

Summary

Week 5/2019 (28 January–3 February 2019)

- Influenza activity is widespread in the European Region and continues to increase. Samples collected from individuals presenting with ILI or ARI to sentinel primary health care sites yielded an influenza positivity rate of 54.7%.
- Influenza type A virus detections dominated with A(H1N1)pdm09 viruses and A(H3N2) viruses co-circulating. Very few influenza B viruses were detected.
- Over 50% of specimens from patients hospitalized with severe acute respiratory infection (SARI) collected in week 5/2019 were positive for influenza, and >99% were type A.
- Pooled data from 22 Member States and areas reporting to the [EuroMOMO](#) project indicated excess mortality in elderly populations overall. However, this result was driven by data from only a few countries.

2018–2019 season overview

- Influenza activity in the European region, based on sentinel sampling, exceeded a positivity rate of 10% in week 49/2018 and has increased continuously into week 5/2019, but may be levelling off. The positivity rate has exceeded 50% since week 3/2019.
- Both influenza A virus subtypes are circulating widely, with co-circulation in some countries while others report dominance of either A(H1N1)pdm09 or A(H3N2) viruses. Countries should continue to promote vaccination. In addition, countries are encouraged to use antivirals in accordance with national guidelines.
- Among hospitalized influenza virus-infected patients admitted to ICU wards, 76% of influenza A virus detections were subtyped; of these 78% were A(H1N1)pdm09 virus. Among influenza virus-infected patients admitted to other wards, 26% of influenza A virus detections were subtyped and 70% were A(H1N1)pdm09 virus.
- Over 90% of influenza A virus positive cases detected from SARI surveillance since week 40/2018 were subtyped and 82% were A(H1N1)pdm09 virus.
- In general, current influenza vaccines tend to work better against influenza A(H1N1)pdm09 and influenza B viruses than against influenza A(H3N2) viruses. [Preliminary results](#) from Canada, where the predominant circulating viruses are influenza A(H1N1)pdm09, indicate good vaccine effectiveness. These results are supported by preliminary vaccine effectiveness [results](#) from Hong Kong, where the vaccine was very effective at preventing A(H1N1)pdm09 virus-related hospitalizations in children.
- The high vaccine effectiveness against A(H1N1)pdm09 viruses is consistent with genetic characterization reports indicating that all circulating viruses belong to clade 6B.1 and remain antigenically similar to the vaccine virus, despite the emergence of a number of subgroups. The lower vaccine effectiveness against A(H3N2) viruses likely reflects the

circulation of multiple genetic clades some of which contain viruses that display low antigenic similarity to the vaccine virus, particularly with egg-propagated vaccine virus as compared to cell culture-propagated vaccine virus.

Primary care data

Syndromic surveillance data

For week 5/2019, 27 (84%) of the 32 Member States that calculated influenza-like illness (ILI) thresholds and 10 (56%) of the 18 Member States that calculated acute respiratory infection (ARI) thresholds reported activity above their baseline levels.

Of those Member States in which thresholds for ILI activity are defined, the following countries in eastern (n=2; Republic of Moldova, Russian Federation), northern (n=9; Denmark, Estonia, Iceland, Ireland, Latvia, Lithuania, Norway, United Kingdom (England and Scotland)), southern (n=7; Greece, Israel, Italy, Montenegro, Romania, Serbia, The Former Yugoslav Republic of Macedonia) and western (n=9; Belgium, Czech Republic, Hungary, Luxembourg, Netherlands, Portugal, Slovakia, Spain, Switzerland) areas of the European Region reported activity above baseline levels.

Of those Member States and areas in which thresholds for ARI activity are defined, the following countries in eastern (n=2; Republic of Moldova, Russian Federation), northern (n=3; Estonia, Latvia, Lithuania), southern (n=3; Albania, Bulgaria, Romania) and western (n=2; Czech Republic, Slovakia) areas of the European Region reported activity above baseline levels.

Influenza activity

Of 48 Member States and areas reporting on intensity, 2 reported baseline (Austria, Kazakhstan), 16 reported low (across the region), 21 reported medium (across the region), and 9 reported high (southern, western areas) intensity for week 5/2019 (Fig. 1).

Of 48 Member States and areas reporting on geographic spread, 1 reported no activity (Uzbekistan), 2 reported sporadic spread (United Kingdom (England and Northern Ireland)), 4 reported local spread (Azerbaijan, Ireland, Slovakia, Kosovo (in accordance with United Nations Security Council Resolution 1244 [1999])), 2 reported regional spread (Belarus, Ukraine) and 39 reported widespread (across the region) (Fig. 2).

