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

Summary

Week 9/2019 (25 February–3 March 2019)

- Influenza activity was widespread in the European Region. Specimens collected from individuals presenting with ILI or ARI to sentinel primary health care sites yielded an influenza virus positivity rate of 41.8%.

- Influenza type A virus detections dominated with slightly more A(H1N1)pdm09 than A(H3N2) viruses. Very few influenza B viruses were detected.

- 27.4% of specimens from patients with severe acute respiratory infection (SARI) in week 9/2019 tested positive for influenza virus, and almost all were type A.

- Pooled data from 23 Member States and areas reporting to the EuroMOMO project indicated that the excess mortality observed in previous weeks is now declining. Excess mortality was seen in persons aged 65 years and above, and to a lesser extent in persons 15-64 years.

2018–2019 season overview

- Influenza activity in the European region, based on sentinel sampling, exceeded a positivity rate of 10% in week 49/2018, exceeded 50% between weeks 3/2019 and 7/2019, and peaked in week 5/2019.

- 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.

- Among hospitalized influenza virus-infected patients admitted to ICU wards, 38% of influenza A viruses were subtyped; of these 73% were A(H1N1)pdm09 viruses. Among influenza virus-infected patients admitted to other wards, 34% of influenza A viruses were subtyped and 65% were A(H1N1)pdm09 viruses.

- Over 90% of influenza A viruses detected from SARI surveillance since week 40/2018 were subtyped and 81% were A(H1N1)pdm09 viruses.

- A recent summary of regional activity from October 2018 to February 2019 was published in Eurosurveillance and can be found here.

- 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 vaccine effectiveness estimates continue to support the use of vaccines. Early data suggest the vaccines are effective, but estimates vary depending on the population studied and the proportions of circulating influenza A

virus subtypes. See data from [six European studies](#), [Canada](#), [Finland](#), [Hong Kong](#), [Sweden](#), and the [United States](#).

- On 21 February 2019, WHO published the recommendations for the influenza vaccine composition to be used in the 2019–2020 northern hemisphere season. The recommendation for type B lineages was unchanged, for A(H1N1)pdm09 it was updated, and for A(H3N2) the decision was postponed until 21 March 2019.

- Circulating viruses remain susceptible to neuraminidase inhibitors supporting early use of antiviral treatment according to national guidelines.

Primary care data

Syndromic surveillance data

For week 9/2019, of the 32 Member States reporting influenza-like illness (ILI) thresholds, 21 (66%) reported ILI activity above baseline levels.

These include countries in eastern areas of the European Region (n=2; Republic of Moldova, Russian Federation), northern areas (n=5; Estonia, Iceland, Latvia, Lithuania, Norway), southern areas (n=6; Cyprus, Greece, Italy, Montenegro, Republic of North Macedonia, Serbia) and western areas (n=8; Belgium, Czech Republic, Hungary, Luxembourg, Netherlands, Poland, Slovakia, Spain).

Of the 18 Member States reporting acute respiratory infection (ARI) thresholds, 6 (33%) reported ARI above baseline levels.

These include countries in eastern areas of the European Region (n=3; Armenia, Republic of Moldova, Russian Federation), northern areas (n=1; Estonia), southern areas (n=1; Albania) and western areas (n=1; Slovakia).

Influenza activity

For week 9/2019, of 48 Member States and areas reporting on intensity, 2 reported high intensity (Republic of North Macedonia, Kosovo[*]), 22 reported medium (across the region), 22 reported low intensity (across the region), and 2 reported baseline (Fig. 1).

Of 48 Member States and areas reporting on geographic spread, 28 reported widespread (across the region), 8 reported regional spread (in eastern, southern and western areas), 5 reported local spread (Azerbaijan, Belarus, Ireland, Slovakia, United Kingdom (Scotland)), 5 reported sporadic cases (Armenia, Bulgaria, Israel, Lithuania, United Kingdom (Northern Ireland)), and 2 reported no activity (Cyprus, Uzbekistan) (Fig. 2).

