

# Influenza Surveillance Report

[www.infectiousdisease.dhh.la.gov](http://www.infectiousdisease.dhh.la.gov)

Week 1: 12/30/18 - 1/5/19

**Influenza activity remained high this week in Louisiana. Rhino/Enteroviruses, RSV, and Coronaviruses represent the majority of non-influenza viruses reported.**

The Influenza Surveillance Summary Report describes the results of the tracking done by the Louisiana Office of Public Health Infectious Disease Epidemiology Section (IDEpi). This report relies on data supplied by sentinel surveillance sites, including hospital emergency departments (ED), laboratories and physicians' offices. Sentinel sites provide weekly data on Influenza Like Illness (ILI) and/or laboratory confirmed cases.

Taken together, ILI surveillance and laboratory surveillance provide a clear picture of the influenza activity occurring in Louisiana each week. If you have any questions about our surveillance system or would like more information, please contact Julie Hand at 504-568-8298 or [julie.hand@la.gov](mailto:julie.hand@la.gov).

**ILI** is defined as an illness characterized by cough and/or cold symptoms and a fever of 100° F or greater in the absence of a known cause. While not every case of ILI is a case of influenza, the CDC has found that trends in ILI from sentinel sites are a good proxy measure of the amount of influenza activity in an area. For this reason, all states and territories participating in the national surveillance program monitor weekly ILI ratios from their sentinel surveillance sites.

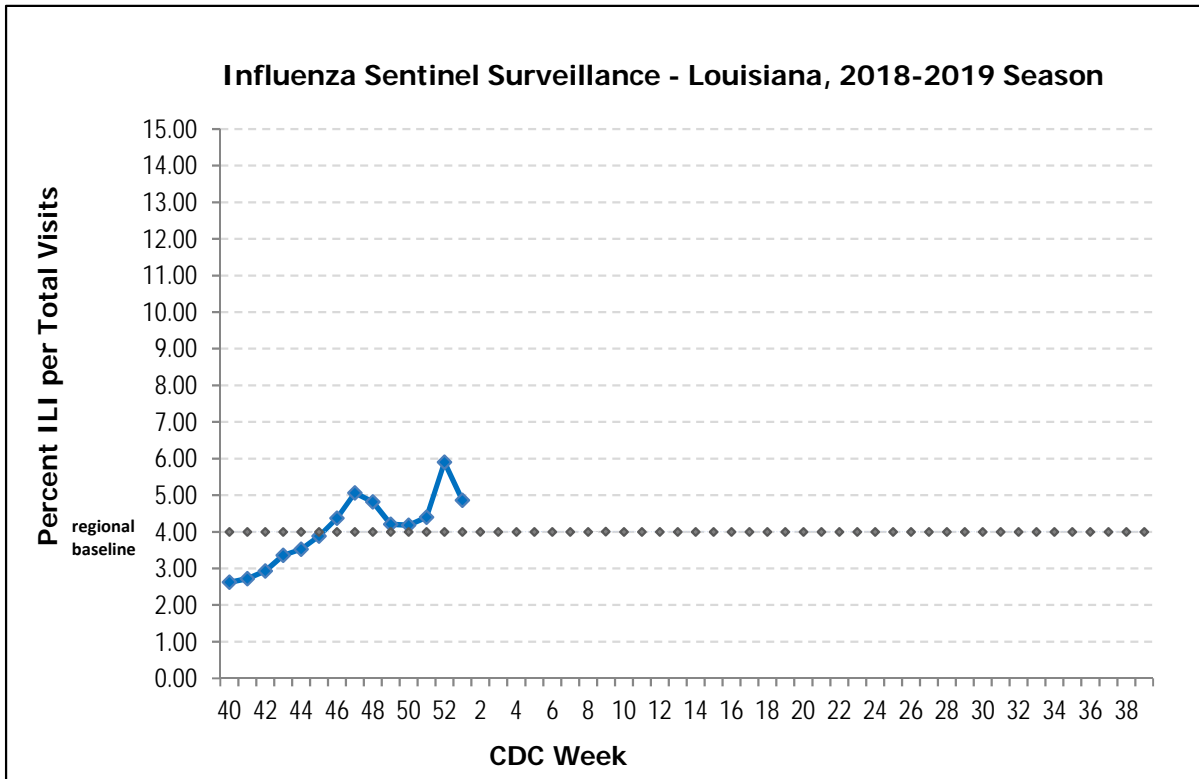


**Laboratory testing:** Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information is included on page 3 of this report.

