Weekly U.S. Influenza Surveillance Report (FluView)

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

A description of the CDC influenza surveillance system, including methodology and detailed descriptions of each data component is available on the [surveillance methods](#) page.
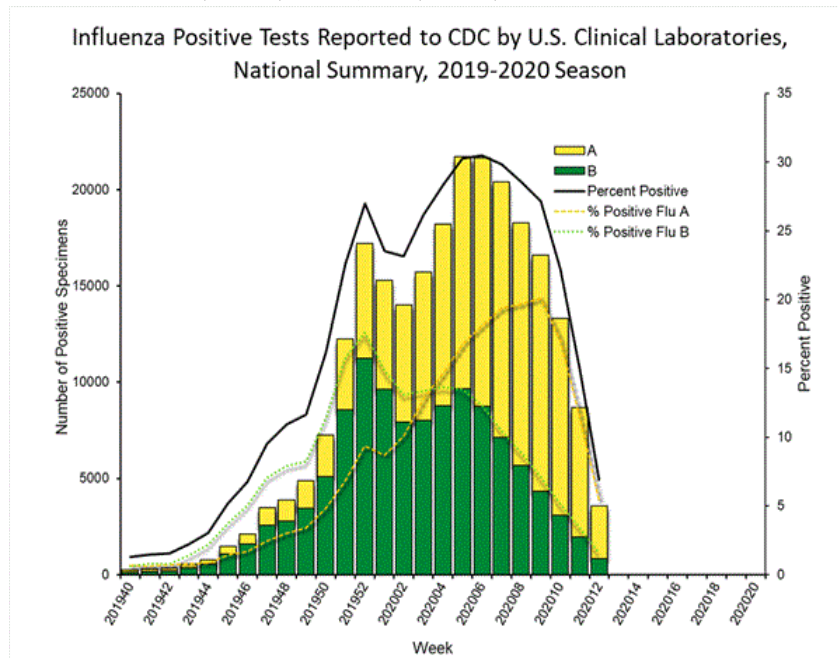
Additional information on the current and previous influenza seasons for each surveillance component are available on [FluView Interactive](#).

U.S. Virologic Surveillance

Clinical Laboratories

The results of tests performed by clinical laboratories nationwide are summarized below. Data from clinical laboratories (the percentage of specimens tested that are positive for influenza) are used to monitor whether influenza activity is increasing or decreasing.

	Week 12	Data Cumulative since September 29, 2019 (week 40)
No. of specimens tested	51,570	1,208,294
No. of positive specimens (%)	3,581 (6.9%)	242,330 (20.1%)
Positive specimens by type		
Influenza A	2,748 (76.7%)	128,676 (53.1 %)
Influenza B	833 (23.3%)	113,654 (46.9%)

Influenza Positive Tests Reported to CDC by U.S. Clinical Laboratories, National Summary, 2019-2020 Season

[View Chart Data](#) | [View Full Screen](#)

Public Health Laboratories

The results of tests performed by public health laboratories nationwide are summarized below. Data from public health laboratories are used to monitor the proportion of circulating viruses that belong to each influenza subtype/lineage.

	Week 12	Data Cumulative since

	September 29, 2019 (week 40)	
No. of specimens tested	2,139	78,778
No. of positive specimens	219	42,510
Positive specimens by type/subtype		
Influenza A	181 (82.6%)	24,087 (56.7%)
(H1N1)pdm09	147 (91.9%)	21,583 (92.5%)
H3N2	13 (8.1%)	1,744 (7.5%)
Subtyping not performed	21	760
Influenza B	38 (17.4%)	18,423 (43.3%)
Yamagata lineage	0 (0.0%)	231 (1.6%)
Victoria lineage	28 (100%)	14,077 (98.4%)
Lineage not performed	10	4,115

While influenza B/Victoria viruses predominated earlier in the season, during recent weeks, influenza A(H1N1)pdm09 viruses have been reported more frequently than B/Victoria viruses nationally and in all surveillance regions. For the season, A(H1N1)pdm09 viruses are the predominant virus nationally. Regional and state level data about circulating influenza viruses can be found on FluView Interactive.