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[*] This designation is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

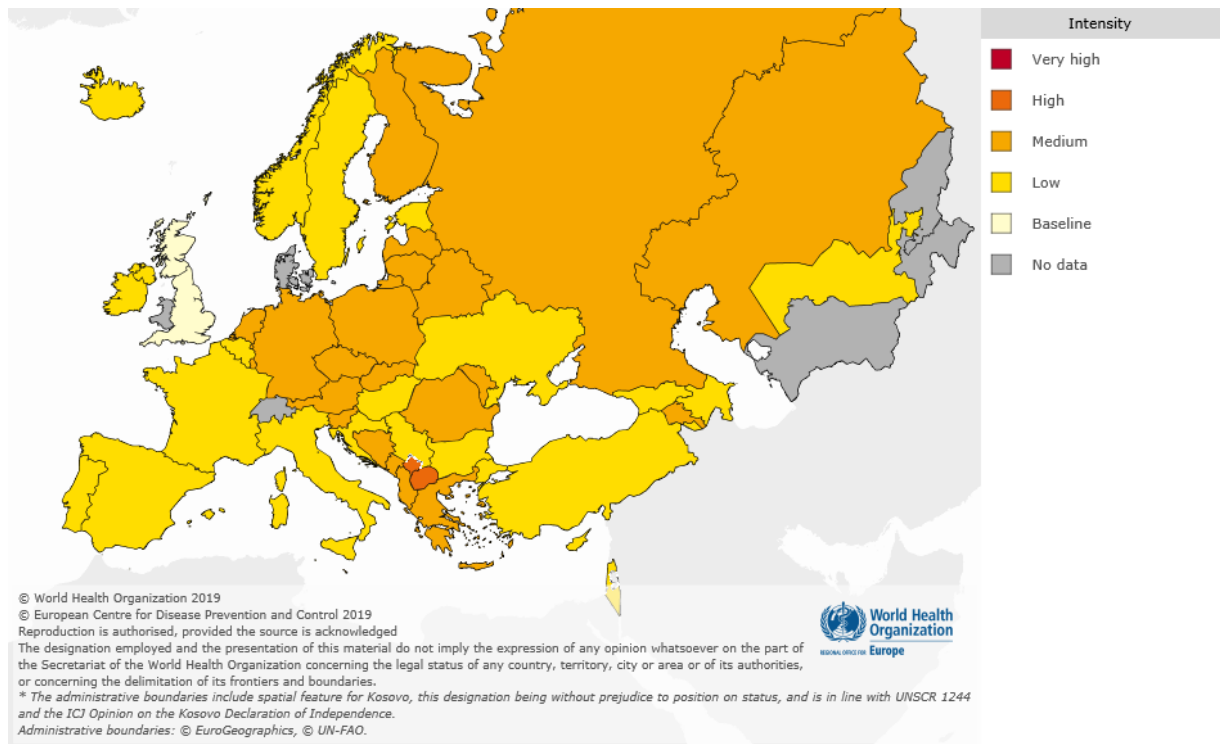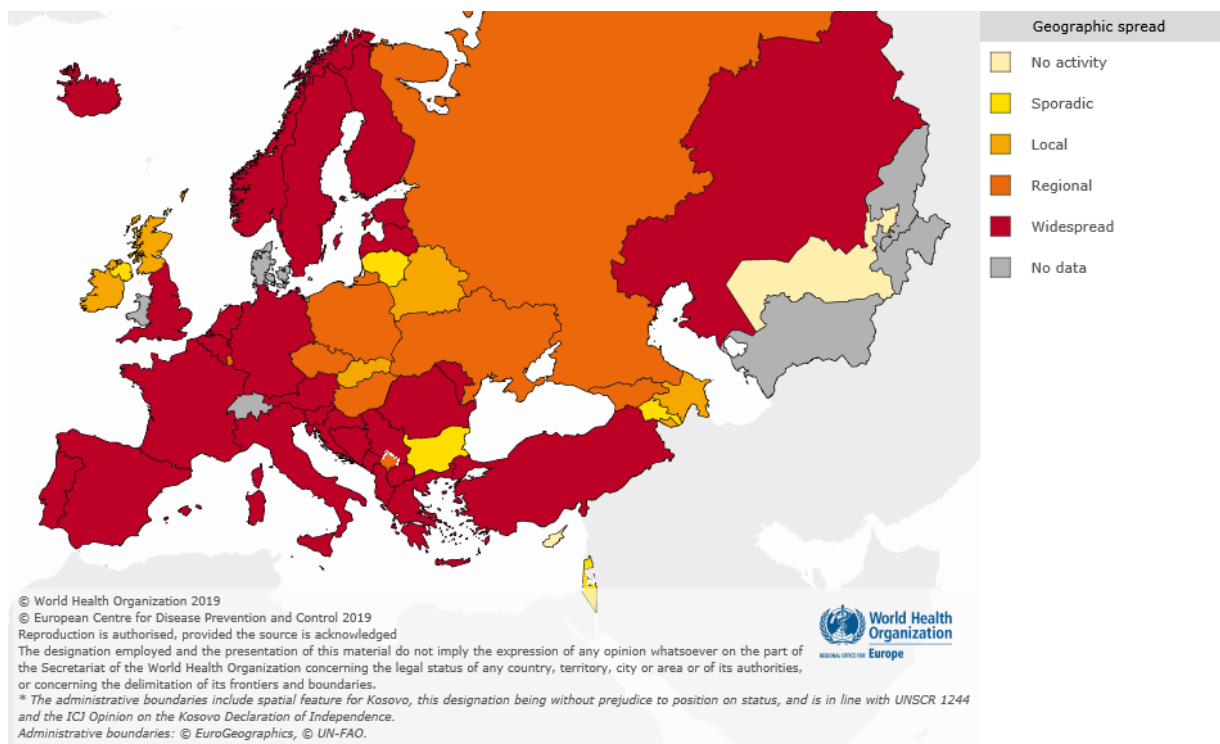## Fig. 1. Intensity in the European Region, week 9/2019

