Flu News Europe
Joint ECDC–WHO/Europe weekly influenza update

# Summary

## Weeks 31–35/2018 (30 July–2 September 2018)

- Influenza activity was at inter-season levels.
- Of all the samples from primary health care settings, only one tested positive for influenza virus.

## 2017–2018 season overview

- Aggregated regional data indicated that influenza viruses circulated at high levels from week 52/2017 through 12/2018 (based on increased proportions of sentinel specimens – 40% and above – testing positive for influenza viruses). This was longer than in recent seasons and may have contributed to the burden observed during the season.
- The majority of influenza viruses detected were type B, representing a high level of circulation of influenza B viruses compared to recent seasons. B/Yamagata lineage viruses greatly outnumbered those of the B/Victoria lineage.
- Different patterns of dominant influenza virus types and A subtypes were observed between the countries of the Region.
- While low in numbers, characterized A(H3N2) viruses were reported mainly as clade 3C.2a (57%) and subclade 3C.2a1 (42%), while 45% of B/Victoria lineage viruses fell in a subclade of clade 1A viruses that are antigenically distinct from the 2017–2018 season trivalent vaccine component.
- The majority of severe cases were due to influenza type B virus infection and occurred mostly in persons older than 15 years of age.
- All-cause excess mortality was increased from December 2017 through March 2018 and was most pronounced among individuals aged 65 years and above, though individuals in the age group 15–64 years also showed marked excess mortality. EuroMOMO. Click here for more information
- Interim results from 5 European studies indicated 25% to 52% vaccine effectiveness against any laboratory-confirmed influenza virus infection.

## Primary care data

Of countries with thresholds based on syndromic surveillance data for influenza-like illness (ILI) and/or acute respiratory infection (ARI), all reported respiratory infections to be at baseline levels.

## Influenza activity

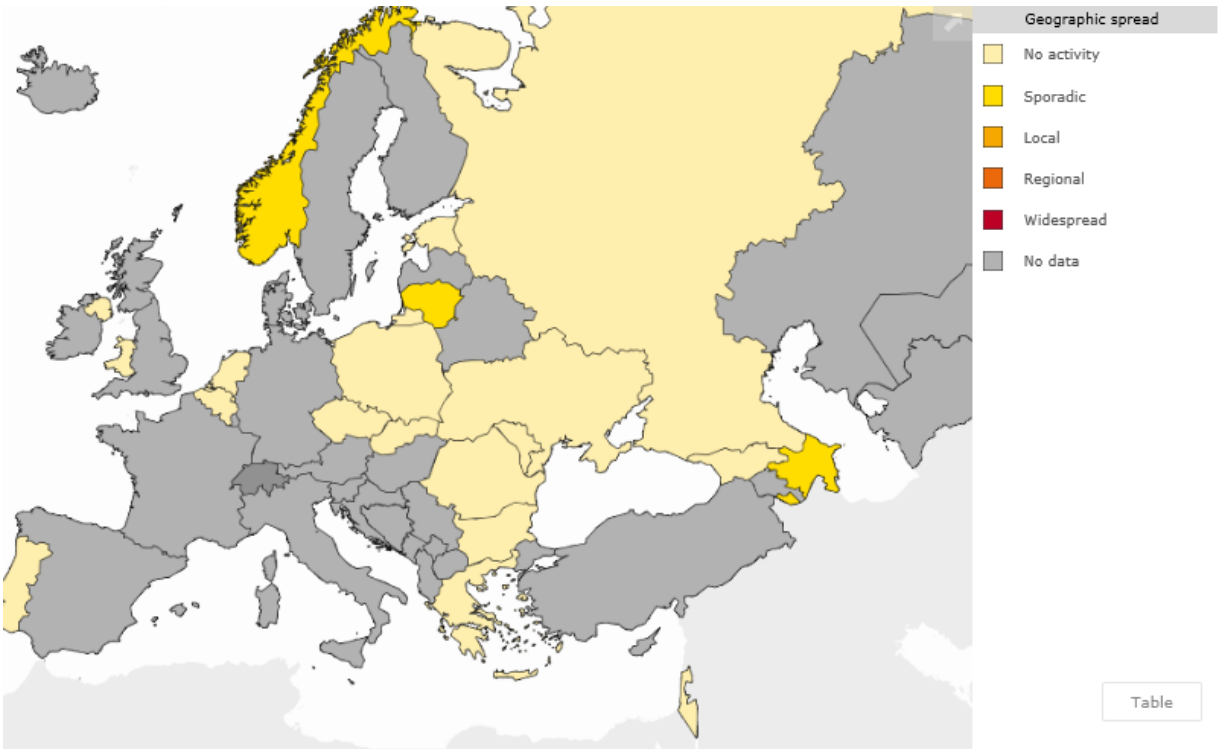
All 29 Member States and areas reporting on intensity for at least one week from week 31/2018 through week 35/2018 reported low intensity (refer to Fig. 1 for week 35/2018 data).