Fig. 1. Intensity in the European Region, week 5/2019

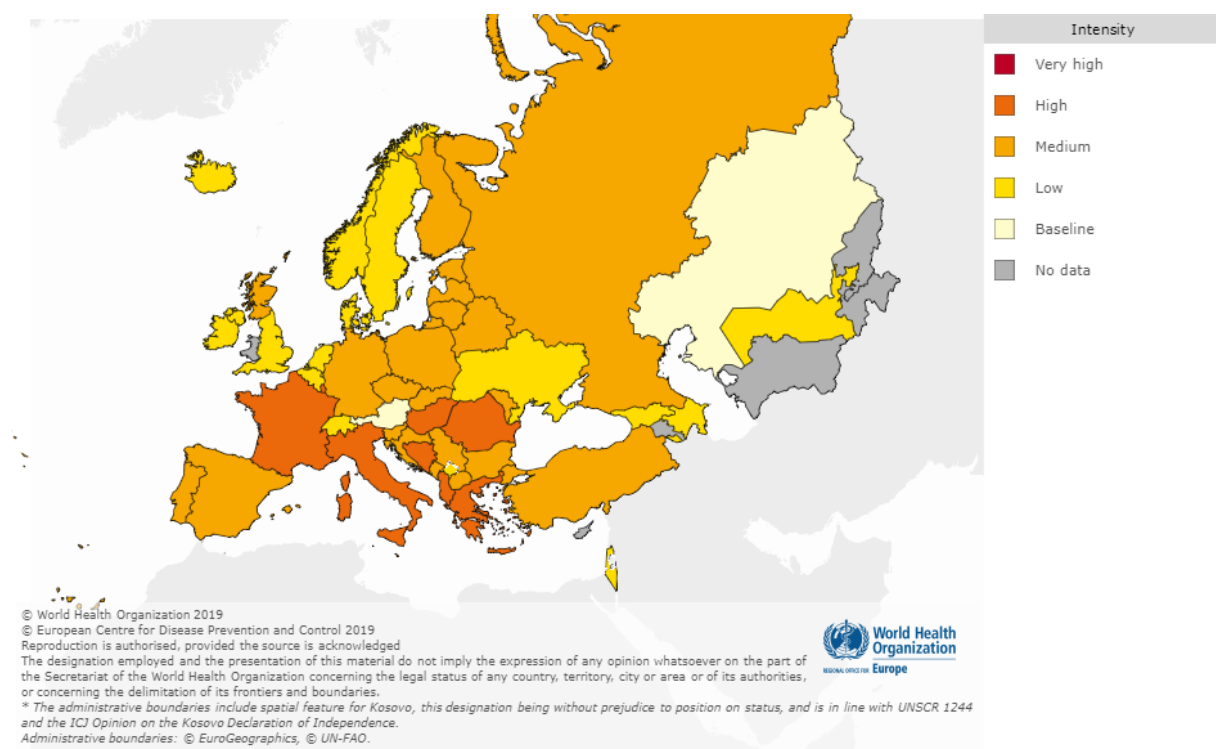
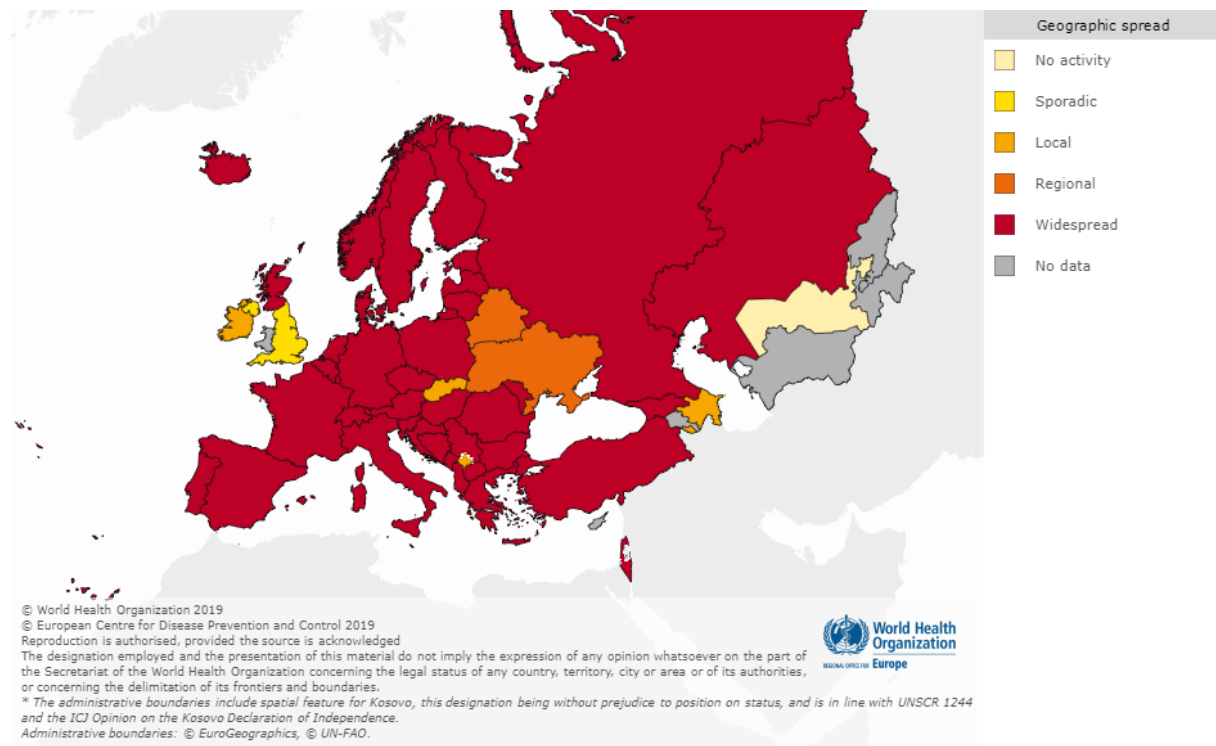