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The designation employed and the presentation of this material do not imply the expression of any opinion whatsoever on the part of
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Fig. 2. Geographic spread in the European Region, week 9/2019

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

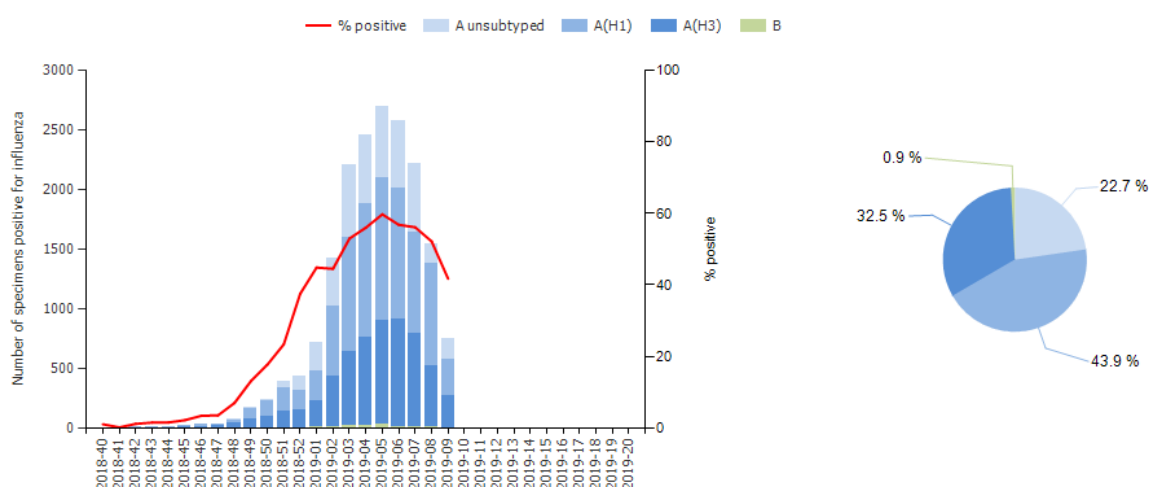## Viruses detected in sentinel-source specimens (ILI and ARI)

For week 9/2019, 751 (41.8%) of 1 796 sentinel specimens tested positive for an influenza virus; 750 were type A and 1 was type B. Of 571 subtyped A viruses, 52.4% were A(H1N1)pdm09 and 47.6% were A(H3N2) (Fig. 3 and Table 1).

