SURVEILLANCE REPORT

Annual Epidemiological Report for 2015

Seasonal influenza

Key facts

- As in previous seasons, influenza activity started in week 51/2015 and lasted until week 20/2016.
- Compared with previous seasons, primary care consultation rates for influenza-like illness (ILI)/acute respiratory infection (ARI) were similar in most EU/EEA countries.
- In almost all countries, the season was dominated by influenza A(H1N1)pdm09 viruses.
- Influenza B virus circulation increased, following the decline of influenza A virus circulation but continued to co-circulate with A(H1N1)pdm09m in Ireland, France and Spain for most of the season.
- The majority of ICU cases were aged less than 65 years and mainly infected with A(H1N1)pdm09, especially middle-aged adults.
- Influenza activity was accompanied by excess all-cause mortality in persons aged 15–64 years.
- There was a good antigenic match between circulating A(H1N1)pdm09 viruses and the vaccine strain. However, vaccine effectiveness against this subtype remained suboptimal.
- Circulating B viruses were mainly of the Victoria lineage and antigenically similar to the quadrivalent B/Victoria vaccine strain but belonged to another lineage than the B/Yamagata lineage included in most commonly used trivalent vaccines.
- The vast majority of viruses tested were susceptible to neuraminidase inhibitors.

Methods

This report includes 2015 events and data and does not follow the entire winter season pattern. For a detailed description of methods used to produce this report, please refer to the *Methods* chapter [1].

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

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

Influenza surveillance for 30 EU/EEA countries is carried out by the European Influenza Surveillance Network (EISN) under the coordination of the European Centre for Disease Prevention and Control (ECDC).

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Stockholm, December 2017

EU/EEA influenza surveillance is based on weekly data reported to ECDC by sentinel general practitioners (in some countries also other physicians, such as paediatricians) and national influenza reference laboratories from week 40 to week 20 of the following year.

Surveillance data include the following indicators:

- Qualitative indicators of influenza activity, namely intensity, geographic 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. Geographic spread, ranging from no activity to widespread, refers to the number of affected areas in a given country. Trend (i.e. increasing, stable or decreasing) compares the level of ILI/ARI sentinel consultations with the previous week.
- The aggregate number of ILI and/or ARI cases seen by sentinel physicians. ILI and a denominator were reported by Austria, Belgium, Croatia, Cyprus, the Czech Republic, Denmark, Estonia, France, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, and the UK. ARI and a denominator were reported by Belgium, Bulgaria, Cyprus, the Czech Republic, Estonia, Germany, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Romania, Slovakia, Slovenia, and the UK. 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 and testing positive for influenza, by type, A subtype and B lineage). 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.
- Antigenic and genetic characterisation and strain-based antiviral susceptibility data for a subset of influenza viruses detected both in sentinel and non-sentinel specimens.
- Case-based hospital data reported by a subset of countries on a voluntary basis (Finland, France, Ireland, Romania, Slovakia, Spain, Sweden, and the UK) including demographic, clinical and virological data.

Since the 2014–2015 season, influenza surveillance in the 53 countries of the WHO European Region is jointly coordinated by ECDC and the WHO Regional Office for Europe. Results are disseminated through a joint weekly bulletin (www.FlunewsEurope.org).

This report presents data from 30 EU/EEA countries and the EuroMOMO project which monitors weekly all-cause excess mortality in Europe. Archived weekly data from October 2014 onwards are available at http://www.flunewseurope.org/Archives.