The predominant virus also varies by age group. Nationally, for the season overall, influenza B viruses are the most commonly reported influenza viruses among persons 5-24 years, while influenza A viruses are the most commonly reported influenza viruses among persons 0-4 years and 25 years and older. In the most recent three weeks, influenza A viruses are the most commonly reported influenza viruses in all age groups.
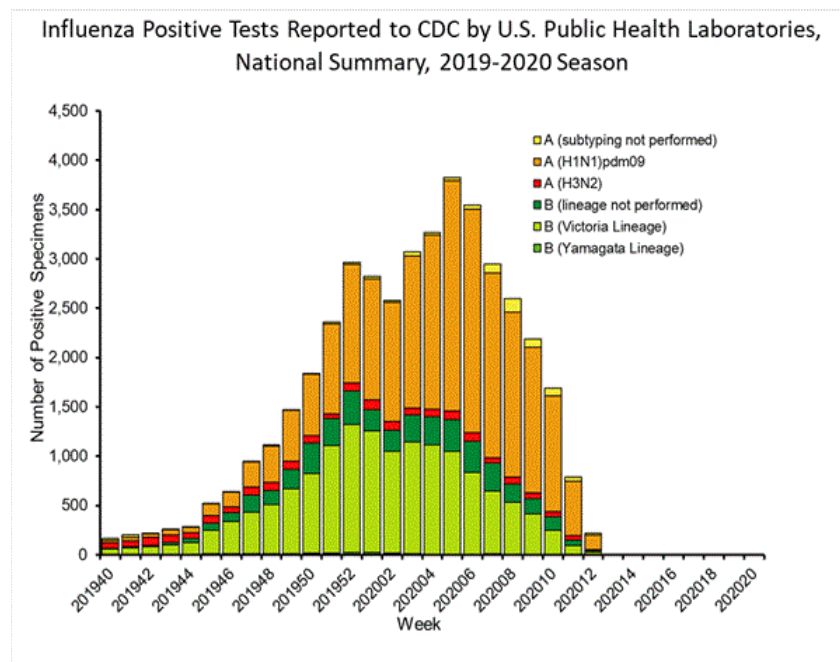
View Chart Data | View Full Screen

Additional virologic surveillance information for current and past seasons:
Surveillance Methods | FluView Interactive: National, Regional, and State Data or Age Data

Influenza Virus Characterization

CDC performs genetic and antigenic characterization of U.S. viruses submitted from state and local health laboratories using Right Size Roadmap submission guidance. These data are used to compare how similar the currently circulating influenza viruses are to the reference viruses used for developing new influenza vaccines and to monitor evolutionary changes that continually occur in circulating influenza viruses. Antigenic characterization data are based on an animal model (influenza-naive ferrets), and do not reflect pre-existing protection provided by

past influenza infections and vaccinations. Additional antigenic characterization studies involving people vaccinated with current influenza vaccines are conducted later in the season; these data account for pre-existing protection in different populations against circulating influenza viruses. Genetic and antigenic characterization data are not used to make calculations about vaccine effectiveness (VE). CDC conducts VE studies each year to measure the benefits of flu vaccines in people. Interim estimates of 2019-2020 flu vaccine effectiveness have been released.

CDC **genetically characterized** 2,336 influenza viruses collected in the U.S. from September 29, 2019, to March 21, 2020.

Virus Subtype or Lineage	Total No. of Subtype/Lineage Tested	Genetic Characterization			
		Clade	Number (% of subtype/lineage tested)	Subclade	Number (% of subtype/lineage tested)
A/H1	840				
		6B.1A	840 (100%)		
A/H3	497				
		3C.2a	467 (94.0%)	2a1	467 (94.0%)
				2a2	0
				2a3	0
				2a4	0
		3C.3a	30 (6.0%)	3a	30 (6.0%)
B/Victoria	909				
		V1A	909 (100%)	V1A	0
				V1A.1	60 (6.6%)
				V1A.3	849 (93.4%)
B/Yamagata	90				
		Y3	90 (100%)		

CDC **antigenically characterizes** a subset of influenza viruses by hemagglutination inhibition (HI) or neutralization based Focus Reduction assays (FRA). 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 antigenically characterized 471 influenza viruses collected in the United States from September 29, 2019, to March 21, 2020. These data are not used to make calculations about vaccine effectiveness (VE). CDC conducts VE studies each year to measure the benefits of flu vaccines in people.

