

2018-2019 Influenza Season Week 42 ending October 20, 2018

All data are preliminary and may change as more reports are received.

An overview of the CDC influenza surveillance system, including methodology and detailed descriptions of each data component, is available at <http://www.cdc.gov/flu/weekly/overview.htm>.

Synopsis:

Influenza activity in the United States remains low. Influenza A(H1N1)pdm09, influenza A(H3N2), and influenza B viruses continue to co-circulate, with influenza A(H1N1)pdm09 viruses reported most commonly by public health laboratories during the most recent three weeks. Below is a summary of the key influenza indicators for the week ending October 20, 2018:

- **Viral Surveillance:** Influenza A viruses have predominated in the United States since the beginning of July. The percentage of respiratory specimens testing positive for influenza in clinical laboratories was low.
 - **Virus Characterization:** The majority of influenza viruses characterized antigenically and genetically are similar to the cell-grown reference viruses representing the 2018–2019 Northern Hemisphere influenza vaccine viruses.
 - **Antiviral Resistance:** All viruses tested since late May show susceptibility to the antiviral drugs oseltamivir, zanamivir, and peramivir.
- **Influenza-like Illness Surveillance:** The proportion of outpatient visits for influenza-like illness (ILI) remained low at 1.5%, which is below the national baseline of 2.2%. All regions reported ILI below their region-specific baseline level.
 - **ILI State Activity Indicator Map:** Puerto Rico and one state experienced low ILI activity; and New York City, the District of Columbia, and 49 states experienced minimal ILI activity..
- **Geographic Spread of Influenza:** The geographic spread of influenza in four states was reported as local; the District of Columbia, Puerto Rico, the U.S. Virgin Islands and 42 states reported sporadic activity; four states reported no activity; and Guam did not report.
- **Pneumonia and Influenza Mortality:** The proportion of deaths attributed to pneumonia and influenza (P&I) was below the system-specific epidemic threshold in the National Center for Health Statistics (NCHS) Mortality Surveillance System.
- **Influenza-associated Pediatric Deaths:** No influenza-associated pediatric deaths were reported to CDC.

National and Regional Summary of Select Surveillance Components

HHS Surveillance Regions*	Out- patient ILI†	Data for current week			Predominant flu virus reported by public health laboratories for the most recent three weeks‡
		Number of jurisdictions reporting regional or widespread activity§	% respiratory specimens positive for flu in clinical laboratories‡		
Nation	Normal	0 of 54	0.6%	Influenza A(H1N1)pdm09	
Region 1	Normal	0 of 6	0.3%	Influenza A	

HHS Surveillance Regions*	Out- patient ILI†	Data for current week		Predominant flu virus reported by public health laboratories for the most recent three weeks‡
		Number of jurisdictions reporting regional or widespread activity§	% respiratory specimens positive for flu in clinical laboratories‡	
Region 2	Normal	0 of 4	0.4%	Influenza A
Region 3	Normal	0 of 6	0.4%	Approximately equal Influenza A and Influenza B
Region 4	Normal	0 of 8	4.3%	Influenza A
Region 5	Normal	0 of 6	0.4%	Influenza A
Region 6	Normal	0 of 5	0.8%	Influenza A
Region 7	Normal	0 of 4	0.2%	Influenza A
Region 8	Normal	0 of 6	1.1%	Influenza A
Region 9	Normal	0 of 5	1.4%	Influenza A
Region 10	Normal	0 of 4	1.2%	Influenza A

*<https://www.hhs.gov/about/agencies/iea/regional-offices/index.html>

† Elevated means the % of visits for ILI is at or above the national or region-specific baseline

§ Includes all 50 states, the District of Columbia, Guam, Puerto Rico, and U.S. Virgin Islands

‡ National data are for current week; regional data are for most recent three weeks

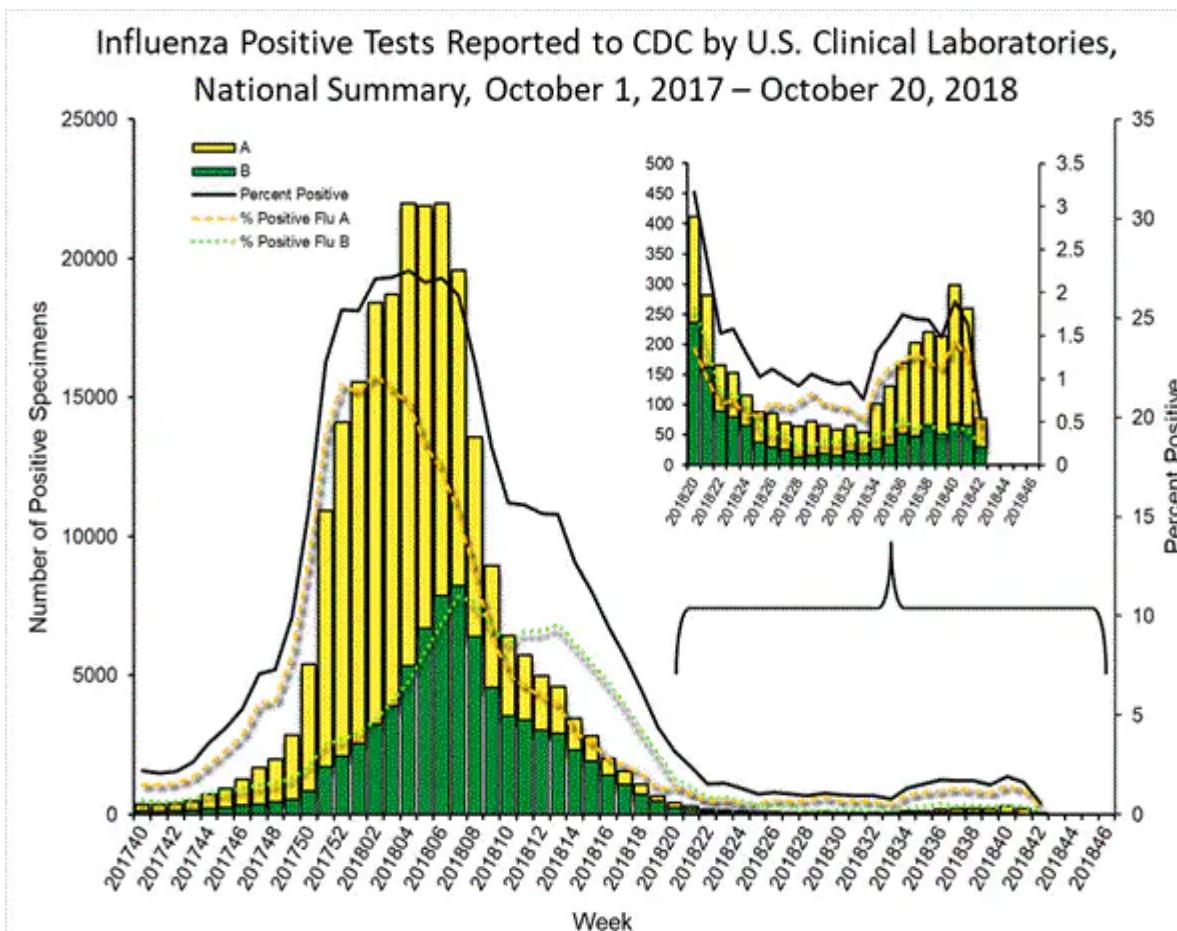
U.S. Virologic Surveillance:

WHO and NREVSS collaborating laboratories, which include both public health and clinical laboratories located in all 50 states, Puerto Rico, Guam, and the District of Columbia, report to CDC the total number of respiratory specimens tested for influenza and the number positive for influenza by virus type. In addition, public health laboratories also report the influenza A subtype (H1 or H3) and influenza B lineage information of the viruses they test and the age or age group of the persons from whom the specimens were collected.

Additional virologic data, including national, regional and select state-level data, can be found at:
<http://gis.cdc.gov/grasp/fluvview/fluportaldashboard.html>. Age group proportions and totals by influenza subtype reported by public health laboratories can be found at:
http://gis.cdc.gov/grasp/fluvview/flu_by_age_virus.html.

The results of tests performed by clinical laboratories are summarized below.

	Week 42	Data Cumulative since September 30, 2018 (Week 40)
No. of specimens tested	13,434	44,998
No. of positive specimens (%)	76 (0.6%)	633 (1.4%)
<i>Positive specimens by type</i>		
Influenza A	47 (61.8%)	470 (74.2%)
Influenza B	29 (38.2%)	163 (25.8%)



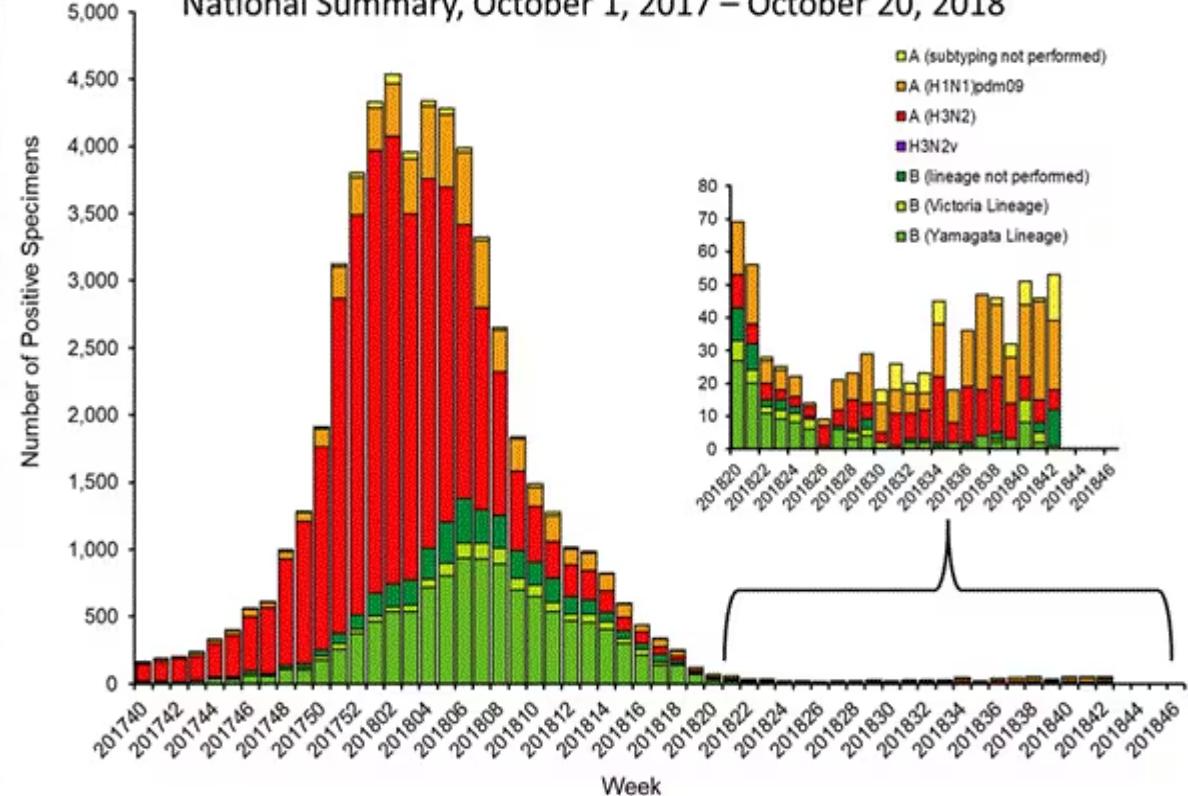
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The results of tests performed by public health laboratories are summarized below.