Of the 29 Member States and areas reporting on geographic spread for at least one week from week 31/2018 through week 35/2018, most reported no activity, a few (4–5 countries) sporadic activity and one local activity (refer to Fig. 2 for week 35/2018 data).

## Maps of qualitative indicators in the European Region

### Fig. 1. Intensity in the European Region, week 35/2018

### Fig. 2. Geographic spread in the European Region, week 35/2018






For interactive maps of influenza intensity and geographic spread, see the Flu News Europe website.

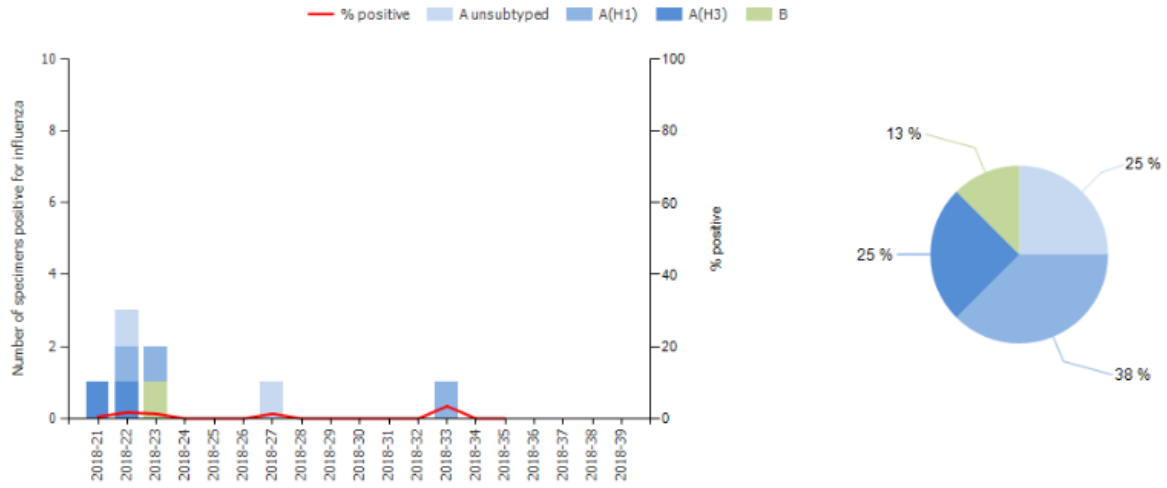
## Viruses detected in sentinel-source specimens (ILI and ARI)

For weeks 21–35/2018, 8 (0.5%) of 1 462 sentinel specimens tested positive for an influenza virus. Of the 7 influenza type A viruses, 5 were subtyped, 3 were A(H1N1)pdm09 and 2 were A(H3N2) (Fig. 3 and Table 1). The single influenza B virus was not ascribed to a lineage.

For weeks 31-35/2018, only one influenza virus A(H1N1)pdm09 was detected.

Details of the distribution of viruses detected in non-sentinel-source specimens can be found in the Virus characteristics section.

## Fig. 3. Influenza virus detections in sentinel-source specimens by type and subtype, by week and cumulatively for weeks 21–35/2018 [a]




[a] Pie chart shows cumulative data for this period.

## Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, weeks 21–35/2018

| | Weeks 21-35/2018 | |
|---|---|---|
| **Virus type and subtype** | **Number** | **%[a]** |
| **Influenza A** | **7** | **87.5** |
| A(H1N1)pdm09 | 3 | 60.0 |
| A(H3N2) | 2 | 40.0 |
| A not subtyped | 2 | - |
| **Influenza B** | **1** | **12.5** |
| B/Victoria lineage | 0 | 0 |
| B/Yamagata lineage | 0 | 0 |
| Unknown lineage | 1 | - |
| **Total detections (total tested)** | **8 (1 462)** | **0.5** |

[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.

## Severity

A subset of Member States monitor severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in intensive care units (ICUs) (n=12 Member States), or other wards (n=8 Member States), or 2) severe acute respiratory infections (SARI; n=16 Member States).

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

Numbers of reported hospitalized laboratory-confirmed influenza cases in ICUs remained low during weeks 21–35/2018, with only the Czech Republic, Spain and Sweden each reporting one case.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

Numbers of reported hospitalized laboratory-confirmed influenza cases in other wards also remained low during weeks 21–35/2018, with only the Czech Republic (n=2) and Spain (n=3) reporting cases.