Influenza A Viruses

- **A (H1N1)pdm09:** 177 A(H1N1)pdm09 viruses were antigenically characterized by HI with ferret antisera, and 143 (80.8%) were antigenically similar (reacting at titers that were within 4-fold of the homologous virus titer) to cell-propagated A/Brisbane/02/2018-like reference viruses representing the A(H1N1)pdm09 component for the 2019-20 Northern Hemisphere influenza vaccines. The decrease in the percent of A(H1N1)pdm09 viruses similar to A/Brisbane/02/2018 is due to some of the recent viruses selected for testing having a single amino acid change that is antigenically distinguishable in antigenic assays using ferret sera. Similar viruses were observed last season as well and these represented a small proportion of virus circulating. We have observed an increase in the proportion of H1N1pdm09 viruses with this change late in the US season.
- **A (H3N2):** 86 A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and 40 (46.5%) were antigenically similar to cell-propagated A/Kansas/14/2017-like reference viruses representing the A(H3N2) component for the 2019-20 Northern Hemisphere influenza vaccines.

Influenza B Viruses

- **B/Victoria:** 180 B/Victoria lineage viruses, including viruses from both co-circulating sub-clades, were antigenically characterized by HI with ferret antisera, and 112 (62.2%) were antigenically similar to cell-propagated B/Colorado/06/2017-like reference viruses representing the B/Victoria component for the 2019-20 Northern Hemisphere influenza vaccines.
- **B/Yamagata:** 28 B/Yamagata lineage viruses were antigenically characterized by HI with ferret antisera, and all 28 (100%) were antigenically similar to cell-propagated B/Phuket/3073/2013-like reference viruses representing the B/Yamagata component for the 2019-20 Northern Hemisphere influenza vaccines.

CDC also assesses **susceptibility of influenza viruses to the antiviral medications** including the neuraminidase inhibitors (oseltamivir, zanamivir, and peramivir) and the PA endonuclease inhibitor baloxavir using next generation sequence analysis supplemented by laboratory assays. Viruses collected in the United States since September 29, 2019, were tested for antiviral susceptibility as follows:
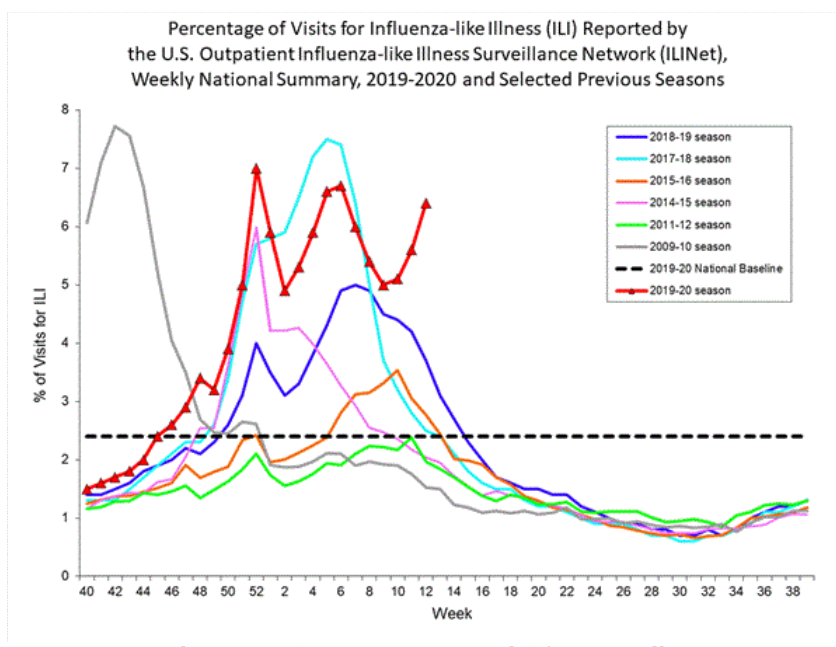
	Antiviral Medication		Total Viruses*	A/H1	A/H3	B/Victoria	B/Yamagata
Neuraminidase Inhibitors	**Oseltamivir**	**Viruses Tested**	2,309	831	488	900	90
		Reduced Inhibition	1 (0.0%)	(0.0%)	(0.0%)	1 (0.1%)	(0.0%)
		Highly Reduced Inhibition	4 (0.2%)	4 (0.5%)	(0.0%)	(0.0%)	(0.0%)
	Peramivir	**Viruses Tested**	2,309	831	488	900	90
		Reduced Inhibition	(0.0%)	(0.0%)	(0.0%)	(0.0%)	(0.0%)
		Highly Reduced Inhibition	5 (0.2%)	4 (0.5%)	(0.0%)	1 (0.1%)	(0.0%)
	Zanamivir	**Viruses Tested**	2,309	831	488	900	90
		Reduced Inhibition	2 (0.1%)	(0.0%)	(0.0%)	2 (0.2%)	(0.0%)
		Highly Reduced Inhibition	(0.0%)	(0.0%)	(0.0%)	(0.0%)	(0.0%)
PA Endonuclease Inhibitor	**Baloxavir**	**Viruses Tested**	2,467	855	573	946	93
		Reduced Susceptibility	(0.0%)	(0.0%)	(0.0%)	(0.0%)	(0.0%)

