

## Summary

### Week 16/2017 (17–23 April 2017)

- Influenza activity across the region decreased further with 38 of 39 countries reporting low influenza activity.
- The proportion of sentinel specimens testing positive for influenza viruses was 13%, slightly lower compared to the previous week (15%).
- The proportion of type B viruses exceeded the proportion of type A viruses in sentinel detections, similar to recent weeks. However, the overall number of type B virus detections remained low.

### Season overview

- After an earlier than usual start (week 46/2016), the influenza season is considered to be over in the majority of countries in the Region, with influenza activity at inter-seasonal levels in 38 of 39 countries that reported for week 16/2017.
- From week 40/2016 through week 10/2017, influenza A viruses predominated, accounting for 90% of all sentinel detections; the great majority (99%) of influenza A viruses from sentinel sites that were subtyped were A(H3N2).
- Since week 11/2017 influenza B viruses have predominated, although absolute numbers of type B detections have remained low.
- Confirmed cases of influenza type A virus infection reported from hospitals have predominantly been in adults aged 65 years or older.
- Significant excess all-cause mortality has been observed in people aged 15–64 years, and markedly so in people aged 65 years or older, in the majority of the 19 reporting countries or regions. This is commonly seen when the predominant viruses circulating are A(H3N2).
- Two-thirds of the A(H3N2) viruses genetically characterized belong to subclade (3C.2a1), but remain antigenically similar to the clade 3C.2a vaccine virus, as described in the [WHO recommendations for vaccine composition for the northern hemisphere 2017–18](#). See also the [WHO CC London February 2017 report](#).
- Vaccine effectiveness estimates for all age groups against A(H3N2) illness suggest moderate effectiveness in [Canada](#) (42%), the [US](#) (43%) and in [Europe](#) (38%).
- Of the viruses tested so far this season, one A(H3N2) virus has shown reduced susceptibility to oseltamivir and a second A(H3N2) virus has shown reduced susceptibility to zanamivir.
- The developments during the season have followed the conclusions of the ECDC [risk assessment](#) on seasonal influenza, [updated](#) on 25 January 2017, suggesting increased severe outcomes in the elderly due to the high prevalence of A(H3N2) viruses, which put some health care systems under pressure.

## Primary care data

### Influenza activity

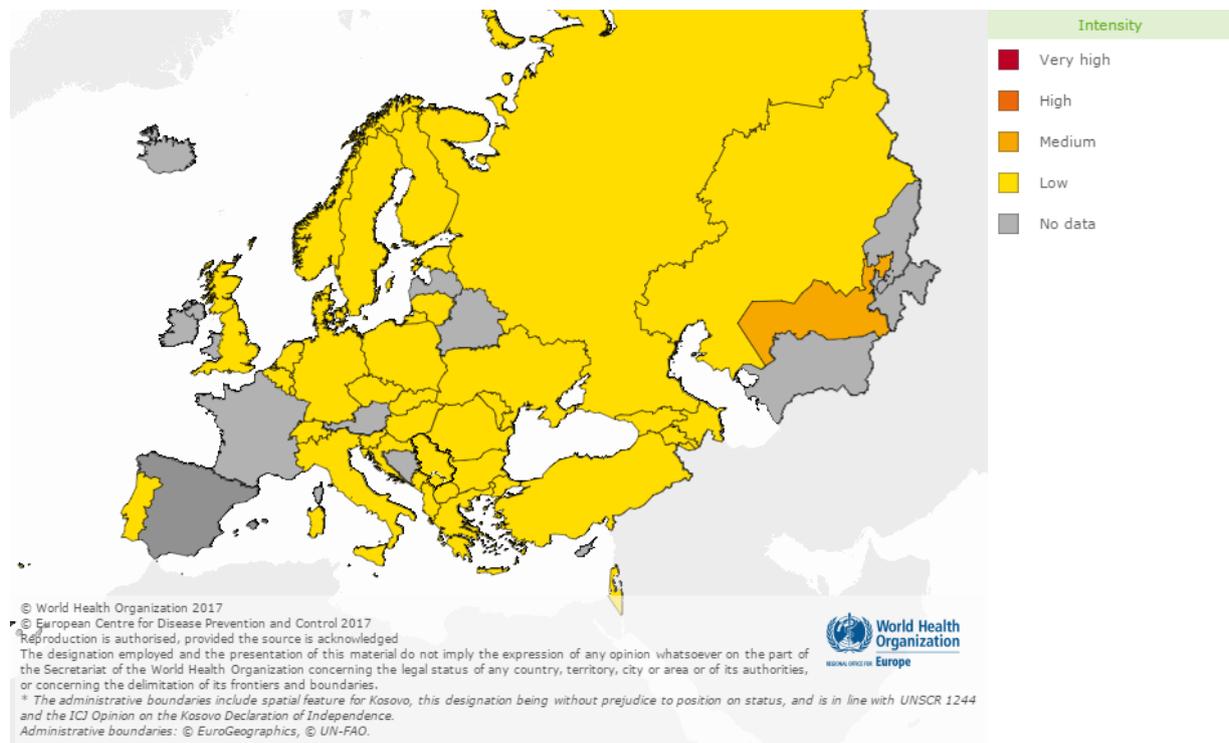
Of 39 countries reporting on influenza activity for week 16/2017, 1 reported medium intensity and 38 reported a return to baseline levels with low intensity (Fig. 1).

