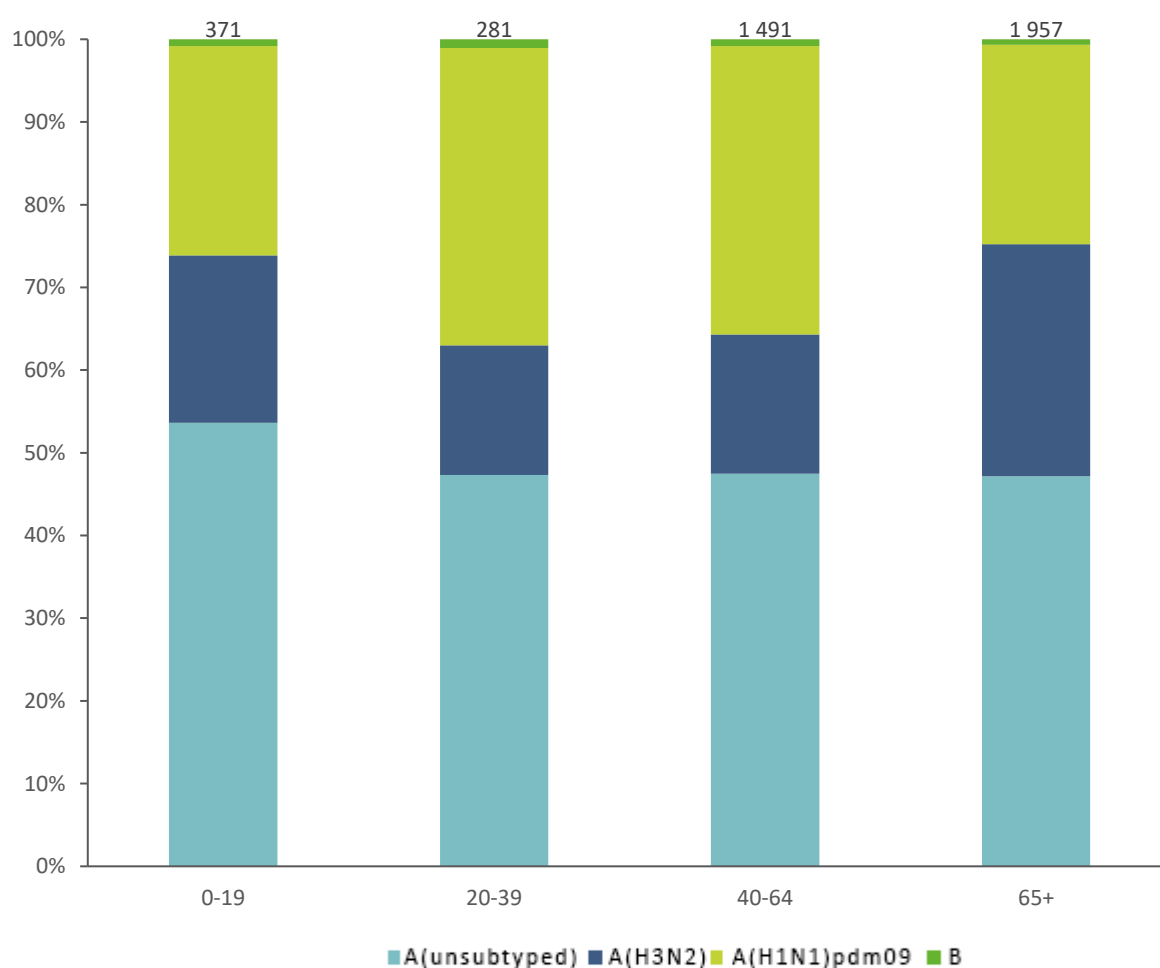
Hospitalisations due to influenza

Thirteen countries reported a total of 7 342 laboratory-confirmed hospitalised influenza cases in intensive care units (ICUs) and eight countries reported a total of 9 561 confirmed cases from other wards during the 2018–2019 influenza season. These numbers include data from all hospitals in some of the reporting countries, while other countries reported only data from selected hospitals.

