

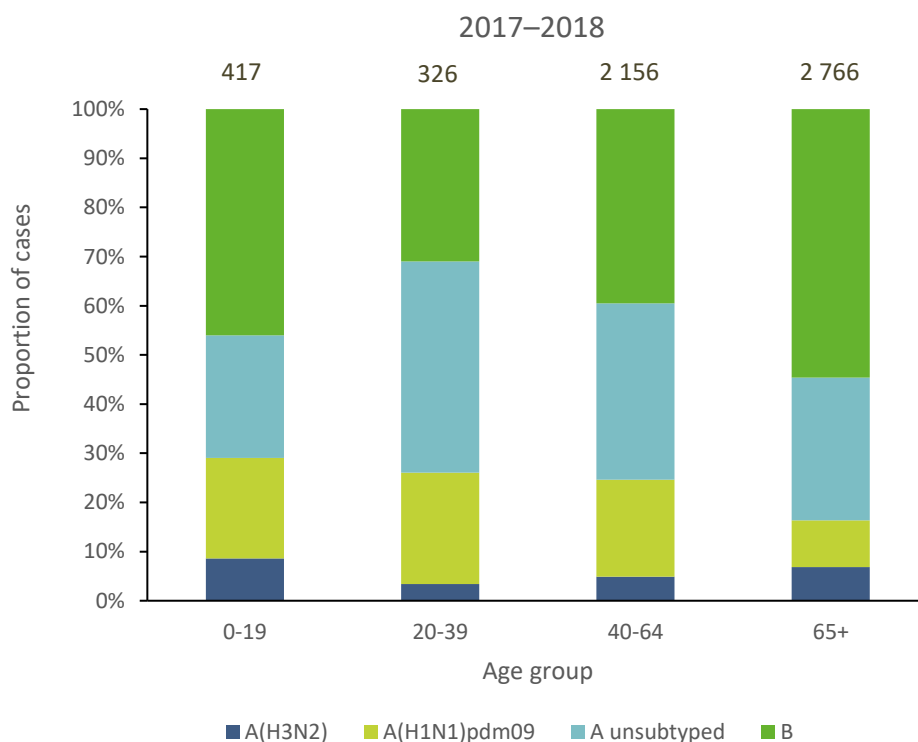
Hospitalisations due to influenza

Ten countries reported a total of 9 317 laboratory-confirmed hospitalised influenza cases in intensive care units (ICUs); 17 410 confirmed cases were reported from other wards during the 2017–2018 influenza season. These numbers include data from all hospitals in some of the reporting countries, while other countries reported only data from selected hospitals. Compared with the previous three seasons, there was an increase in the number of reported laboratory-confirmed influenza cases in ICUs and other wards in the countries that provided data in all of the seasons.

Influenza type A viruses were detected in 53% of all laboratory-confirmed influenza cases admitted to ICUs, with type B accounting for 47%. The majority of severe cases occurred in persons aged over 39 years (Figure 3). France and the UK accounted for 31% and 38% of ICU cases, respectively.

For laboratory-confirmed influenza cases reported from wards other than ICUs, type B viruses were detected more frequently (61%) than type A viruses (39%). Among the influenza A detections in patients 65 years of age and older, A(H3N2) accounted for the highest proportion of cases.

Figure 3. Laboratory-confirmed influenza cases admitted to ICU, by age group (year) and (sub)type, 10 EU/EEA countries, season 2017–2018



Virus characterisations

Virus characterisation data were reported from both sentinel and non-sentinel sources. Of 996 influenza A(H3N2) viruses attributed to a clade, 554 (56%) fell in the vaccine virus component clade (3C.2a), 430 (43%) in subclade 3C.2a1 — with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin — and seven (<1%) fell in clade 3C.3a. Five A(H3N2) viruses were not attributed to any of the predefined clades.

All 560 A(H1N1)pdm09 viruses fell in the A/Michigan/45/2015 vaccine component clade (6B.1).

A reassortant influenza A(H1N2) virus was detected in the Netherlands during the 2017–18 season. The variant virus originated from the reassortment of seasonal influenza A(H3N2) and A(H1N1)pdm09 viruses and was considered to be antigenically similar to the circulating strains [8].