However, of the 40 countries reporting on geographic spread of influenza, 1 reported widespread, 2 regional and 22 local or sporadic influenza activity, indicating that influenza viruses are still circulating; 15 countries reported no influenza activity (Fig. 2).

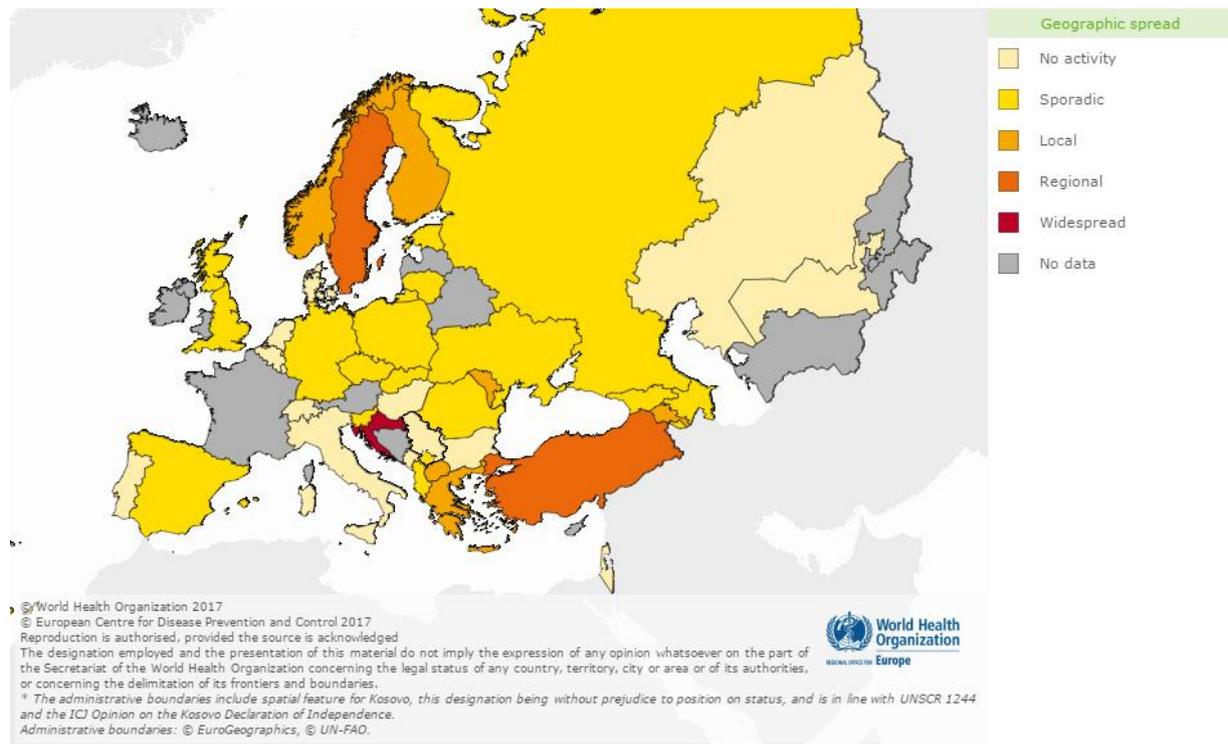
The proportion of influenza virus detections among sentinel specimens was 13%, which is slightly lower compared to week 15/2017 (15%), with 12 of 35 countries reporting dominance of influenza B viruses.