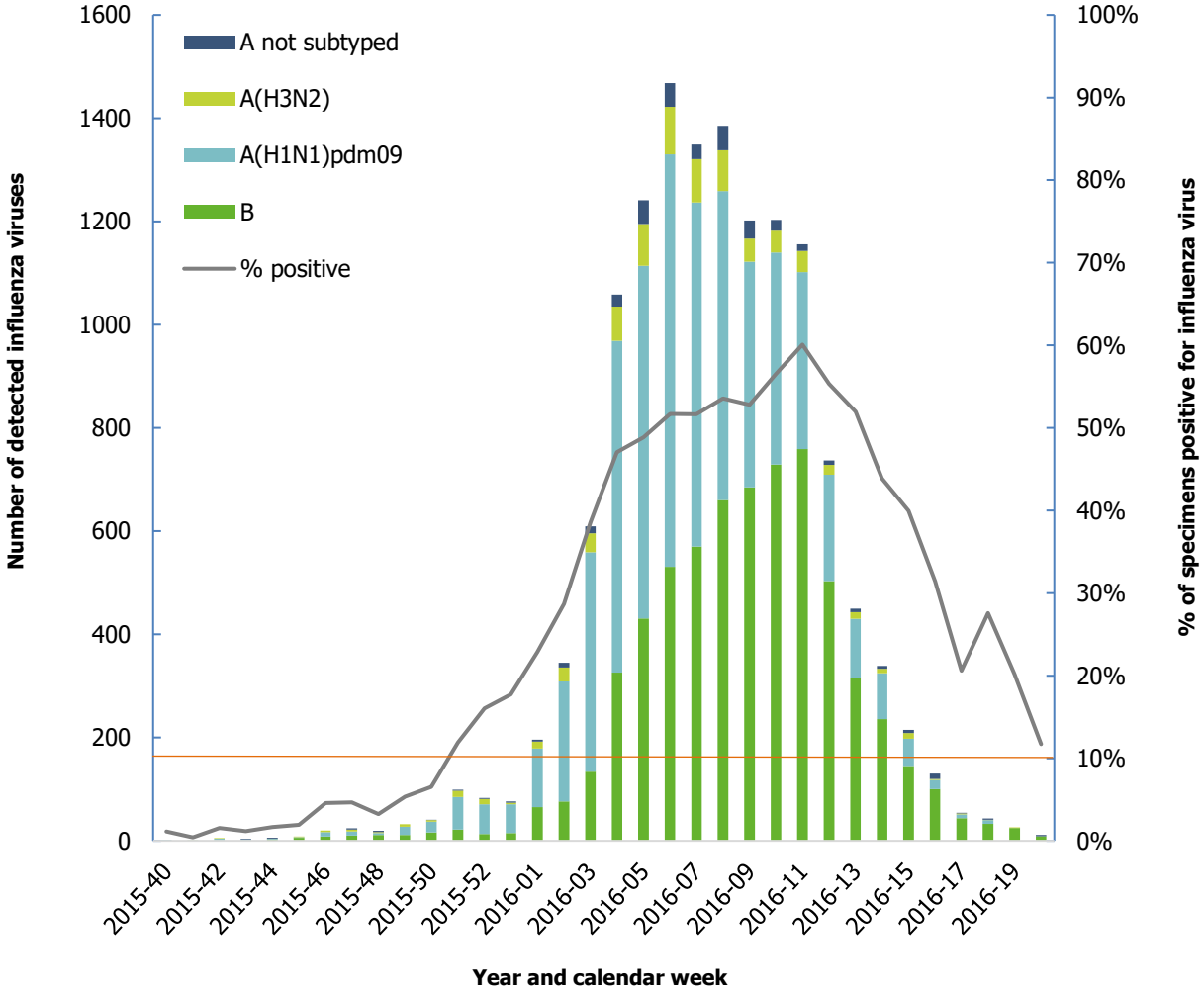
Sentinel surveillance

The proportion of sentinel specimens testing positive for influenza virus crossed the 10% threshold in week 50/2015 in Belgium, the Czech Republic, Ireland, the Netherlands, and Sweden. In week 51/2015, the 10% threshold for pooled EU/EEA data was reached, indicating the start of the influenza season. The percentage of positive specimens peaked between weeks 4/2016 and 14/2016, with a maximum of 60% during week 11/2016. The percentage of positive specimens remained above the threshold level until the last week of the season (week 20/2016) (Figure 1).

During the season, 33 756 specimens from sentinel primary care providers were tested; 13 640 (40%) of which were positive for influenza virus. Of the positive specimens, 7 146 (52%) were type A and 6 494 (48%) were type B.

Of 6 804 A viruses subtyped, 6 093 (90%) were A(H1N1)pdm09 and 711 (10%) were A(H3N2) viruses. A(H3N2) was dominant only in Slovenia and Italy, with 89% and 73% of A viruses subtyped, respectively. Of 3 724 influenza B viruses ascribed to a lineage, 3 586 (96%) were B (Victoria), which was more prevalent in all reporting countries. Influenza B viruses co-circulated with A(H1N1)pdm09m in Ireland, France and Spain for most of the season. In other EU countries, influenza B viruses became dominant in most of EU countries, following the decline of influenza A viruses circulation during week 9/2016.

Figure 1. Weekly proportion of sentinel specimens positive for influenza virus and number of detections by type and subtype, EU/EEA, 2015–2016



Note: A 10% threshold is used to indicate the start of the seasonal epidemic (horizontal line in orange). Overall positivity rates of sentinel specimens are used to estimate the start, duration and end of influenza activity.