	Week 42	Data Cumulative since September 30, 2018 (Week 40)
No. of specimens tested	580	1,894
No. of positive specimens*	53	150
<i>Positive specimens by type/subtype</i>		
Influenza A	41 (77.4%)	115 (76.7%)
(H1N1)pdm09	21 (77.8%)	73 (78.5%)
H3N2	6 (22.2%)	20 (21.5%)
Subtyping not performed	14	22
Influenza B	12 (22.6%)	35 (23.3%)
Yamagata lineage	0 (0.0%)	10 (47.6%)
Victoria lineage	1 (100.0%)	11 (52.4%)
Lineage not performed	11	14

*The percent of specimens testing positive for influenza is not reported because public health laboratories often receive samples that have already tested positive for influenza at a clinical laboratory and therefore percent positive would not be a valid indicator of influenza activity. Additional information is available at <http://www.cdc.gov/flu/weekly/overview.htm>.

Influenza Positive Tests Reported to CDC by U.S. Public Health Laboratories, National Summary, October 1, 2017 – October 20, 2018



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Influenza Virus Characterization:

Close monitoring of influenza viruses is required to better assess the potential impact on public health. CDC characterizes influenza viruses through one or more tests including [genomic sequencing](#), [hemagglutination inhibition \(HI\)](#) and/or neutralization assays based Focus Reduction assays (FRA). These data are used to compare how similar currently circulating influenza viruses are to the reference viruses used for developing new influenza vaccines and to monitor evolutionary changes that continually occur in influenza viruses circulating in humans. Antigenic and genetic characterization of circulating influenza viruses gives an indication of the influenza vaccine's ability to induce an immune response against the wide array of influenza viruses that are co-circulating every season. However, annual [vaccine effectiveness estimates](#) are needed to determine how much protection was provided to the population by vaccination.

For nearly all influenza-positive surveillance samples received at CDC, next-generation sequencing is performed to determine the genetic identity of circulating influenza viruses and to monitor the evolutionary trajectory of viruses circulating in our population. Virus gene segments are classified into genetic clades/subclades based on phylogenetic analysis. However, genetic changes that classify the clades/subclades do not always result in antigenic changes. “Antigenic drift” is a term used to describe gradual antigenic change that occurs as viruses evolve changes to escape host immune pressure. Antigenic drift is evaluated by comparing antigenic properties of cell-propagated reference viruses representing currently recommended vaccine components with those of cell-propagated circulating viruses.

CDC has antigenically or genetically characterized 177 influenza viruses collected May 20, 2018 – October 20, 2018, and submitted by U.S. laboratories, including 74 influenza A(H1N1)pdm09 viruses, 60 influenza A(H3N2) viruses, and 43 influenza B viruses.