## Maps of qualitative indicators in the European Region

**Fig. 1. Intensity in the European Region, week 16/2017**



**Fig. 2. Geographic spread in the European Region, week 16/2017**



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

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

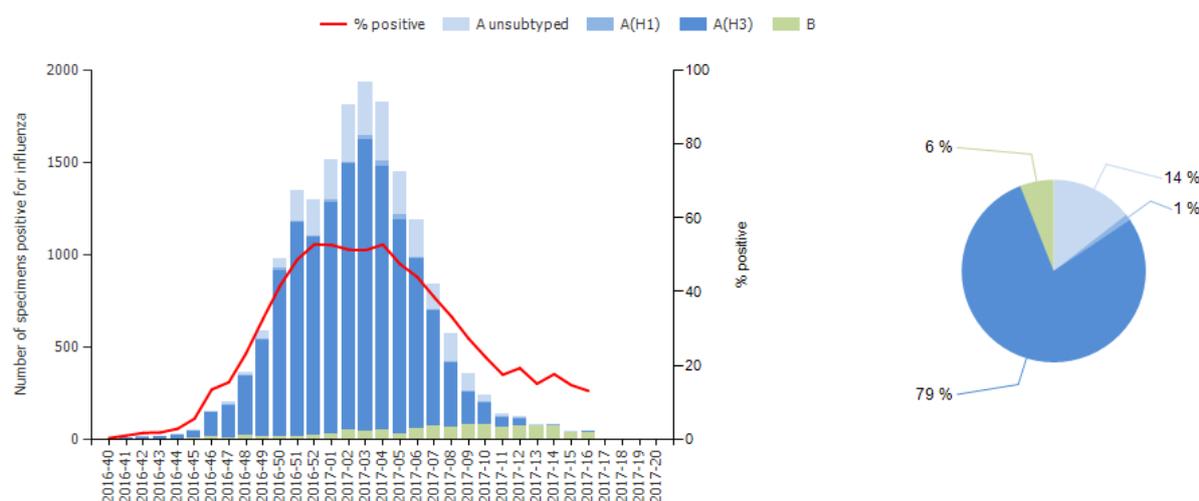
For week 16/2017, 43 (13%) of 326 sentinel specimens tested positive for influenza viruses (Table 1). Of these, 91% were type B and 9% type A viruses. The proportion of type B viruses commonly increases in the second half of an influenza season.

Of 7 countries across the region that each tested at least 10 sentinel specimens, only 1 reported a proportion of influenza virus detections of 30% or above (Republic of Moldova; 35%).

Of 4 subtyped influenza A viruses, all were A(H3N2). The lineage of 3 influenza B viruses was determined; all were of the B/Victoria lineage.

Since week 40/2016, of all typed viruses, 90% were type A, with 99% of those subtyped being A(H3N2) (Fig. 3, Table 1). Of the 763 influenza B viruses that have been ascribed to a lineage since week 40/2016, 430 (56%) were of the B/Yamagata lineage and 333 (44%) were of the B/Victoria lineage.