Fig. 2. Geographic spread in the European Region, week 5/2019



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

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

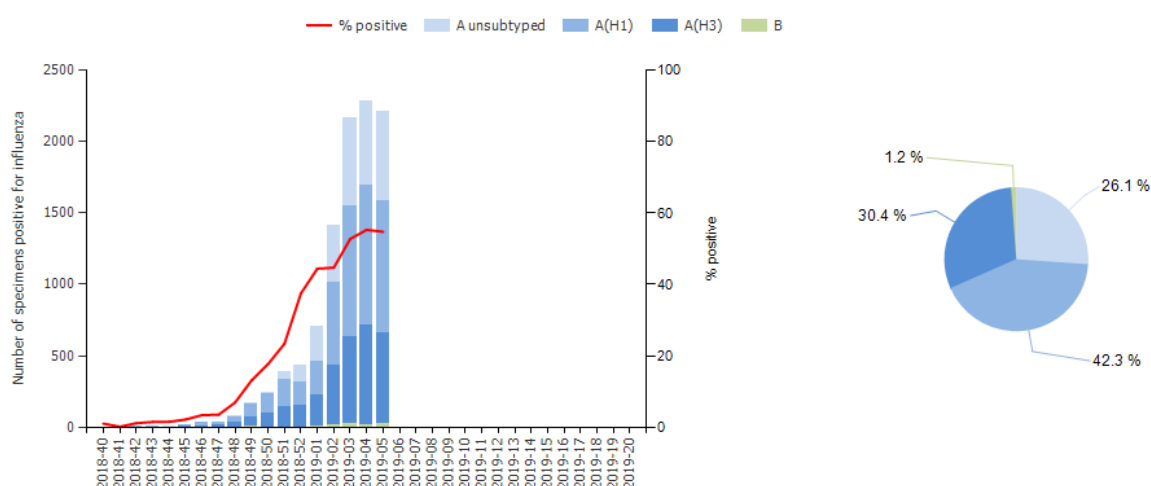
For week 5/2019, 2 203 (54.7%) of 4 026 sentinel specimens tested positive for an influenza virus; 98.8% were type A and 1.2% were type B. Of 1 557 subtyped A viruses, 59.3% were A(H1N1)pdm09 and 40.7% A(H3N2). Of 6 type B viruses ascribed to a lineage, 4 (66.7%) were B/Victoria and 2 (33.3%) were B/Yamagata (Fig. 3 and Table 1).

Of 40 Member States or areas across the region that each tested at least 10 sentinel specimens in week 5/2019, 37 reported rates of influenza virus detections above 30% (median 52.8%; range 36.2% to 92.6%).

For the season to date, more influenza type A (n=10 085, 98.8%) than type B (n=120, 1.2%) viruses have been detected. Of 7 424 subtyped A viruses, 4 320 (58.2%) were A(H1N1)pdm09 and 3 104 (41.8%) were A(H3N2). Of 120 influenza type B viruses detected, 40 (33.3%) were ascribed to a lineage and 32 (80.0%) were B/Yamagata (Fig. 3 and Table 1).