A total of 556 additional viruses (211 A(H1N1)pdm09, 32 A(H3N2), and 313 B) collected in Alabama, Alaska, Florida, Illinois, Iowa, Louisiana, Massachusetts, Michigan, Nevada, New York, North Carolina, Pennsylvania, South Dakota, Virginia and Wisconsin were analyzed for resistance to neuraminidase inhibitors by pyrosequencing assay. Three (1.4%) of the 211 A(H1N1)pdm09 viruses tested had the H275Y amino acid substitution in the neuraminidase and showed highly reduced inhibition by oseltamivir and peramivir. No molecular markers associated with reduced or highly reduced inhibition by neuraminidase inhibitors were detected in A(H3N2) and type B viruses tested.

Outpatient Illness Surveillance

ILINet

Nationwide during week 12, 6.4% 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 above the national baseline of 2.4%.

Percentage of Visits for Influenza-like Illness (ILI) Reported by the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet), Weekly National Summary, 2019-2020 and Selected Previous Seasons

View Chart Data (current season only) | View Full Screen

On a regional level, the percentage of outpatient visits for ILI ranged from 4.7% to 11.8% during week 12. Eight of the 10 surveillance regions reported an increase in percentage of outpatient visits for ILI, and all regions reported a percentage of outpatient visits for ILI above their region-specific baselines.

ILI Activity Map

Data collected in ILINet are used to produce a measure of ILI activity* by state.

During week 12, the following ILI activity levels were experienced:

- High – the District of Columbia, New York City, Puerto Rico, and 34 states (Alabama, California, Colorado, Connecticut, Georgia, Illinois, Kansas, Kentucky, Louisiana, Maine, Maryland, Massachusetts, Michigan, Minnesota, Mississippi, Montana, Nebraska, New Jersey, New Mexico, New York, North Carolina, North Dakota, Oklahoma, Oregon, Pennsylvania, South Carolina, Tennessee, Texas, Utah, Vermont, Virginia, Washington, West Virginia, and Wisconsin)
- Moderate – 10 states (Arkansas, Hawaii, Idaho, Indiana, Iowa, Missouri, Nevada, Ohio, South Dakota, and Wyoming)
- Low - two states (Alaska and Delaware)
- Minimal - four states (Arizona, Florida, New Hampshire, and Rhode Island)
- Data were insufficient to calculate an ILI activity level from the U.S. Virgin Islands.

Among the 37 jurisdictions with high ILI activity, ILI increased relative to the previous week in 20, remained stable in 10 and declined in 7. Thirty-four of the jurisdictions with high ILI activity also had clinical laboratory data available and in those, the percent of specimens testing positive for influenza decreased in 32 and increased in only 2.