**Fig. 3. Influenza virus detections in sentinel-source specimens by type and subtype, by week<sup>a</sup>**



<sup>a</sup>The data in the pie chart is cumulative.

**Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 16/2017 and cumulatively**

Virus type and subtype	Current Week		Season 2016-2017	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>4</b>	<b>9</b>	<b>16 224</b>	<b>90</b>
A(H1N1)pdm09	0	0	186	1
A(H3N2)	4	100	13 544	99
A not subtyped	0	-	2 494	-
<b>Influenza B</b>	<b>39</b>	<b>91</b>	<b>1791</b>	<b>10</b>
B/Victoria lineage	3	100	333	44
B/Yamagata lineage	0	0	430	56
Unknown lineage	36	-	1 028	-
<b>Total detections / Total tested</b>	<b>43 / 326</b>	<b>13</b>	<b>18 015 / 49 410</b>	<b>36</b>

<sup>a</sup>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.

## Severity

Ten of the 12 countries that conduct sentinel surveillance of severe acute respiratory infections (SARI) and routinely report data reported 713 SARI cases for week 16/2017. Among these cases, 108 respiratory specimens were collected, 18 (17%) of which tested positive for influenza viruses in 3 countries (Armenia, Republic of Moldova and the Russian Federation).

Since week 40/2016, a total of 16 countries have reported 37 790 SARI cases. Of these 10 294 were tested for influenza viruses, 3 527 (34%) of which were positive: 2 706 (77%)

were type A and 821 (23%) type B viruses. Of the influenza A viruses, 2 493 (92%) were A(H3N2), 7 (<1%) were A(H1N1)pdm09 and 206 (8%) were not subtyped.

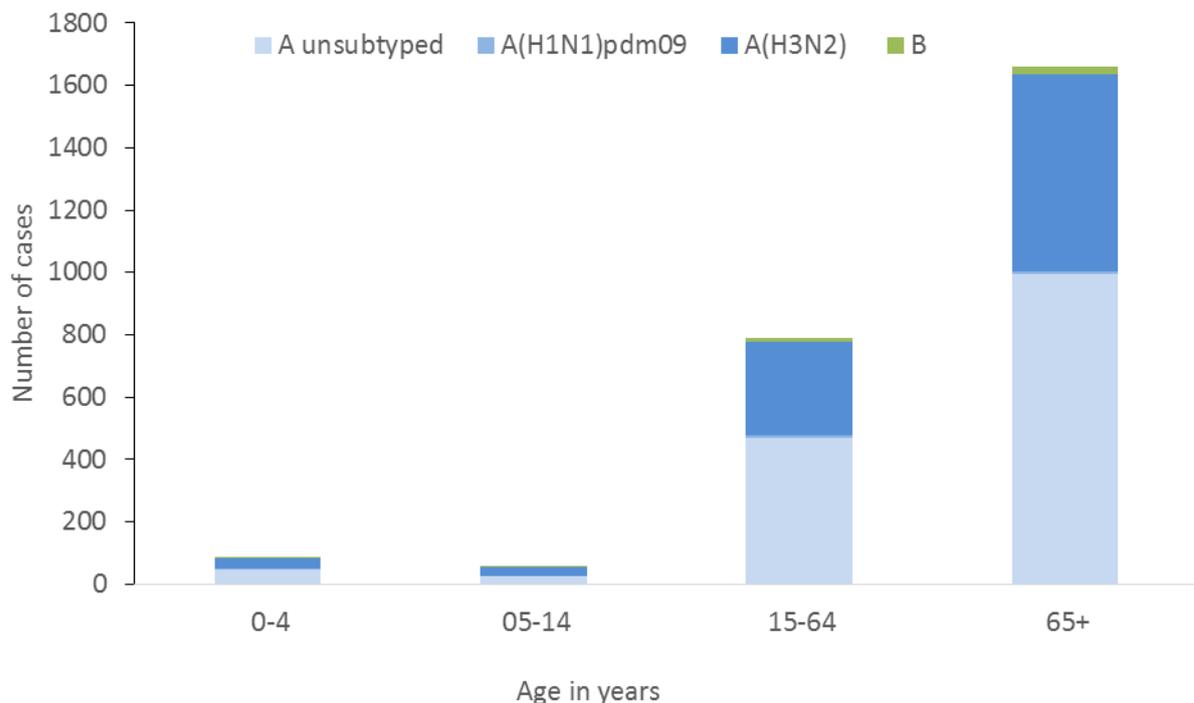
For week 16/2017, of 9 countries that conduct surveillance of hospitalized laboratory-confirmed influenza cases 2 (Estonia and Finland) reported a total of 2 cases, both in intensive care units (ICU). Of the patients admitted to ICU, 1 was infected with influenza subtype A(H3N2) virus and 1 with influenza B virus.