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^a



^a Pie chart shows cumulative data for this period.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 5/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	2 176	98.8	10 085	98.8
A(H1N1)pdm09	924	59.3	4 320	58.2
A(H3N2)	633	40.7	3 104	41.8
A not subtyped	619	-	2 661	-
Influenza B	27	1.2	120	1.2
B/Victoria lineage	4	66.7	8	20.0
B/Yamagata lineage	2	33.3	32	80.0
Unknown lineage	21	-	80	-
Total detections (total tested)	2 203 (4 026)	54.7	10 205 (29 268)	34.9

^aFor 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 and areas monitors severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in ICUs (12 Member States or areas), or other wards (8 Member States or areas), or 2) severe acute respiratory infections (SARI; 17 Member States or areas).

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

Among laboratory-confirmed influenza cases in ICUs reported for week 5/2019, influenza type A viruses (n=488, 99.6%) were detected much more frequently than influenza type B viruses (n=2, 0.4%).

Since week 40/2018, more influenza type A (n=3 390, 98.9%) than type B (n=36, 1.1%) viruses were detected. Of 1 230 subtyped influenza A viruses, 961 (78.1%) were A(H1N1)pdm09 and 269 (21.8%) were A(H3N2). No influenza B viruses were ascribed to a lineage. Of 1 502 cases with known age, 49% were 15–64 years old and 42.1% were 65 years and older.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

Among laboratory-confirmed influenza cases reported in wards other than ICUs for week 5/2019 (n=566), influenza type A viruses (n=563, 99.5%) were detected more frequently than influenza type B viruses (n=3, 0.5%).

Cumulatively since week 40/2018, more influenza type A (n=4 620, 99.0%) than type B (n=45, 1.0%) viruses were detected. Of 1 216 subtyped influenza A viruses, 854 (70.2%) were A(H1N1)pdm09 and 362 (29.8%) were A(H3N2). The one influenza B virus ascribed to a lineage was B/Yamagata. Of 4 665 cases with known age, 37.0% were 15–64 years old and 39.6% were 65 years and older.

2. SARI surveillance

For week 5/2019, 1 532 SARI cases were reported by 13 Member States or areas. Of 478 specimens tested for influenza viruses, 256 (53.6%) were positive. Of these, 255 were influenza type A and only one was type B.

Of 22 766 SARI cases reported since week 40/2018, 22 358 had a recorded age and, of these, 61.7% were 0–4 years old and 21.4% were 15–64 years old. For SARI cases testing positive for influenza virus since week 40/2018 (n=1 495), type A viruses were the most common (99.9%). Of the 1 389 influenza type A infected cases for which subtyping was performed, 1 144 (82.4%) were infected by A(H1N1)pdm09 viruses and 245 (17.6%) were infected by A(H3N2) viruses.

Mortality monitoring

For week 5/2019, the [EuroMOMO](#) project received data from 22 Member States or areas that were included in pooled analyses. The pooled estimates of all-cause mortality showed elevated levels in elderly populations. However, these trends appeared to be driven by a few 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 week 5/2019, 15 644 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 an influenza virus; 15 547 (99.4%) were type A and 97 (0.6%) type B. Of 4 868 subtyped A viruses, 2 971 (61.0%) were A(H1N1)pdm09 and 1 897 (39.0%) were A(H3N2). No influenza B viruses were ascribed to a lineage.

For the season so far, a substantially greater number of influenza type A (n=67 340, 98.9%) than type B viruses (n=761, 1.1%) has been detected. Of 22 989 subtyped A viruses, 15 198 (66.1%) were A(H1N1)pdm09 and 7 791 (33.9%) were A(H3N2). Of 29 influenza type B viruses ascribed to a lineage, 16 (55.2%) were B/Yamagata and 13 (44.8%) were B/Victoria; 761 type B viruses were reported without a lineage (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, week 5/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	15 547	99.4	67 340	98.9
A(H1N1)pdm09	2 971	61.0	15 198	66.1
A(H3N2)	1 897	39.0	7 791	33.9
A not subtyped	10 679	-	44 351	-
Influenza B	97	0.6	761	1.1
B/Victoria lineage	0	-	13	44.8
B/Yamagata lineage	0	-	16	55.2
Unknown lineage	97	-	732	-
Total detections (total tested)	15 644 (38 058)	41.1	68 101 (379 976)	17.9

^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 and antigenic characterization

Genetic and antigenic characterization of influenza viruses is routinely performed to understand how similar currently circulating influenza viruses are to the viruses used in influenza vaccines for an ongoing season.