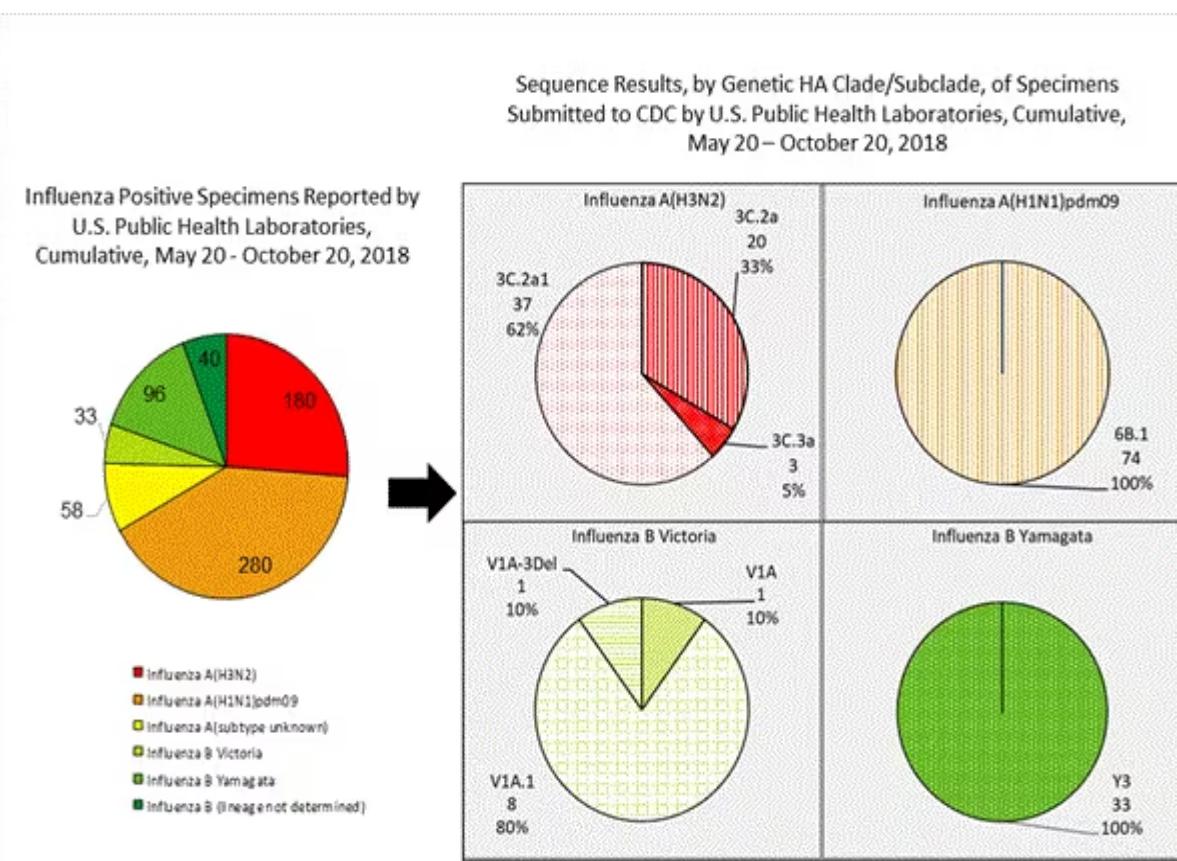
Influenza A Viruses

- **A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 74 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Sixty-nine A(H1N1)pdm09 viruses were antigenically characterized, and all 69 (100%) were antigenically similar (analyzed using HI with ferret antisera) to A/Michigan/45/2015 (6B.1), a cell-propagated A/Michigan/45/2015-like reference virus representing the A(H1N1)pdm09 component for the 2018-19 Northern Hemisphere influenza vaccines.
- **A (H3N2):** Phylogenetic analysis of the HA genes from 60 A(H3N2) viruses revealed extensive genetic diversity with multiple clades/subclades co-circulating. The HA genes of circulating viruses belonged to clade 3C.2a (n=20), subclade 3C.2a1 (n=37) or clade 3C.3a (n=3). Forty-three influenza A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and 40 (93.0%) A(H3N2) viruses tested were well-inhibited (reacting at titers that were within fourfold of the homologous virus titer) by ferret antisera raised against A/Singapore/INFIMH-16-0019/2016 (3C.2a1), a cell-propagated A/Singapore/INFIMH-16-0019/2016 -like reference virus representing the A(H3N2) component of 2018-19 Northern Hemisphere influenza vaccines. The number of H3N2 viruses reported this week is lower than previously reported due to the removal of duplicate data.

Influenza B Viruses

- **B/Victoria:** Phylogenetic analysis of 10 B/Victoria-lineage viruses indicate that all HA genes belonged to genetic clade V1A, however genetic subclades which are antigenically distinct have emerged. The majority of recent B/Victoria-lineage viruses belonged to a subclade of viruses with a 6-nucleotide deletion (encoding amino acids 162 and 163) in the HA (V1A.1, previously abbreviated as V1A-2Del). In addition, a small number of B/Victoria-lineage viruses have a three amino acid deletion (162-164) in the HA protein (abbreviated as V1A-3Del). Nine (90%) B/Victoria lineage viruses were well-inhibited by ferret antisera raised against cell-propagated B/Colorado/06/2017-like (V1A.1) reference virus, representing the B/Victoria lineage component of 2018-19 Northern Hemisphere influenza vaccines. One (10%) B/Victoria lineage virus reacted poorly (at titers that were 8-fold or greater reduced compared with the homologous virus titer) with ferret antisera raised against cell-propagated B/Colorado/06/2017-like reference virus, and belonged to clade V1A.
- **B/Yamagata:** Phylogenetic analysis of 33 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 32 influenza B/Yamagata-lineage viruses were antigenically characterized, and all were antigenically similar to cell-propagated B/Phuket/3073/2013 (Y3), the reference vaccine virus representing the influenza B/Yamagata-lineage component of the 2018-19 Northern Hemisphere quadrivalent vaccines.

The majority of U.S. viruses submitted for characterization come from state and local public health laboratories. Due to [Right Size Roadmap](#) considerations, specimen submission guidance to laboratories is that, if available, 2 influenza A(H1N1)pdm09, 2 influenza A(H3N2), and 2 influenza B viruses be submitted every other week. Therefore, the numbers of each virus type/subtype characterized should be more balanced across subtypes/lineages but will not reflect the actual proportion of circulating viruses. In the figure below, the results of tests performed by public health labs are shown on the left and CDC sequence results (by genetic clade/subclade) are shown on the right.



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Antiviral Resistance:

During May 20–October 20, 2018, 164 specimens (63 influenza A(H1N1)pdm09, 57 influenza A(H3N2), and 44 influenza B viruses) collected in the United States were tested for susceptibility to the neuraminidase inhibitors (oseltamivir, zanamivir, and peramivir).¹ All tested viruses were sensitive to all three recommended antiviral medications.

While all of the recently circulating influenza viruses are susceptible to the neuraminidase inhibitor antiviral medications oseltamivir, zanamivir, and peramivir; rare sporadic instances of oseltamivir-resistant and peramivir-resistant influenza A(H1N1)pdm09 viruses and oseltamivir-resistant influenza A(H3N2) viruses have been detected worldwide. Antiviral treatment as early as possible is recommended for patients with confirmed or suspected influenza who have severe, complicated, or progressive illness; who require hospitalization; or who are at [high risk](#) for serious influenza-related complications. Additional information on recommendations for treatment and chemoprophylaxis of influenza virus infection with antiviral agents is available at <http://www.cdc.gov/flu/antivirals/index.htm>.