Of 34 countries or areas across the region that each tested at least 10 sentinel specimens in week 9/2019, 25 reported a proportion of influenza virus detections at or above 30% (median 45.9%; range 30.0% – 80.0%).

For the season to date, almost all viruses detected were influenza type A (n=17 853, 99.1%) with type B accounting for only 0.9% (n=158). Of 13 765 subtyped A viruses, 7 914 (57.5%) were A(H1N1)pdm09 and 5 851 (42.5%) were A(H3N2). Of 52 influenza type B viruses ascribed to a lineage, 84.6% were B/Yamagata (67.1% of type B viruses were reported without a lineage) (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.

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Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 9/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	%[a]	Number	%[a]
Influenza A	**750**	**99.9**	**17 853**	**99.1**
A(H1N1)pdm09	299	52.4	7 914	57.5
A(H3N2)	272	47.6	5 851	42.5
A not subtyped	179	-	4 088	-
Influenza B	**1**	**0.1**	**158**	**0.9**
B/Victoria lineage	0	-	8	15.4
B/Yamagata lineage	0	-	44	84.6
Unknown lineage	1	-	106	-
Total detections (total tested)	**751 (1 796)**	**41.8**	**18 011 (43 362)**	**41.5**

[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 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 reported in ICUs in week 9/2019 (n=232), influenza type A viruses (n=229, 98.7%) were detected almost exclusively.

Since week 40/2018, overwhelmingly more influenza type A (n=5 999, 99.2%) than type B viruses (n=50, 0.8%) were detected. Of 2 283 subtyped influenza A viruses, 73.4% were A(H1N1)pdm09 and 26.6% were A(H3N2). No influenza type B viruses were ascribed to a lineage. Of 3 217 cases with known age, 45.9% were 15–64 years old and 46.0% 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 in week 9/2019 (n=191), influenza type A viruses (99.5%) were detected almost exclusively.

Since week 40/2018, overwhelmingly more influenza type A (n=7 601, 99.3%) than type B viruses (n=53, 0.7%) were detected. Of 2 564 subtyped influenza A viruses, 64.8% were A(H1N1)pdm09 and 35.2% were A(H3N2). The 1 influenza type B virus ascribed to a lineage was B/Yamagata. Of 7 654 cases with known age, 43.5% were 65 years and older and 34.1% were 15–64 years old.

<u>2. SARI surveillance</u>

For week 9/2019, 1 474 SARI cases were reported by 13 Member States or areas. Of 343 specimens tested for influenza viruses, 27.4% were positive. Of these, influenza type A viruses (97.9%) were detected much more frequently than influenza type B viruses (2.1%).

Of 29 917 SARI cases reported since week 40/2018, 28 859 had a recorded age and, of these, 58.0% were 0–4 years old and 23.7% were 15–64 years old. For SARI cases testing positive for influenza virus since week 40/2018 (n=2 387), almost all were type A viruses (99.6%). Of the 2 163 influenza type A virus-infected cases for which subtyping was performed, 81.0% were infected by A(H1N1)pdm09 viruses and 19.0% by A(H3N2) viruses. The 1 influenza type B virus ascribed to a lineage was B/Yamagata.

Mortality monitoring

For week 9/2019, the EuroMOMO project received data from 23 countries or areas that were included in pooled analyses. The pooled estimates indicated that the excess mortality among persons aged 15–64 years and 65 years and older observed in recent weeks has now started to decline.

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 9/2019, 9 046 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; 99.5% were type A and 0.5% were type B. Of 3 574 subtyped A viruses, 50.8% were A(H1N1)pdm09 and 49.2% were A(H3N2) (Table 2).