Additional information about medically attended visits for ILI for current and past seasons:
Surveillance Methods | FluView Interactive: National, Regional, and State Data or ILI Activity Map

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.

During week 12, the following influenza activity was reported:

- Widespread – Puerto Rico and 38 states (Alabama, Colorado, Connecticut, Delaware, Georgia, Idaho, Illinois,

Indiana, Iowa, Kansas, Kentucky, Louisiana, Maine, Maryland, Massachusetts, Michigan, Mississippi, Missouri, Nevada, New Hampshire, New Jersey, New Mexico, New York, North Carolina, Ohio, Oklahoma, Oregon, Pennsylvania, Rhode Island, South Carolina, Tennessee, Texas, Utah, Vermont, Virginia, Washington, West Virginia and Wisconsin)
- Regional – 10 states (Arizona, Arkansas, California, Florida, Minnesota, Montana, Nebraska, North Dakota, South Dakota and Wyoming)
- Local – the District of Columbia and two states (Alaska and Hawaii)
- Sporadic – the U.S. Virgin Islands
- Guam did not report.

Additional geographic spread surveillance information for current and past seasons:
Surveillance Methods | FluView Interactive

Influenza-Associated Hospitalizations

The Influenza Hospitalization Surveillance Network (FluSurv-NET) conducts 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.

A total of 19,543 laboratory-confirmed influenza-associated hospitalizations were reported by FluSurv-NET sites between October 1, 2019 and March 21, 2020; 14,100 (72.1%) were associated with influenza A virus, 5,335 (27.3%) with influenza B virus, 56 (0.3%) with influenza A virus and influenza B virus co-infection, and 52 (0.3%) with influenza virus for which the type was not determined. Among those with influenza A subtype information, 3,747 (94.5%) were A(H1N1)pdm09 virus and 219 (5.5%) were A(H3N2).

The overall cumulative hospitalization rate was 67.3 per 100,000 population, which is higher than all recent seasons at this time of year except for the 2017-18 season. Rates in children 0-4 years old and adults 18-49 years old are now the highest CDC has on record for these age groups, surpassing the rate reported during the 2009 H1N1 pandemic. Hospitalization rates for school-aged children are higher than any recent regular season but lower than rates during the pandemic.
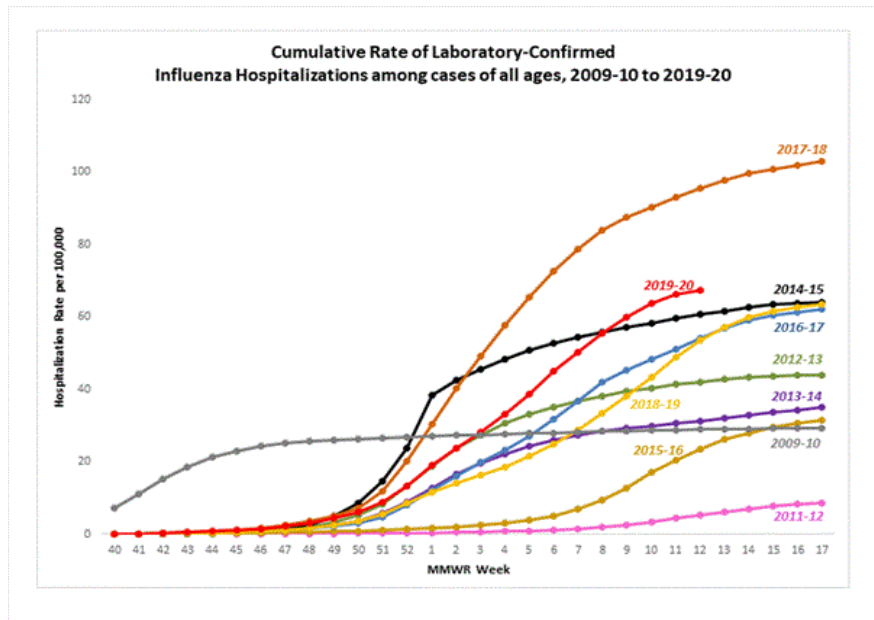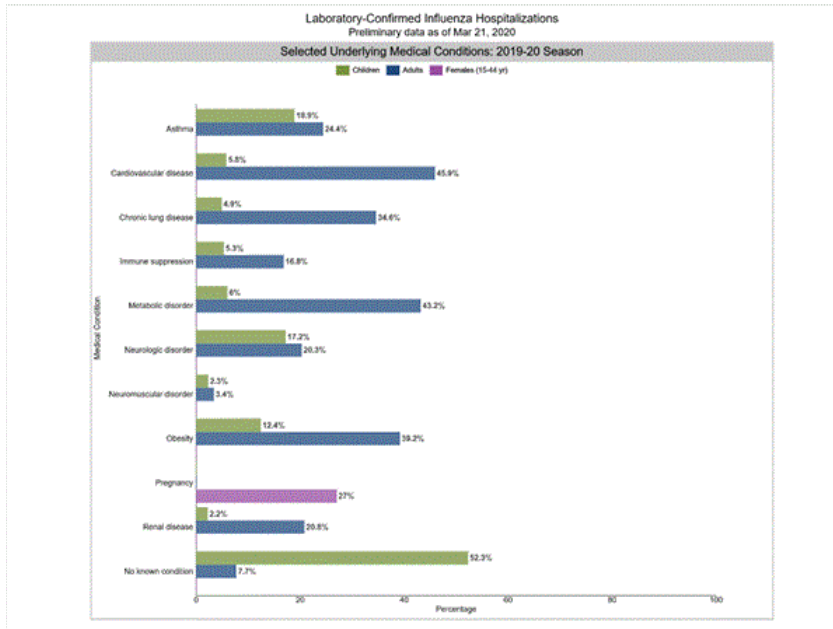