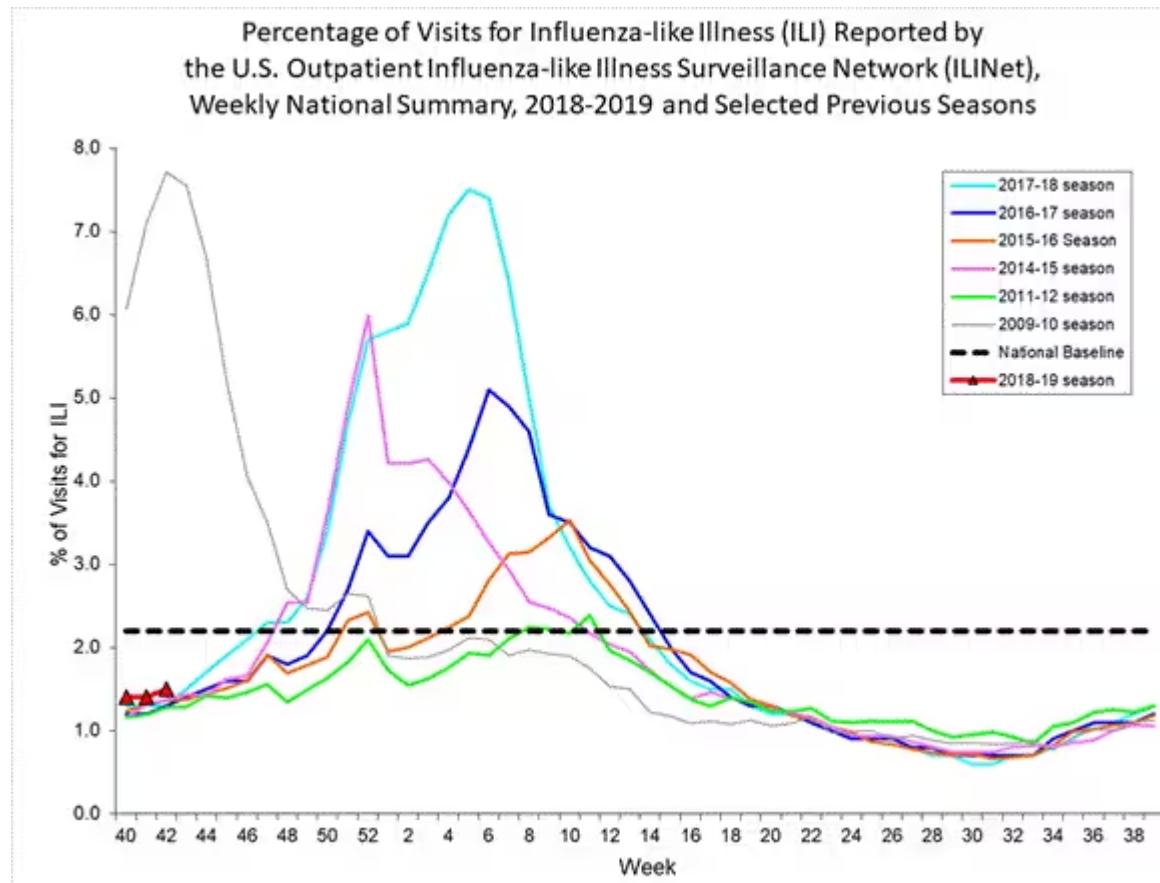
Outpatient Illness Surveillance:

Nationwide during week 42, 1.5% of patient visits reported through the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet) were due to influenza-like illness (ILI). This percentage

is below the national baseline of 2.2%. (ILI is defined as fever (temperature of 100°F [37.8°C] or greater) and cough and/or sore throat.)

On a regional level, the percentage of outpatient visits for ILI ranged from 0.6% to 2.5% during week 42. All regions reported a percentage of outpatient visits for ILI below their region-specific baseline.

Additional data on medically attended visits for ILI for current and past seasons and by geography (national, HHS region, or select states) are available on FluView Interactive <http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html>.



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ILINet State Activity Indicator Map:

Data collected in ILINet are used to produce a measure of ILI activity* by state. Activity levels are based on the percent of outpatient visits in a state due to ILI and are compared to the average percent of ILI visits that occur during weeks with little or no influenza virus circulation. Activity levels range from minimal, which would correspond to ILI activity from outpatient clinics being below, or only slightly above, the average, to high, which would correspond to ILI activity from outpatient clinics being much higher than average.

The ILI Activity Indicator Map displays state-specific activity levels for multiple seasons and allows a visual representation of relative activity from state to state. More information is available on

FluView Interactive at <https://gis.cdc.gov/grasp/fluview/main.html>.

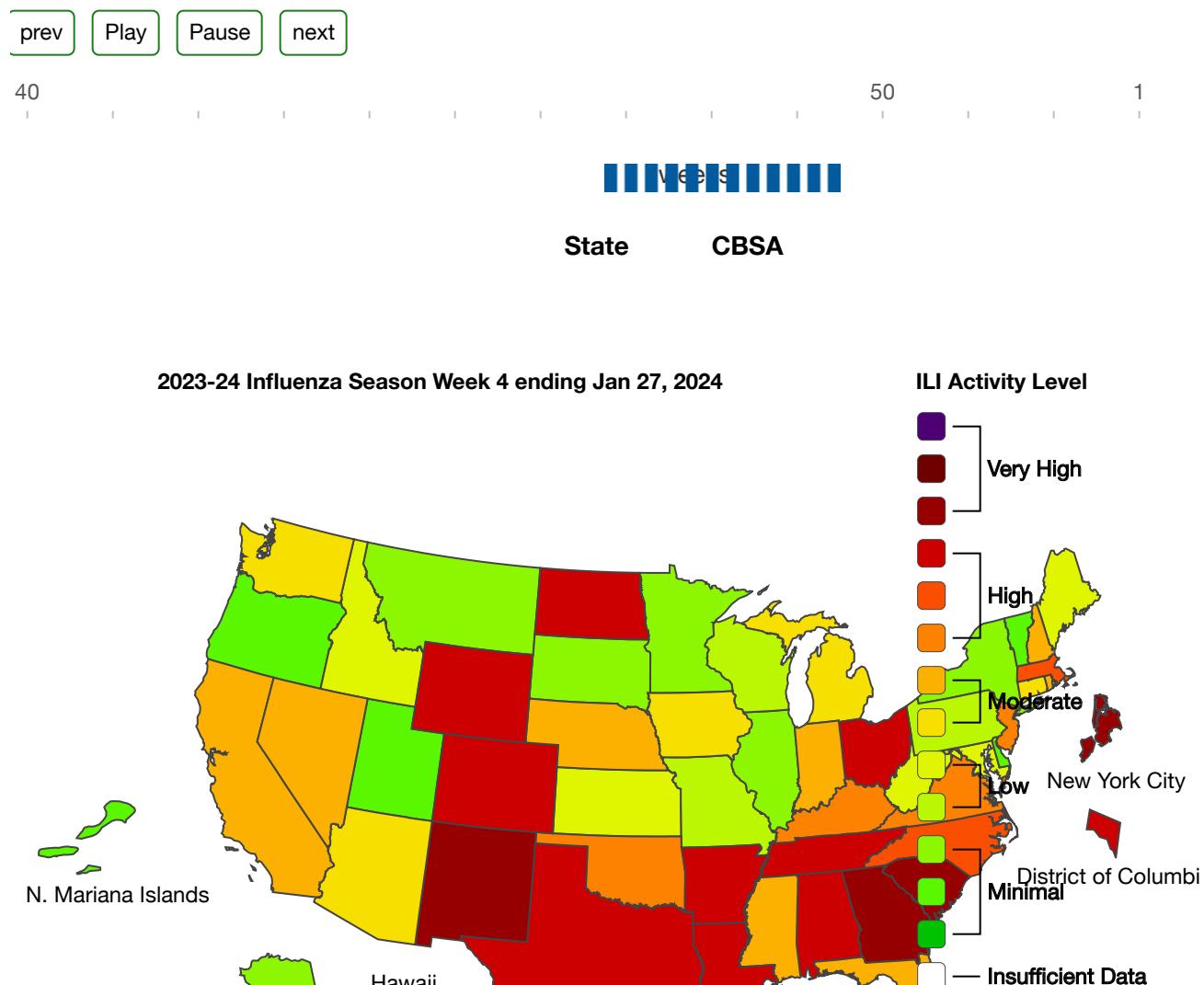
During week 42, the following ILI activity levels were experienced:

- Puerto Rico and one state (Georgia) experienced low ILI activity.
- New York City, the District of Columbia, and 49 states (Alabama, Alaska, Arizona, Arkansas, California, Colorado, Connecticut, Delaware, Florida, Hawaii, Idaho, Illinois, Indiana, Iowa, Kansas, Kentucky, Louisiana, Maine, Maryland, Massachusetts, Michigan, Minnesota, Mississippi, Missouri, Montana, Nebraska, Nevada, New Hampshire, New Jersey, New York, New Mexico, North Carolina, North Dakota, Ohio, Oklahoma, Oregon, Pennsylvania, Rhode Island, South Carolina, South Dakota, Tennessee, Texas, Utah, Vermont, Virginia, Washington, West Virginia, Wisconsin, and Wyoming) experienced minimal ILI activity.

A Weekly Influenza Surveillance Report Prepared by the Influenza Division

Outpatient Respiratory Illness Activity Map Determined by Data Reported to ILINet

This system monitors visits for respiratory illness that includes fever plus a cough or sore throat, also referred to as ILI, not laboratory confirmed influenza and may capture patient visits due to other respiratory pathogens that cause similar symptoms.



*This map uses the proportion of outpatient visits to health care providers for ILI to measure the ILI activity level within a state. It does not, however, measure the extent of geographic spread of flu within a state. Therefore, outbreaks occurring in a single city could cause the state to display high activity levels.

Data collected in ILINet may disproportionately represent certain populations within a state, and therefore, may not accurately depict the full picture of influenza activity for the whole state.

Data displayed in this map are based on data collected in ILINet, whereas the State and Territorial flu activity map is based on reports from state and territorial epidemiologists. The data presented in this map are preliminary and may change as more data are received.

Differences in the data presented here by CDC and independently by some state health departments likely represent differing levels of data completeness with data presented by the state likely being the more complete.

Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists

The influenza activity reported by state and territorial epidemiologists indicates geographic spread of influenza viruses, but does not measure the severity of influenza activity. Additional data displaying the influenza activity reported by state and territorial epidemiologists for the current and past seasons are available on FluView Interactive at <https://gis.cdc.gov/grasp/fluview/FluView8.html>

During week 42, the following influenza activity was reported::

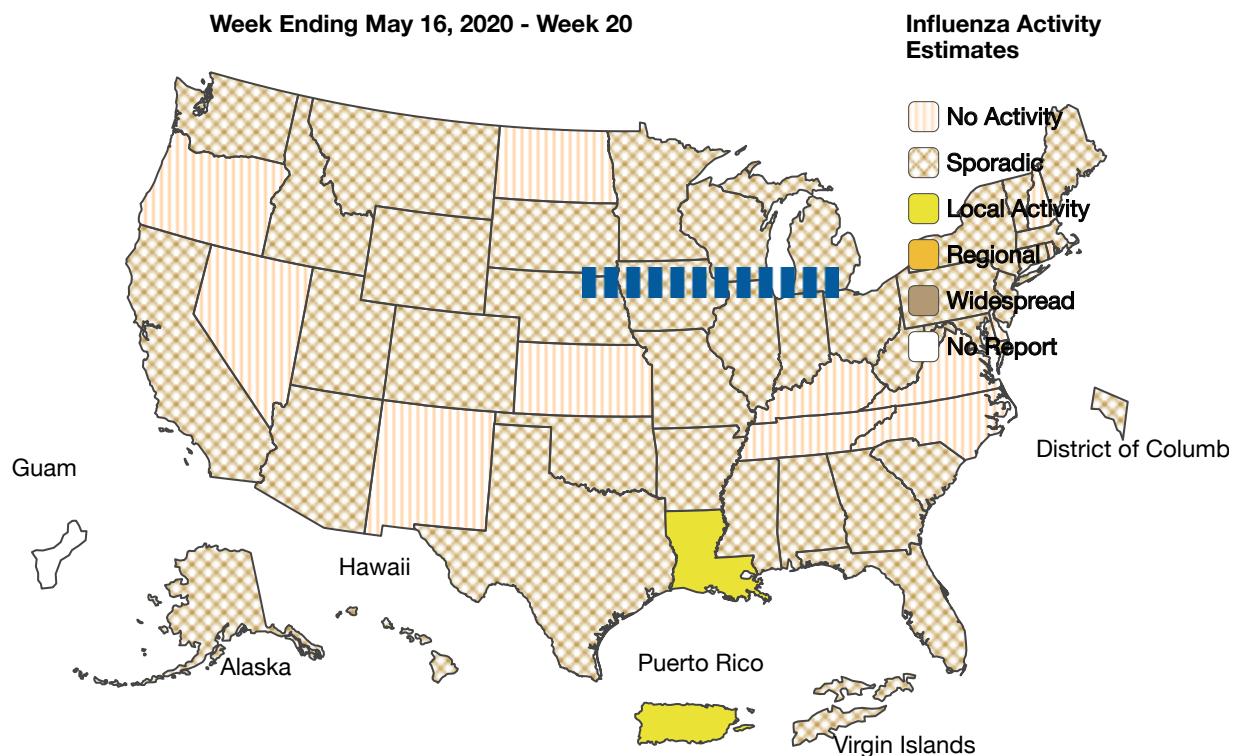
- Local influenza activity was reported by four states (Massachusetts, New Hampshire, North Dakota, and Oregon).
- Sporadic influenza activity was reported by the District of Columbia, Puerto Rico, the U.S. Virgin Islands and 42 states (Alabama, Alaska, Arizona, Arkansas, California, Colorado, Connecticut, Delaware, Florida, Georgia, Hawaii, Idaho, Indiana, Iowa, Kansas, Kentucky, Louisiana, Maine, Maryland, Michigan, Minnesota, Missouri, Montana, Nebraska, Nevada, New Jersey, New Mexico, New York, North Carolina, Ohio, Oklahoma, Pennsylvania, South Carolina, South Dakota, Tennessee, Texas, Utah, Vermont, Washington, West Virginia, Wisconsin, and Wyoming).
- No influenza activity was reported by four states (Illinois, Mississippi, Rhode Island, and Virginia).
- Guam did not report.