2. SARI surveillance

For weeks 31–35/2018, 1 139 SARI cases were reported. Of 101 specimens tested, none were positive for influenza viruses.

## Mortality monitoring

For week 35/2018, the EuroMOMO project received data from 23 EU/EEA Member States or regions that were included in pooled analyses. Overall, the pooled estimates of all-cause mortality showed expected mortality levels for the participating countries.

## Virus characteristics

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

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

For weeks 21–35/2018, 488 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 influenza viruses, which was an increase of 68 compared to weeks 21–30/2018. Of the 488, 76% were type A and 24% type B viruses (Table 2). Of the influenza A viruses that were subtyped, 54% were A(H3N2). The majority of influenza B viruses from non-sentinel specimens were not tested for lineage; 12 were tested, 10 of which were found to be B/Yamagata.

### Table 2. Influenza virus detections in non-sentinel-source specimens by type and subtype, weeks 21–35/2018

| | Weeks 21-35/2018 | |
|---|---|---|
| **Virus type and subtype** | **Number** | **%[a]** |
| **Influenza A** | **369** | **75.6** |
| A(H1N1)pdm09 | 117 | 45.7 |
| A(H3N2) | 139 | 54.3 |
| A not subtyped | 113 | - |
| **Influenza B** | **119** | **24.4** |
| B/Victoria lineage | 2 | 16.7 |
| B/Yamagata lineage | 10 | 83.3 |
| Unknown lineage | 107 | - |
| **Total detections (total tested)** | **488 (33 397)** | **-** |

[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

For specimens collected since week 21/2018, genetic characterization of 35 viruses has been reported (Table 3). All 24 influenza A(H1N1)pdm09 viruses fell in the A/Michigan/45/2015 vaccine component clade (6B.1), 1 A(H3N2) virus was reported as clade 3C.2a and 3 A(H3N2) viruses as subclade 3C.2a1 (with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin). All 7 influenza B viruses belonged to clade 3 of the B/Yamagata lineage (represented by B/Phuket/3073/2013).

For more information on virus characterizations for EU/EEA countries, see the latest WHO CC London Influenza virus characterisation reports).

### Table 3. Viruses attributed to genetic groups, cumulative for weeks 21/2018–35/2018

| Phylogenetic group | Number of viruses |
|---|---|
| A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a] | 24 |
| A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1)[b] | 3 |
| A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a) | 1 |
| B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, d] | 7 |

[a]Vaccine component of vaccines for northern (2017–2018 and 2018-2019 seasons) and southern (2018 season) hemispheres

[b]Vaccine component for southern hemisphere 2018 and northern hemisphere 2018-2019 seasons

[c]Vaccine component of quadrivalent vaccines for use in northern hemisphere 2017–2018 and 2018-2019 seasons

[d]Vaccine component for southern hemisphere 2018

The recommended composition of trivalent influenza vaccines for the 2017–2018 season in the northern hemisphere included an A/Michigan/45/2015 (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 also recommended.

On 21 February 2018, WHO published influenza vaccine recommendations for the 2018–2019 season in the northern hemisphere. Two changes were recommended compared to the current trivalent and quadrivalent vaccine formulations used in the 2017–2018 season in the northern hemisphere. Similar to the recommended composition for the 2018 southern hemisphere vaccine, the A(H3N2) component was changed to an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus. In trivalent vaccines the B component was switched to a B/Colorado/06/2017-like virus, representing the emergent strain of B/Victoria-lineage viruses with deletion K162 and N163 in the HA1 subunit. The A(H1N1)pdm09 component in trivalent and quadrivalent vaccines and the B/Yamagata component in quadrivalent vaccines remained the same.

## Antiviral susceptibility testing

Neuraminidase (NA) inhibitor susceptibility has been assessed for 3 703 viruses with collection dates from week 40/2017: 1 539 type B, 990 A(H3N2), and 1 174 A(H1N1)pdm09. Two type B viruses carried the NA amino acid substitution D197N associated with reduced inhibition (RI) by oseltamivir and zanamivir, and 2 type B viruses showed RI by oseltamivir only. Nineteen A(H1N1)pdm09 viruses carried the NA amino acid substitution H275Y associated with highly reduced inhibition (HRI) by oseltamivir and 2 showed RI by zanamivir only. Two A(H3N2) viruses carried NA amino acid substitution R292K associated with HRI by oseltamivir and RI by zanamivir.

This weekly update was prepared by an editorial team at the European Centre for Disease Prevention and Control (Cornelia Adlhoch, Angeliki Melidou, Pasi Penttinen, Phillip Zucs) 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 (Raquel Guiomar, Instituto Nacional de Saúde Doutor Ricardo Jorge, Portugal; Vladimir Mikic, Institute of Public Health, The former Yugoslav Republic of Macedonia) 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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