Influenza type A viruses were detected in 99% of all laboratory-confirmed influenza cases admitted to ICUs, with type B accounting only for 1%. Of severe cases admitted to ICUs, 48% were reported in persons aged 65 years and over, but a substantial proportion of hospitalised patients belonged to the 40–64 year age group (Figure 3). Among the 40–64 aged ICU admitted patients, influenza A(H1N1)pdm09 accounted for the highest proportion of cases, while among the elderly, A(H3) slightly outnumbered A(H1N1)pdm09 virus infections admitted in ICU (Figure 3). The United Kingdom, France and Spain accounted for 45%, 26% and 15% of ICU cases, respectively.

For laboratory-confirmed influenza cases reported from wards other than ICUs, type A viruses were detected almost exclusively (99%). Among the influenza A detections, A(H1N1)pdm09 accounted for the highest proportion of cases reported from wards other than ICUs.

Figure 3. Laboratory-confirmed influenza cases with age information admitted to ICU, by age group (year) and (sub)type, 13 EU/EEA countries, season 2018–2019



Virus characterisations

Virus characterisation data were reported from both sentinel and non-sentinel sources.

Of 2 662 influenza A(H3N2) viruses attributed to a clade, 73 (3%) were reported as subclade 3C.2a1 similar to the 2018–2019 vaccine virus component A/Singapore/INF16H-16-0019/2016 (H3N2) and 1 966 (74%) belonged to other 3C.2a clades/subclades that are considered to be antigenically similar to the vaccine virus component [7,8]: 11 in clade 3C.2a, 9 in subclade 3C.2a1a, 1 828 in subclade 3C.2a1b, 83 in subclade 3C.2a2 and 35 in subclade 2C.2a3. In total, 618 (23%) fell in clade 3C.3a which is antigenically distinct from the vaccine virus component [7,8]. Five A(H3N2) viruses were not attributed to any of the predefined clades.

Of 2 014 A(H1N1)pdm09 viruses attributed to a clade, 2 011 fell in the A/Michigan/45/2015 vaccine component clade (6B.1), specifically subclade 6B.1A, the majority with an additional amino acid substitution S183P in haemagglutinin (HA). Three viruses were not attributed to any of the predefined clades.

Two reassortant seasonal influenza A(H1N2) viruses were detected during the 2018–2019 season, one in Sweden and one in Denmark [9,10]. The variant viruses originated from the reassortment of seasonal influenza A(H1N1)pdm09 and A(H3N2) viruses and were considered to be antigenically similar to the circulating strains. Phylogenetic analysis indicated that these two viruses originated independently [9,10].

All 36 B/Yamagata lineage viruses belonged to clade 3, represented by the quadrivalent vaccine virus component B/Phuket/3073/2013. All 35 B/Victoria lineage viruses belonged to clade 1A. Five (14%) of them belonged to a subgroup represented by the trivalent and quadrivalent vaccine virus component B/Colorado/06/2017, which carries a double amino acid deletion (Δ 162-163) in HA. Twenty-three B/Victoria lineage viruses (66%) belonged to a subgroup represented by B/Hong Kong/269/2017, characteristic of an antigenically distinct subgroup of viruses with a triple amino acid deletion (Δ 162-164) in HA. Seven viruses (20%) did not carry any deletion, similar to B/Brisbane/60/2008.

For more information on virus characterisations for EU/EEA countries, see the [February report](#) by the WHO Collaborating Centre for Reference and Research on Influenza in London [7] and the [May monthly characterisation report](#) published by ECDC [8].

Vaccine effectiveness

Interim results on vaccine effectiveness (VE) from six studies in Europe indicated 2018–2019 influenza VE estimates among all ages in primary care to be 32–43% against influenza A [11]. The season estimates for the VE against A(H3N2) using data from nine European countries confirmed that VE was higher against A(H1N1)pdm09 and lower against A(H3N2) [12].

All-cause excess mortality

Pooled data from 22 EU/EEA countries reporting to the [EuroMOMO](#) project showed an excess mortality from all causes between the second week of January 2019 and the end of February 2019. Excess mortality mainly affected people aged 65 years or older but was also observed in the 15–64 years age group [6].