A Weekly Influenza Surveillance Report Prepared by the Influenza Division
Weekly Influenza Activity Estimates Reported by State and Territorial Epidemiologists*

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Weeks

Week Ending May 16, 2020 - Week 20



Season: 2019-20 ▾

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(<http://gis.cdc.gov/grasp/fluview/FluView8.html>)

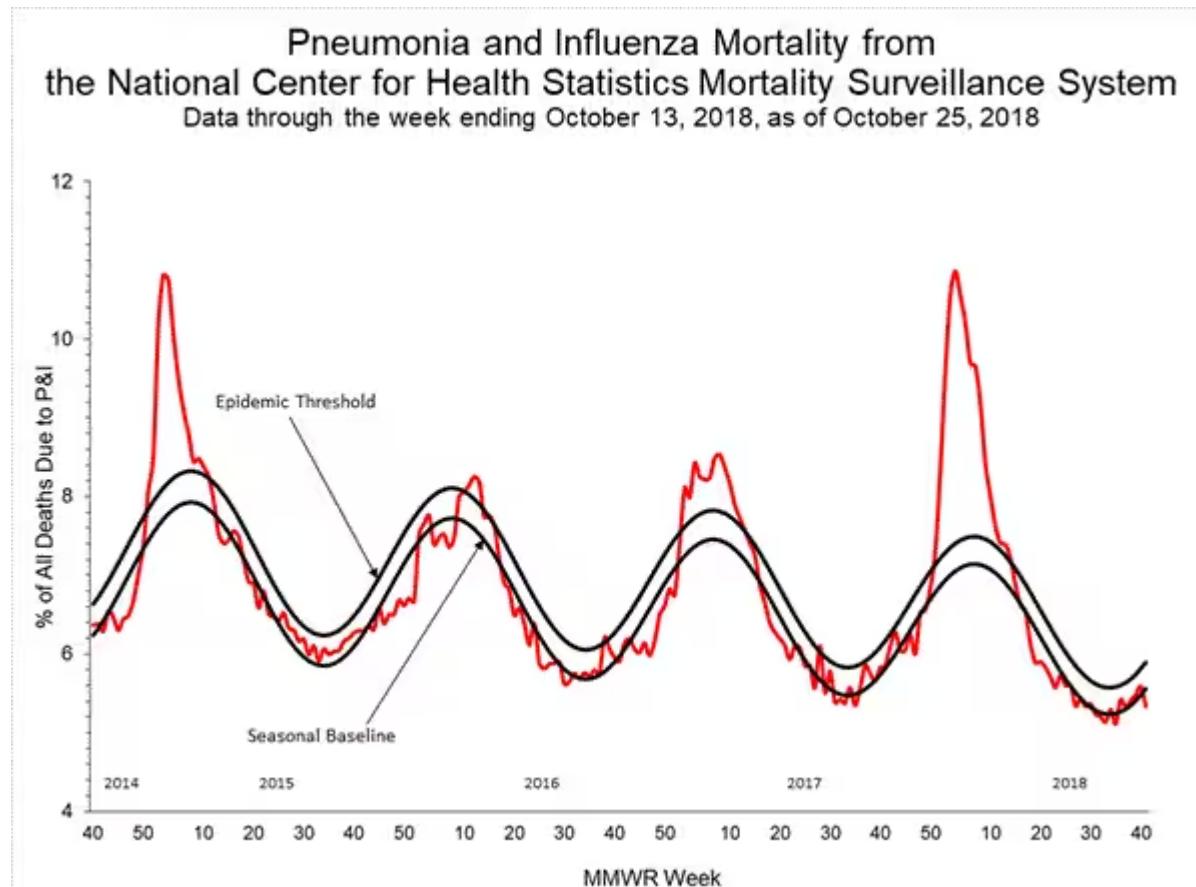
Influenza-Associated Hospitalizations:

The Influenza Hospitalization Surveillance Network (FluSurv-NET) conducts all age population-based surveillance for laboratory-confirmed influenza-related hospitalizations in select counties in the Emerging Infections Program (EIP) states and Influenza Hospitalization Surveillance Project (IHSP) states. FluSurv-NET estimated hospitalization rates will be updated weekly starting later this season. Additional FluSurv-NET data can be found at:
<http://gis.cdc.gov/GRASP/Fluview/FluHospRates.html> and
<http://gis.cdc.gov/grasp/fluview/FluHospChars.html>.