Hospitalisations due to influenza

Eight countries reported a total of 8 691 laboratory-confirmed hospitalised influenza cases during the 2015–2016 influenza season, with France, Ireland, Spain and the UK accounting for 8 118 (93%) of all cases (Table 1). The level of care was known for 4 984 patients from a total of four countries; 25% of these almost 5 000 cases were admitted to an intensive care unit (ICU).

Table 1. Number of hospitalised laboratory-confirmed influenza cases by level of care, eight EU countries, 2015–2016

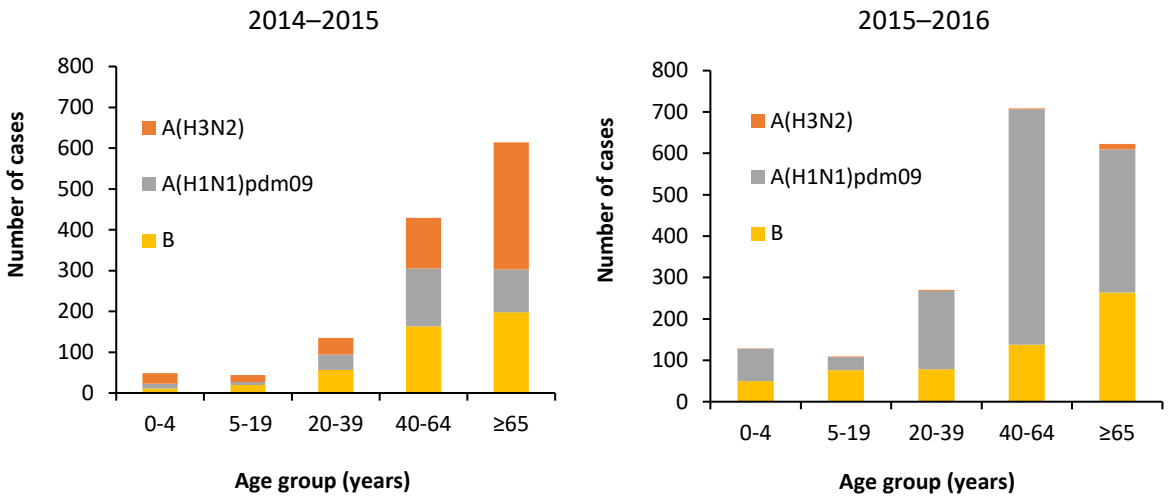
Country	2015–2016			
	General care	ICU	Unknown	Total
Finland	·	71	·	71
France	·	1 102	·	1 102
Ireland	1 712	159	·	1 871
Romania	51	51	·	102
Slovakia	5	3	4	12
Spain	1 958	1 045	47	3 050
Sweden	·	362	·	362
UK	·	2 121	·	2 121
Total	**3 726**	**4 914**	**51**	**8 691**

In 2015–2016, influenza virus type A was detected in 81% of the cases reported in ICUs; type B was detected in 19% of reported ICU cases.

Among ICU cases, A(H1N1)pdm09 was dominant in most age groups and accounted for the highest proportion of cases in middle-aged adults (40–64 years), while patients aged 5–19 years were mostly infected with B viruses. (Figure 2). Of 1 359 ICU patients with known medical status, 960 (71%) did not have underlying conditions. A(H3N2) virus played only a marginal role, with 55 cases reported.

As opposed to season 2014–2015, which was dominated by A(H3N2) viruses, the elderly (≥ 65years of age) were not the most affected age group during the 2015–2016 season. As in season 2014–2015, B viruses were responsible for severe cases in all age groups, and especially in the elderly in season 2015–2016 (Figure 2).

Figure 2. Number of influenza cases admitted to selected intensive care units, by (sub-)type and age group; Finland, France, Ireland, Romania, Slovakia, Spain and Sweden; 2014–2015 and 2015–2016



All-cause excess mortality

Mortality data from 17 countries or regions reported to the European EuroMOMO project suggested excess all-cause mortality among those aged 15–64 years between the end of 2015 and week 14/2016, a time period with influenza activity in the reporting European countries. The main affected age group corresponded to the main affected age group as determined by hospital/ICU surveillance. The level of mortality from all causes was similar to that observed during the 2012–2013 winter season, when A(H1N1)pdm09 was the dominant type A virus, and slightly lower than that during the 2014–2015 season during which A(H3N2) predominated.