Since week 40/2018, genetic characterizations of 1 201 viruses have been reported by the network laboratories.

Of the genetically characterized viruses 707 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade; 477 were A(H3) viruses, with 301 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 32 to the A/Switzerland/8060/2017 (3C.2a2) subclade, 14 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 63 to the A/England/538/2018 (3C.3a) clade, 37 to the A/Singapore-16-0019/2016 (3C.2a1) subclade, 1 to the A/Hong Kong/4801/2014 (3C.2a) clade, 3 attributed to a subgroup not listed, and 26 not attributed to a clade. Of the 17 genetically characterized influenza B viruses, 9 were B/Yamagata viruses belonging to the B/Phuket/3073/2013 clade (clade 3). Of the 8 B/Victoria viruses characterized, 1 was not attributed to a clade. All others belonged to the B/Brisbane/60/2008 clade (clade 1A), but 2 fell in subclades with a two amino acid deletion in HA (1A.Δ2; represented by B/Colorado/06/2017) and 3 fell in subclades with a three amino acid deletion in HA (1A.Δ3; represented by B/Hong Kong/269/2017) (Table 3).

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2018–5/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015 ^a	707
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	301
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup ^b	32
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	14
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	63
A(H3) clade 3c.2a1 representative A/Singapore-16-0019/2016 subgroup ^d	37
A(H3) clade 3c.2a representative A/Hong Kong/4801/2014 subgroup	1
A(H3) attributed to recognized group in current guidance but not listed here	3
A(H3) not attributed to a clade	26
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	2
B(Vic)-lineage clade 1A representative B/Colorado/06/2017	2
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	3
B(Vic) lineage not attributed to a clade	1
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^c	9

^a Vaccine component for 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

^b Vaccine component for 2019 southern hemisphere season.

^c Vaccine component of quadrivalent vaccines for use in 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

^d Vaccine component for 2018–2019 northern hemisphere season.

A summary of recent antigenic characterization data for type A influenza viruses from the WHO collaborating centres in the WHO Global Influenza Surveillance and Response System (GISRS) is given below. A summary for influenza type B viruses is not included as very low numbers have been detected globally.

A(H1N1)pdm09 Viruses

The great majority of A(H1N1)pdm09 viruses characterized so far were antigenically similar to the vaccine virus for use in the 2018–2019 northern hemisphere and 2019 southern hemisphere influenza seasons, A/Michigan/45/2015 (clade 6B.1), as assessed in HI assays using post-infection ferret antisera.

A(H3N2) Viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult, requiring the use of modified HI and/or virus neutralization assays for analysis. In virus neutralization assays or HI assays using post-infection ferret antisera, the majority of recent A(H3N2) viruses have shown similarity to cell culture-propagated A/Singapore/INFIMH-16-0019/2016 (subclade 3C.2a1) vaccine virus, but those falling in the re-emerging 3C.3a clade have shown poor reactivity with the antisera.

The recommended composition of the trivalent influenza vaccine for the northern hemisphere 2018–2019 season included an A/Michigan/45/2015 (H1N1)pdm09-like virus, an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus and a B/Colorado/06/2017-like virus (B/Victoria lineage). For quadrivalent vaccines, a B/Phuket/3073/2013-like virus (B/Yamagata lineage) was recommended. The full report can be found [here](#). A comment by ECDC can be seen [here](#). The majority of influenza vaccines used in Europe are egg-based.

On 27 September 2018, WHO announced the recommended vaccine composition for the southern hemisphere 2019 season. The recommendations matched the A(H1N1)pdm09 and B components for the 2018–2019 northern hemisphere season, but the A(H3N2) component was changed for egg-based vaccines. The full report can be found [here](#).

The northern hemisphere Vaccine Composition Meeting for 2019–2020 has been planned for 18–20 February 2019 in Beijing, China. More information can be found [here](#).

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility was assessed for 897 viruses with collection dates since week 40/2018 [602 A(H1N1)pdm09, 283 A(H3N2), and 12 type B]. 3 A(H1N1)pdm09 viruses carried amino acid substitution H275Y in NA indicative of highly reduced inhibition (HRI) by oseltamivir of which 2 were confirmed by phenotypic test. 1 A(H3N2) virus showed evidence of reduced inhibition (RI) by oseltamivir only. 1 type B virus showed evidence of RI by zanamivir only.

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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.

Suggested citation:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 5/2019.

Tables and figures should be referenced:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 5/2019.

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