Since week 40/2016, 9 countries reported a total of 3 650 cases that have been admitted to ICU; 3 557 (97%) were infected with influenza type A viruses (2 113 - unsubtype, 1 317 - A(H3N2) and 127 - A(H1N1)pdm09) and 93 with type B viruses.

Since week 40/2016, 5 countries have reported 3 742 laboratory-confirmed influenza cases admitted to non-ICU wards; 3 694 (99%) were infected with influenza type A viruses (2 063 - unsubtype, 1 624 - A(H3N2), 7 - A(H1N1)pdm09), and 48 were infected with type B influenza viruses.

Since the start of the season, information on patient age and influenza virus (sub)types was available for 2 594 cases admitted to ICU; the majority of cases (64%; n=1 661) were aged ≥65 years, 791 (31%) were aged 15–64 years and 142 (5%) were aged under 15 years (Fig. 4). In total, 925 deaths have been reported, 526 from ICUs and 399 from other wards, with 753 (81%) of the patients aged 65 years or older. Of all fatal cases, 916 (99%) were due to influenza A with 452 (99%) of those subtyped being A(H3N2) viruses.

**Fig. 4. Distribution of virus (sub)types in influenza-confirmed cases admitted to ICU by age-group, cumulatively, during weeks 40/2016-16/2017**



## Mortality monitoring

Data from 20 countries or regions reporting to the [Euromomo](#) project were received for week 16/2017 and included in the pooled analyses of excess all-cause mortality.

The majority of participating European countries experienced a [marked excess](#) in all-cause mortality between December 2016 and the end of February 2017, in particular among the elderly (those aged 65 years and above). Mortality levels have since decreased to expected levels. This season's excess mortality coincided with circulation of influenza A(H3N2) viruses, which usually leads to increased mortality among the elderly.