Pneumonia and Influenza (P&I) Mortality Surveillance:

Based on National Center for Health Statistics (NCHS) mortality surveillance data available on October 25, 2018, 5.3% of the deaths occurring during the week ending October 13, 2018 (week 41) were due to P&I. This percentage is below the epidemic threshold of 5.9% for week 41.

Additional pneumonia and influenza mortality data for current and past seasons and by geography (national, HHS region, or state) are available at on FluView Interactive <http://gis.cdc.gov/grasp/fluvview/mortality.html>. Data displayed on the regional and state-level are aggregated by the state of residence of the decedent.



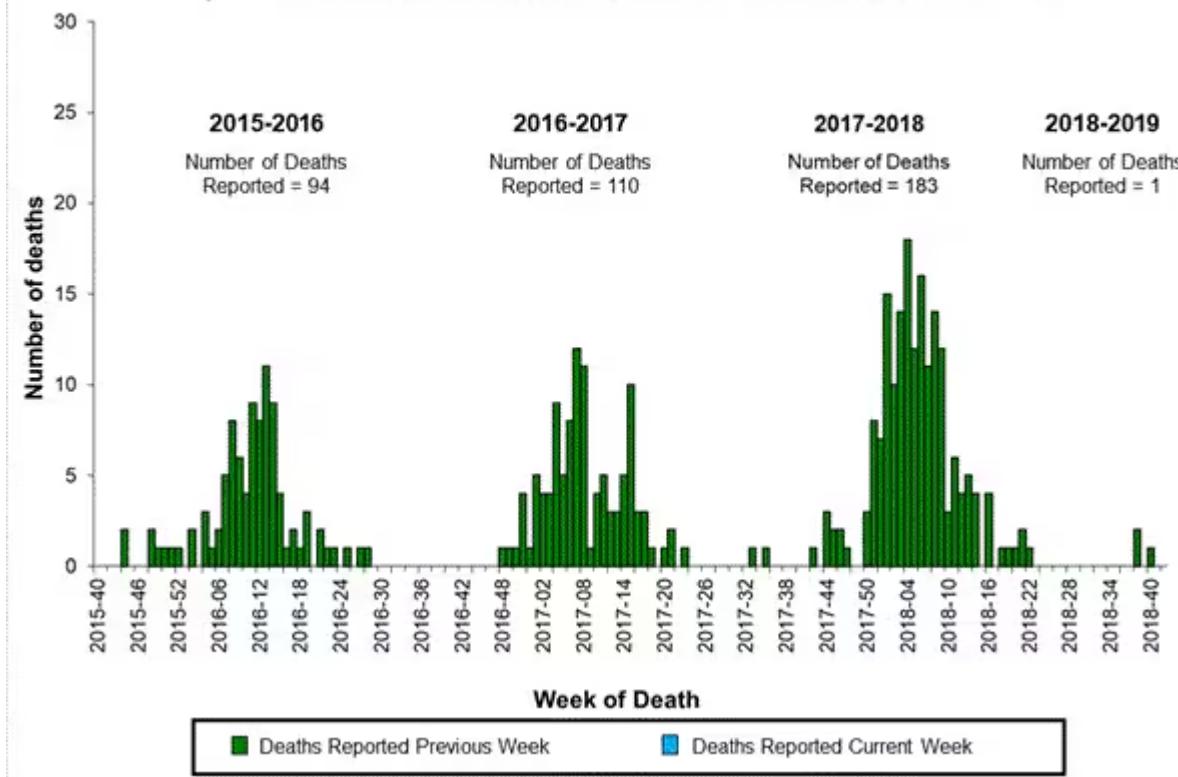
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Influenza-Associated Pediatric Mortality:

No influenza-associated pediatric deaths were reported to CDC during week 42.

Additional information on influenza-associated pediatric deaths including basic demographics, underlying conditions, bacterial co-infections, and place of death for the current and past seasons, is available on FluView Interactive <http://gis.cdc.gov/GRASP/Fluview/PedFluDeath.html>.

Number of Influenza-Associated Pediatric Deaths by Week of Death: 2015-2016 season to present



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Additional National and International Influenza Surveillance Information

FluView Interactive: FluView includes enhanced web-based interactive applications that can provide dynamic visuals of the influenza data collected and analyzed by CDC. These FluView Interactive applications allow people to create customized, visual interpretations of influenza data, as well as make comparisons across flu seasons, regions, age groups and a variety of other demographics. To access these tools, visit <http://www.cdc.gov/flu/weekly/fluvviewinteractive.htm>.

U.S. State and local influenza surveillance: Click on a jurisdiction below to access the latest local influenza information.

[Alabama](#)

[Alaska](#)

[Arizona](#)

[Arkansas](#)

[California](#)

[Colorado](#)

[Connecticut](#)

[Delaware](#)

[District of Columbia](#)

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[West Virginia](#)

[Virgin Islands](#)

[Rhode Island](#)

[Utah](#)

[Wisconsin](#)

World Health Organization: Additional influenza surveillance information from participating WHO member nations is available through [FluNet](#) and the [Global Epidemiology Reports](#).

WHO Collaborating Centers for Influenza located in [Australia](#), [China](#), [Japan](#), the [United Kingdom](#), and the [United States](#) (CDC in Atlanta, Georgia).

Europe: For the most recent influenza surveillance information from Europe, please see WHO/Europe and the European Centre for Disease Prevention and Control at <http://www.flunewseurope.org/>.

Public Health Agency of Canada: The most up-to-date influenza information from Canada is available at <http://www.phac-aspc.gc.ca/fluwatch/>

Public Health England: The most up-to-date influenza information from the United Kingdom is available at <https://www.gov.uk/government/statistics/weekly-national-flu-reports>

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