All 1 460 B/Yamagata lineage viruses belonged to clade 3, represented by B/Phuket/3073/2013. Of 123 B/Victoria lineage clade 1A viruses, 66 (54%) belonged to a subgroup represented by B/Norway/2409/2017, which carries HA1 double amino acid deletion, Δ162–163 (deletion of amino acids K162 and N163 in the HA1 subunit), characteristic of a new antigenically distinct subgroup of viruses that has been detected in several countries during the season [9,10].

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 [11].

All-cause excess mortality

Pooled data from 20 EU/EEA countries reporting to the EuroMOMO project showed an excess mortality from all causes between the beginning of January 2018 and the end of February 2018 [7]. Excess mortality mainly affected people aged 65 years or older.

Antiviral susceptibility and vaccine effectiveness

There was little detection of antiviral resistance to neuraminidase inhibitors (<1% of viruses tested). Interim results on vaccine effectiveness from five European studies indicated that, in all age groups, influenza vaccine effectiveness was 25 to 52% against any type of influenza, 55 to 68% against influenza A(H1N1)pdm09, no effectiveness (-47 to -7) against influenza A(H3N2), and 36 to 54% against influenza B [12], which was consistent with estimates from the United Kingdom [13], Canada [14] and the United States of America [15].

Discussion

The influenza season 2017–2018 was a severe season compared with previous seasons. It lasted longer than previous seasons, which might have contributed to the large number of severe cases. When the overall 10% positivity rate was exceeded, most EU/EEA countries reported low intensity of influenza activity, suggesting a lower sensitivity of intensity as indicator of influenza activity.

For sentinel specimens, the proportion of type B viruses was higher than the proportion of type A viruses, and A(H1N1)pdm09 viruses outnumbered A(H3N2) viruses.

For type B viruses, B/Yamagata lineage viruses greatly outnumbered B/Victoria lineage viruses. B/Yamagata lineage was not included in the 2017–2018 trivalent seasonal influenza vaccine. Nevertheless, the vaccine effectiveness estimates indicated 36–54% vaccine effectiveness against influenza B, a result that likely indicates cross protection from the vaccine against B/Yamagata lineage viruses [12]. Limited circulation of B/Victoria lineage viruses was reported; 54% of these viruses belonged to the newly emerged deletion variant subclade, which is antigenically distinct from the 2017–2018 vaccine virus.

Different patterns of dominant type and A subtype were observed across countries, which may be due to the differences between surveillance systems or natural variation in influenza virus characteristics and epidemiology across Europe. 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 haemagglutinin.

ICU cases were mainly persons aged 40 years and older, while excess mortality from all causes was mainly observed in persons aged 65 years and older, which was similar to the previous season.

On 21 February 2018, WHO published recommendations for the influenza vaccine composition for the 2018–2019 season in the northern hemisphere [11]. Compared with the northern hemisphere 2017–2018 trivalent and quadrivalent vaccines, two changes in the vaccine virus components were recommended. The A(H3N2) component was replaced with an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus. For trivalent vaccines, the B component was replaced with a B/Colorado/06/2017-like virus, representing the emergent strain of B/Victoria-lineage viruses with Δ 162-163 deletion in HA1. The A(H1N1)pdm09 component in both trivalent and quadrivalent vaccines and the B/Yamagata component in quadrivalent vaccines remained the same [11].

Public health implications

Early estimates showed 25–52% vaccine effectiveness against any type of influenza and 36–54% against influenza B, which was mismatched with the B virus trivalent vaccine component. Influenza vaccination should continue to be recommended along the lines of the recommendations of the European Council (2009), as it remains the best preventive measure against influenza [16]. In addition, appropriate use of neuraminidase inhibitors should be continued, in accordance with national and international guidelines.

Regarding the influenza vaccine for 2018–2019, WHO has recommended that the A(H3N2) and the B/Victoria vaccine components should be changed. In addition, as this was the fourth consecutive season in which the circulating B virus was dissimilar from the B strain included in the most widely used trivalent vaccine, close monitoring of circulating B 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.

Surveillance of severe influenza cases should be further improved, with participation of more reporting countries. Antigenic and genetic characterisation of circulating influenza viruses should be continued.

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