Antiviral susceptibility and vaccine effectiveness

Antiviral resistance to neuraminidase inhibitors was detected at very low levels (<1% of viruses tested).

Discussion

The start of the epidemic in Europe was in week 49/2018, two weeks later than in the 2017–2018 season, and it peaked in week 7/2019. Influenza viruses circulated at high levels between weeks 52/2018 and 12/2019 and returned to baseline levels in week 17/2019. This meant that the season was shorter than 2017–2018, but longer than previous seasons.

In sentinel specimens, type A influenza viruses were detected almost exclusively and both influenza subtypes A(H1N1)pdm09 and A(H3N2) co-circulated. Different distributions of A subtypes across countries may be explained by differences between surveillance systems (e.g. collecting samples mostly from one age-group), levels of pre-existing immunity or natural variation in influenza epidemiology across Europe.

Countries reporting severe influenza data saw a lower number of hospitalisations in ICU and other wards compared to 2017–2018. This subset of data from 13 countries, however, may not fully reflect the situation in those EU/EEA countries not reporting severe influenza data which may have experienced a more severe influenza season. ICU cases were mainly aged 65 years and older, but there was a substantial number of hospitalisations in persons aged 40–64 years. Similarly, excess mortality from all causes was mainly observed in persons aged 65 years and older but also in those aged 15–64 years. Influenza type A viruses were detected in 99% of all laboratory-confirmed influenza cases admitted to ICUs and from wards other than ICUs.

A(H1N1)pdm09 viruses remained antigenically similar to the 2018–2019 vaccine virus, despite a fixation of an amino acid substitution S183P on an antigenic epitope of HA observed in the vast majority of circulating viruses. Viruses in the 3C.2a groups are considered to be antigenically similar, but they are evolving rapidly, with the emergence of several virus subclusters defined by additional amino acid substitutions in the HA. Viruses belonging to subclade 3C.3a also circulated in lower numbers but increased compared to the previous season; these viruses were antigenically distinct from the 2018–2019 vaccine component. The co-circulation of different A(H3N2) subclades may have contributed to the reduced vaccine effectiveness against this subtype [11].

For type B viruses, both B/Yamagata and B/Victoria lineage viruses co-circulated at very low levels. B/Yamagata lineage viruses were all similar to the quadrivalent vaccine virus component, but B/Yamagata lineage was not included in the 2018–2019 trivalent seasonal influenza vaccine. Very limited circulation of B/Victoria lineage viruses was reported: in total 86% of the characterised B/Victoria viruses belonged to clades antigenically distinct from the 2018–2019 vaccine virus.

In February and March 2019, WHO published the recommendations for the influenza vaccine composition for the 2019–2020 season in the northern hemisphere [13,14]. Compared to the northern hemisphere 2018–2019 trivalent and quadrivalent vaccines, two changes in the vaccine virus components were recommended. The A(H3N2) component was replaced with an A/Kansas/14/2017(H3N2)-like virus and the A(H1N1)pdm09 component was replaced with an A/Brisbane/02/2018(H1N1)pdm09-like virus [14]. The B/Victoria virus component in both trivalent and quadrivalent vaccines and the B/Yamagata component in quadrivalent vaccines remained the same [13].

Public health implications

- Early estimates showed 32–43% vaccine effectiveness against any type of influenza A. Influenza vaccination for the 2019–2020 influenza season should follow the recommendations of the European Council (2009), as it remains the best preventive measure against influenza [15].
- Appropriate use of neuraminidase inhibitors should be continued in the 2019–2020 influenza season in accordance with national and international guidelines [16].
- Surveillance of severe influenza cases should be further improved, with participation of more reporting countries.
- WHO recommended that the A(H3N2) and the A(H1N1)pdm09 vaccine components be changed in the influenza vaccine for 2019–2020. The co-circulation of genetically and antigenically diverse A(H3N2) and B/Victoria influenza strains poses a challenge to the vaccine selection and may have implications to the VE during 2019–2020 influenza season. Close monitoring and antigenic and genetic characterisation of circulating viruses is required. The quadrivalent vaccine, which includes viruses from both B lineages, provides better protection when both lineages are circulating or the circulating strain does not match the trivalent vaccine B virus component.

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