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The highest rate of hospitalization is among adults aged ≥ 65, followed by children aged 0-4 years and adults aged 50-64 years.

Age Group	2019-2020 Season Cumulative Rate per 100,000 Population
Overall	67.3
0-4 years	93.9

Age Group	2019-2020 Season Cumulative Rate per 100,000 Population
5-17 years	24.4
18-49 years	35.2
50-64 years	88.9
65+ years	176.8

Among 3,161 hospitalized adults with information on underlying medical conditions, 92.3% had at least one reported underlying medical condition, the most commonly reported were cardiovascular disease, metabolic disorder, obesity, and chronic lung disease. Among 535 hospitalized children with information on underlying medical conditions, 47.7% had at least one underlying medical condition; the most commonly reported was asthma. Among 551 hospitalized women of childbearing age (15-44 years) with information on pregnancy status, 27% were pregnant.
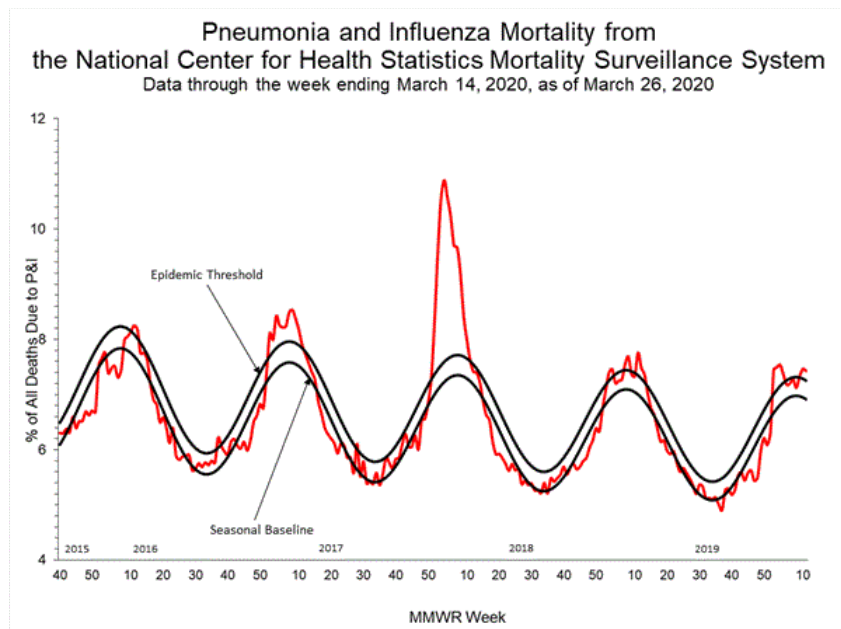