For the season to date, more influenza type A (n=143 645, 99.3%) than type B viruses (n=1 083, 0.7%) have been detected. Of 48 352 subtyped A viruses, 30 226 (62.5%) were A(H1N1)pdm09 and 18 126 (37.5%) were A(H3N2). Of 40 influenza type B viruses ascribed to a lineage, 47.5% were B/Yamagata (96.3% of 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 9/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	%ᵃ	Number	%ᵃ
Influenza A	**8 999**	**99.5**	**143 645**	**99.3**
A(H1N1)pdm09	1 816	50.8	30 226	62.5
A(H3N2)	1 758	49.2	18 126	37.5
A not subtyped	5 425	-	95 293	-
Influenza B	**47**	**0.5**	**1 083**	**0.7**
B/Victoria lineage	0	-	21	52.5
B/Yamagata lineage	0	-	19	47.5
Unknown lineage	47	-	1 043	-
Total detections (total tested)	**9 046 (36 964)**		**144 728 (584 758)**	

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

Genetic 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 1 921 viruses have been reported by the network laboratories.

Of the genetically characterized viruses, 1 100 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade with a further 3 attributed to a subgroup not listed; 784 were A(H3) viruses, with 509 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 43 to the A/Switzerland/8060/2017 (3C.2a2) subclade, 16 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 135 to the A/England/538/2018 (3C.3a) clade, 46 to the A/Singapore-16-0019/2016 (3C.2a1) subclade, 4 to the A/Hong Kong/4801/2014 (3C.2a) clade, 5 attributed to a subgroup not listed, and 26 not attributed to a clade.

Of the 34 genetically characterized influenza B viruses, 20 were B/Yamagata viruses belonging to the B/Phuket/3073/2013 clade (clade 3). Of the 14 B/Victoria viruses characterized, 1 was not attributed to a clade. All others belonged to clade 1A, but 4 fell in subclades with a two amino acid deletion in HA (1A.Δ2; represented by B/Colorado/06/2017) and 7 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 40/2018–9/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015[a]	1 100
A(H1)pdm09 attributed to recognised group in the guidance but not listed here	3
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	509
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup[b]	43
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	16
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	135
A(H3) clade 3c.2a1 representative A/Singapore-16-0019/2016 subgroup[d]	46
A(H3) clade 3c.2a representative A/Hong Kong/4801/2014 subgroup	4
A(H3) not attributed to clade	26
A(H3) attributed to recognized group in current guidance but not listed here	5
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	2
B(Vic)-lineage clade 1A representative B/Colorado/06/2017[a]	4
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	7
B(Vic) lineage not attributed to a clade	1
B(Yam)-lineage clade representative B/Phuket/3073/2013[c]	20

[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

Vaccine composition

The recommended composition of the trivalent influenza vaccine for the current 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.

On 21 February 2019, WHO published the recommendations for quadrivalent vaccines for use in the 2019–2020 northern hemisphere influenza season to contain the following:

- an A/Brisbane/02/2018 (H1N1)pdm09-like virus;

- an A(H3N2) virus to be announced on 21 March 2019[*];

- a B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage); and

- a B/Phuket/3073/2013-like virus (B/Yamagata/16/88 lineage).

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[*] In light of recent changes in the proportions of genetically and antigenically diverse A(H3N2) viruses, the recommendation for the A(H3N2) component has been postponed.

It is recommended that the influenza B virus component of trivalent vaccines for use in the 2019-2020 northern hemisphere influenza season be a B/Colorado/06/2017-like virus of the B/Victoria/2/87-lineage.

The full report and a "Frequently Asked Questions" document are available on the WHO website at:
http://www.who.int/influenza/vaccines/virus/recommendations/2019_20_north/en/

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility was assessed for 1 224 viruses with collection dates since week 40/2018 [819 A(H1N1)pdm09, 408 A(H3N2), and 15 type B]. 6 A(H1N1)pdm09 viruses carried amino acid substitution H275Y in NA indicative of highly reduced inhibition (HRI) by oseltamivir and 2 of them 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.

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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Tables and figures should be referenced:

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