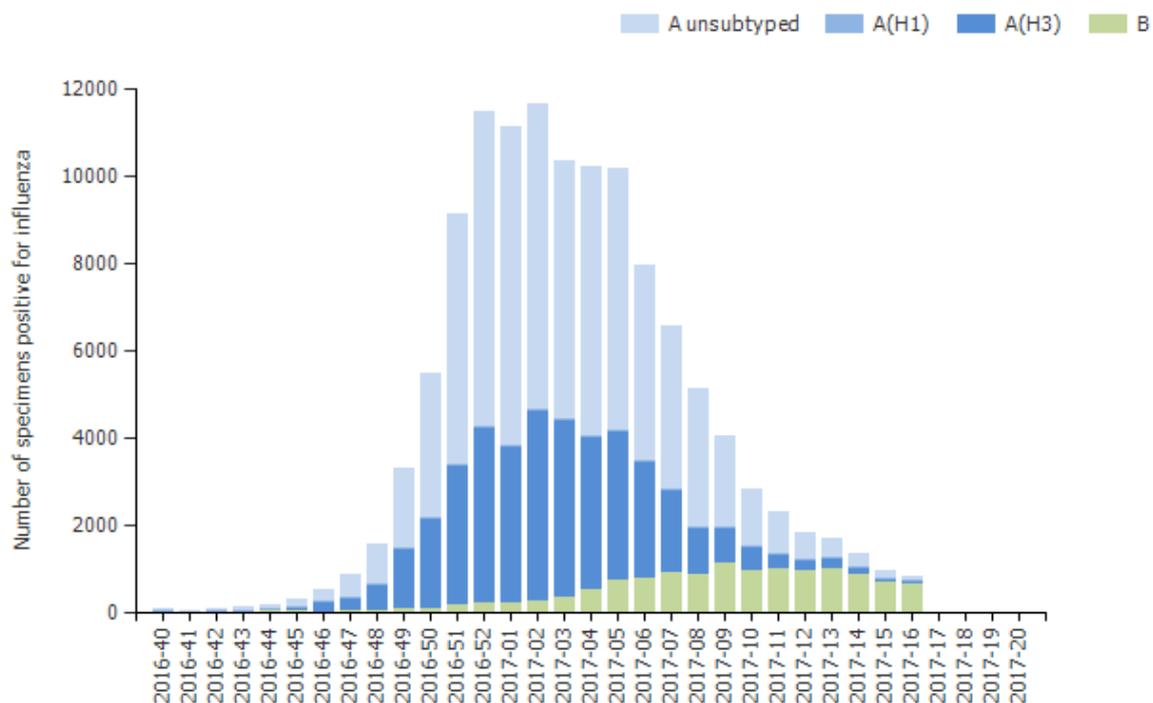
## Virus characteristics

### Viruses detected in non-sentinel-source specimens

For week 16/2017, 847 specimens from non-sentinel sources (such as hospitals, schools, non-sentinel primary care facilities, nursing homes and other institutions) tested positive for influenza viruses (Fig. 5, Table 2).

Of these, 21% were type A (with 94% of the subtyped viruses being A(H3N2)), and 79% type B. The increase in proportion of type B viruses corresponds to the sentinel detection data, however the number of influenza B viruses detected remained relatively low and similar to that seen in recent weeks.

**Fig. 5. Influenza virus detections in non-sentinel-source specimens by type and subtype, by week**



Whilst no subtype or lineage was determined for the majority of influenza viruses since week 40/2016, cumulative distributions of types and type A subtypes similar to those among sentinel detections have been observed: of all typed viruses, 89% were type A, with 99% of those subtyped being A(H3N2). Of 1 319 influenza type B viruses ascribed to a lineage, 76% were B/Yamagata lineage and 24% were B/Victoria lineage (Table 2), which differs from sentinel detections where B/Victoria lineage and B/Yamagata lineage viruses have been more evenly distributed this season. The difference is mainly driven by the proportion of influenza B lineage detections in sentinel specimens in Latvia, Norway and Slovenia (B/Yamagata lineage predominant).

**Table 2. Influenza viruses detected in non-sentinel-source specimens, by virus (sub)type, week 16/2017 and cumulatively**

Virus type and subtype	Current Week		Season 2016-2017	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>178</b>	<b>21</b>	<b>109 502</b>	<b>89</b>
A(H1N1)pdm09	3	6	358	1
A(H3N2)	49	94	39 152	99
A not subtyped	126	-	69 992	-
<b>Influenza B</b>	<b>669</b>	<b>79</b>	<b>13 890</b>	<b>11</b>
B/Victoria lineage	0	0	315	24
B/Yamagata lineage	4	100	1 004	76
Unknown lineage	665	-	12 571	-
<b>Total detections / Total tested</b>	<b>847 / 8 173</b>	<b>-</b>	<b>123 392 / 557 804</b>	<b>-</b>

<sup>a</sup>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; as not all countries have a true non-sentinel testing denominator, no percentage calculations for total tested are shown.

## Genetic characterization

For specimens collected since week 40/2016, genetic characterizations of 3 425 viruses have been reported (Table 3). Among 3 104 A(H3N2) viruses, 916 fell in the vaccine component clade (3C.2a) and 2 149 in the 3C.2a1 subclade defined by N171K amino acid substitution, and often with N121K, in the haemagglutinin. Viruses in these two clades have been antigenically similar, but both clades are evolving rapidly with emergence of several virus clusters defined by additional amino acid substitutions in the haemagglutinin, thereby requiring continued monitoring of antigenic characteristics. See also the [WHO CC London February 2017 report](#).

**Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2016–16/2017**

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (subgroup 6B.1) <sup>b, c</sup>	28
A(H1N1)pdm09 A/South Africa/3626/2013 (subgroup 6B)	5
A(H3N2) A/Bolzano/7/2016 (subgroup 3C.2a1)	2149
A(H3N2) A/Hong Kong/4801/2014 (subgroup 3C.2a) <sup>a, b, c</sup>	916
A(H3N2) A/Samara/73/2013 (subgroup 3C.3)	1
A(H3N2) A/Switzerland/9715293/2013 subgroup (3C.3a)	31
A(H3N2) A/Stockholm/28/2014 (subgroup 3C.3b)	1
A(H3N2), subgroup not listed	6
B/Brisbane/60/2008 (Victoria lineage clade 1A) <sup>a, b, c</sup>	64
B/Phuket/3073/2013 (Yamagata lineage clade 3) <sup>d</sup>	224

<sup>a</sup> Vaccine component for Northern Hemisphere 2016–2017 season

<sup>b</sup> Vaccine component for Southern Hemisphere 2017 season

<sup>c</sup> Vaccine component for Northern Hemisphere 2017–2018 season

<sup>d</sup> Vaccine component of quadrivalent vaccines for use in both Northern and Southern Hemisphere

The recommended composition of trivalent influenza vaccines for the 2016–2017 season in the [northern hemisphere](#) was for inclusion of an A/California/7/2009 (H1N1)pdm09-like virus; an A/Hong Kong/4801/2014 (H3N2)-like virus; and a B/Brisbane/60/2008-like virus (B/Victoria lineage). For quadrivalent vaccines a B/Phuket/3073/2013-like virus (B/Yamagata lineage) was recommended. On 2 March 2017 WHO announced the recommended vaccine composition for the 2017–2018 season in the [northern hemisphere](#). The recommendations matched those for the 2016–2017 season, but for the A(H1N1)pdm09 component being changed to an A/Michigan/48/2015-like virus (clade 6B.1).

Early monitoring of vaccine effectiveness (VE) in [Finland and Sweden](#) (Stockholm County) suggested levels of effectiveness in persons aged 65 years or older (32% and 28% VE, respectively) similar to estimates from annual multi-country studies covering the 2011–2012 and 2014–2015 seasons. More recent VE estimates for all age groups against A(H3N2) illness from Canada (42%), from the US (43%) and from Europe (38%) were consistent with the early estimates from Finland and Sweden.

### Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility has been assessed for 1 816 influenza viruses (1 662 A(H3N2), 29 A(H1N1)pdm09 and 125 type B) with collection dates since week 40/2016. One A(H3N2) virus, from a specimen collected in week 4/2017, showed reduced inhibition by oseltamivir in phenotypic assay. One A(H3N2) virus, from a specimen collected in week 01/2017, showed reduced inhibition by zanamivir in phenotypic assay.

This weekly update was prepared by an editorial team at the European Centre for Disease Prevention and Control (Cornelia Adlhoch, Eeva Broberg, René Snacken, Pasi Penttinen) and the WHO Regional Office for Europe (Caroline Brown, Piers Mook, Dmitriy Pereyaslov and Tamara Meerhoff, Temporary Advisor to WHO). It was reviewed by country experts (AnnaSara Carnahan, Public Health Agency, Sweden; Veronica Eder, National Public Health Center, Republic of Moldova), and by experts from the network (Adam Meijer, National Institute for Public Health and the Environment (RIVM), the Netherlands; Rod Daniels and John McCauley, WHO Collaborating Centre for Reference and Research on Influenza, Francis Crick Institute, United Kingdom; Tyra Grove Krause, Statens Serum Institut and EuroMOMO network, Denmark).

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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