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Additional hospitalization surveillance information for current and past seasons and additional age groups:
[Surveillance Methods](#) | FluView Interactive: [Rates by Age](#) or [Patient Characteristics](#)

Pneumonia and Influenza (P&I) Mortality Surveillance

Based on National Center for Health Statistics (NCHS) mortality surveillance data available on March 26, 2020, 7.4% of the deaths occurring during the week ending March 7, 2020 (week 11) were due to P&I. This percentage is above the epidemic threshold of 7.3% for week 11.

Pneumonia and Influenza Mortality from
the National Center for Health Statistics Mortality Surveillance System
Data through the week ending March 14, 2020, as of March 26, 2020
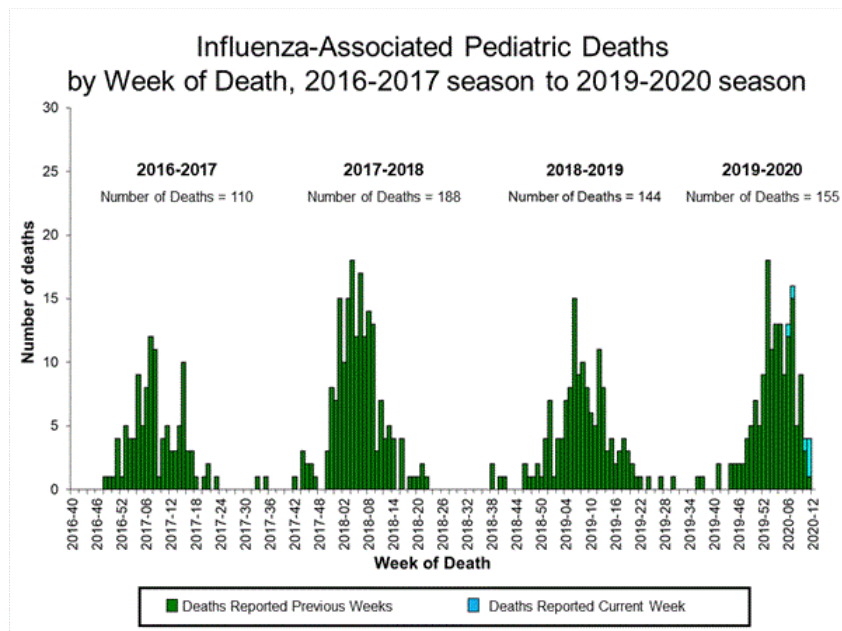
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Additional pneumonia and influenza mortality surveillance information for current and past seasons:
Surveillance Methods | FluView Interactive

Influenza-Associated Pediatric Mortality

Six influenza-associated pediatric deaths occurring during the 2019-2020 season between weeks 6 and 11 (the weeks ending February 8, 2020 and March 14, 2020) were reported to CDC during week 12. Three were associated with influenza A viruses, and one was subtyped as an A(H1N1)pdm09 virus. Three were associated with influenza B viruses and all were B/Victoria viruses.

Of the 155 influenza-associated pediatric deaths occurring during the 2019-2020 season and reported to CDC:

- 99 deaths were associated with influenza B viruses, and 24 had a lineage determined; all were B/Victoria viruses.
- 56 deaths were associated with influenza A viruses, and 31 were subtyped; 30 were A(H1N1)pdm09 viruses, and one was an A(H3) virus.

Influenza-Associated Pediatric Deaths by Week of Death, 2016-2017 season to 2019-2020 season

View Full Screen

Additional pediatric mortality surveillance information for current and past seasons:
Surveillance Methods | FluView Interactive

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/fluviewinteractive.htm

National Institute for Occupational Safety and Health: Monthly surveillance data on the prevalence of health-related workplace absenteeism among full-time workers in the United States are available from NIOSH at https://www.cdc.gov/niosh/topics/absences/default.html

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

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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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.