Virus characterisations and antiviral susceptibility

Despite the genetic evolution of A(H1N1)pdm09 viruses in newly emerging subgroups 6B.1 and 6B.2, most viruses remained antigenically closely related to the A(H1N1)pdm09 vaccine virus. Reports of severe disease associated with A(H1N1)pdm09, evidence of vaccine failure in a number of cases, and dominance of subclade 6B.1 viruses led WHO to recommend in September 2016 to include a subclade 6B.1 virus in the vaccine recommendation for the 2017 southern hemisphere influenza season [4].

Circulating A(H3N2) viruses belonged to different genetic groups and showed antigenic properties similar to the vaccine strain A/Switzerland/9715293/2013 [5].

The characterised B/Victoria viruses were antigenically closely related to the B/Brisbane/60/2008 Victoria lineage strain included in the quadrivalent influenza vaccine. However, only a B/Yamagata lineage strain was included in the most widely used trivalent vaccine.

Since week 40/2015, 3136 A(H1N1)pdm09, 295 A(H3N2), and 721 B viruses have been tested for susceptibility to neuraminidase inhibitors (NAIs) by genetic and/or phenotypic methods. Twenty seven A(H1N1)pdm09 viruses carried the NA-H275Y amino acid substitution associated with highly reduced inhibition by oseltamivir. One A(H3N2) virus carried the NA-E119V amino acid substitution associated with reduced inhibition by oseltamivir. One type B/ Victoria lineage influenza virus carried a NA-D197N amino acid substitution, conferring highly reduced inhibition by oseltamivir and zanamivir. None of the test results of the other viruses showed evidence for reduced or highly reduced inhibition by NAIs.

Discussion

Start, intensity and duration of the 2015–2016 influenza season were similar to those of previous seasons.

In primary care, influenza A(H1N1)pdm09 virus predominated in almost all reporting countries, followed by an increasing dominance of B viruses of mainly the Victoria lineage when the circulation of A(H1N1)pdm09 viruses declined. This contrasts with the 2014–2015 season, when A(H3N2) was the dominant circulating virus in Europe.

Both circulating virus types were also detected in severe hospitalised influenza cases. Since the 2009 influenza pandemic, A(H1N1)pdm09 has been was the dominant type A virus (2010–2011, 2012–2013, 2013–2014 and 2015–2016), with a high proportion of severe outcomes in middle-aged adults. This is in accordance with high proportions of deaths among patients below 65 years of age reported during the decade after each previous pandemic [6]. This pattern of severe outcomes may also explain the excess mortality from all causes in 15–64-year-olds coinciding with influenza activity in EU/EEA countries.

Despite genetic changes with newly emerging clades of A(H1N1)pdm09 viruses, there was a good antigenic match between circulating strains and the vaccine strain. However, vaccine effectiveness estimates against this subtype before the end of the season were suboptimal and ranged from 44% [5] to 49% [6], comparable to estimates from seasons 2013–14 [9] and 2014–2015 [10]. While similar genetic changes in the circulating A(H1N1)pdm09 viruses were also observed in north America, estimated vaccine effectiveness was higher in the USA [9] and Canada [12] at 51% and 64%, respectively.

Circulating B/Victoria virus was very similar to the B/Victoria vaccine strain included in the quadrivalent vaccine but not to the B/Yamagata vaccine strain included in the trivalent vaccine, which is the one most widely used [13].

Public health implications

Two public health conclusions can be drawn from the past season:

Season 2015–2016 was the fourth season since the 2009 influenza pandemic where A(H1N1)pdm09 was the dominant A virus circulating in the EU/EEA and responsible for severe outcomes, especially in middle-aged adults. Over the coming years, public health authorities should continue to closely follow-up severe cases and monitor antigenic characterisation and vaccine effectiveness. Vaccine effectiveness was only moderate because the A(H1N1)pdm09 vaccine component has not been changed since the pandemic while the virus has continued to evolve. A change in the A(H1N1)pdm09 vaccine component for the northern hemisphere is possibly warranted (as already recommended for the southern hemisphere 2017 influenza season).

As in previous seasons, B viruses circulated later in the season and were responsible for severe cases, especially in the elderly. As this was the second consecutive season in which the circulating B virus was dissimilar from the B strain included in the most widely used vaccine, close monitoring of circulating B viruses is also needed. The quadrivalent vaccine, which included viruses from both B-lineages provides a better opportunity of protection when both lineages are circulating or when lineage changes occur.

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