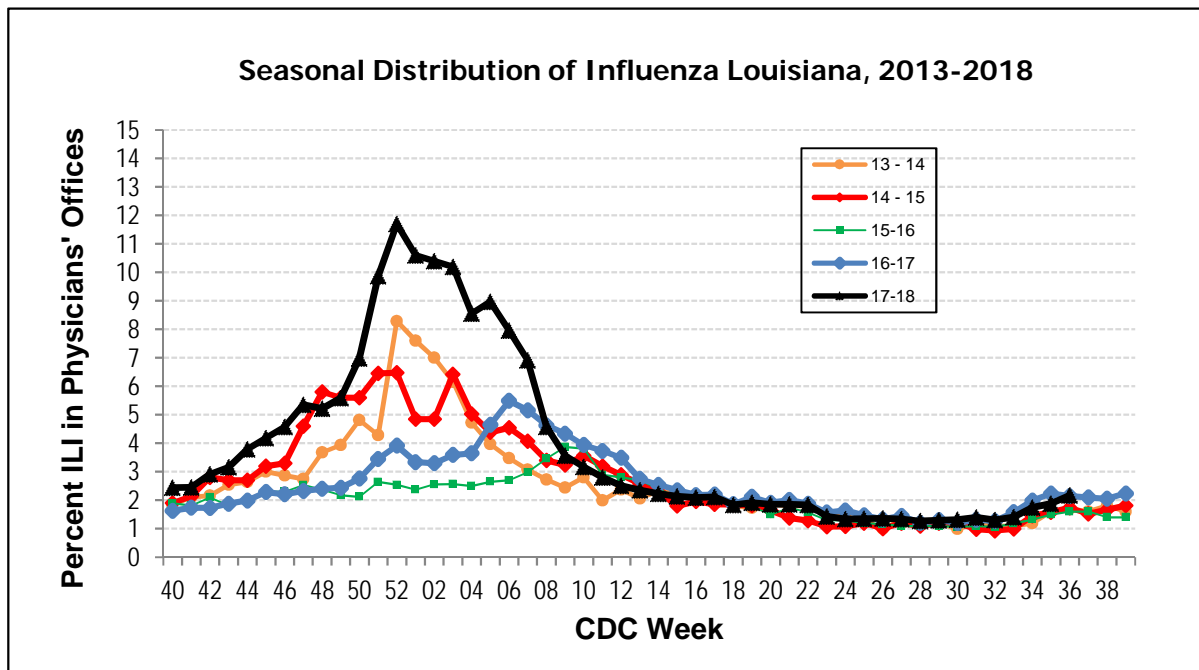
Page 2 : ILI Activity  
Page 3: Virologic Surveillance  
Page 4: Geographic Distribution  
Page 5 & 6: Regional & National Data

## 2018-2019 Season

This graph shows the percentage of visits for ILI over the total number of visits for sentinel surveillance sites. This is the best approach to estimate the magnitude of influenza transmission. ILI counts do include some viral infections other than influenza, but experience over the last 50 years has shown that this approach is a reliable method to estimate influenza transmission. It does not show which strain of influenza virus is responsible. The page on lab surveillance does show the proportion of specimens attributable to each virus strain.

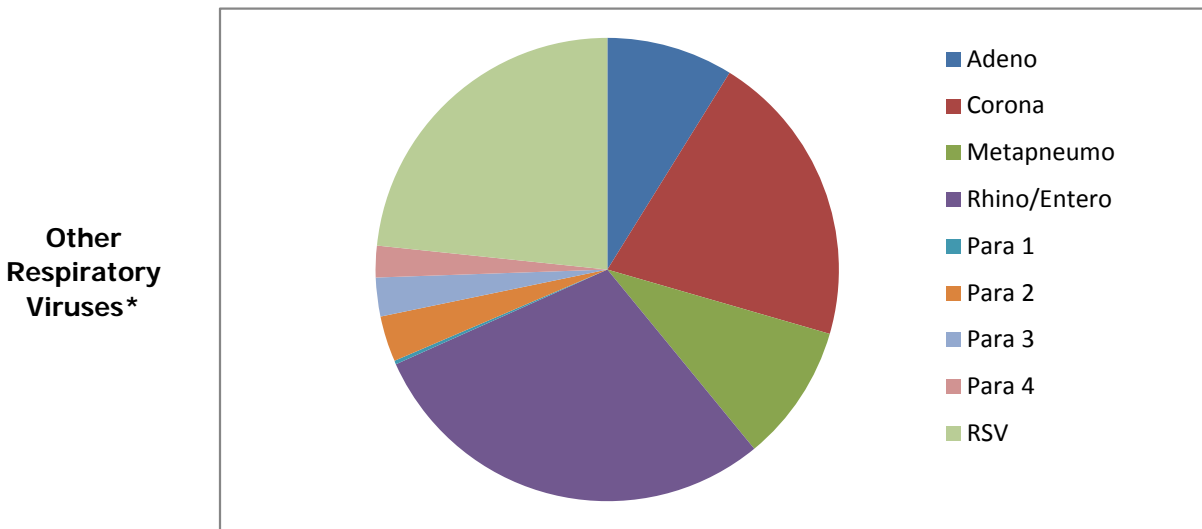
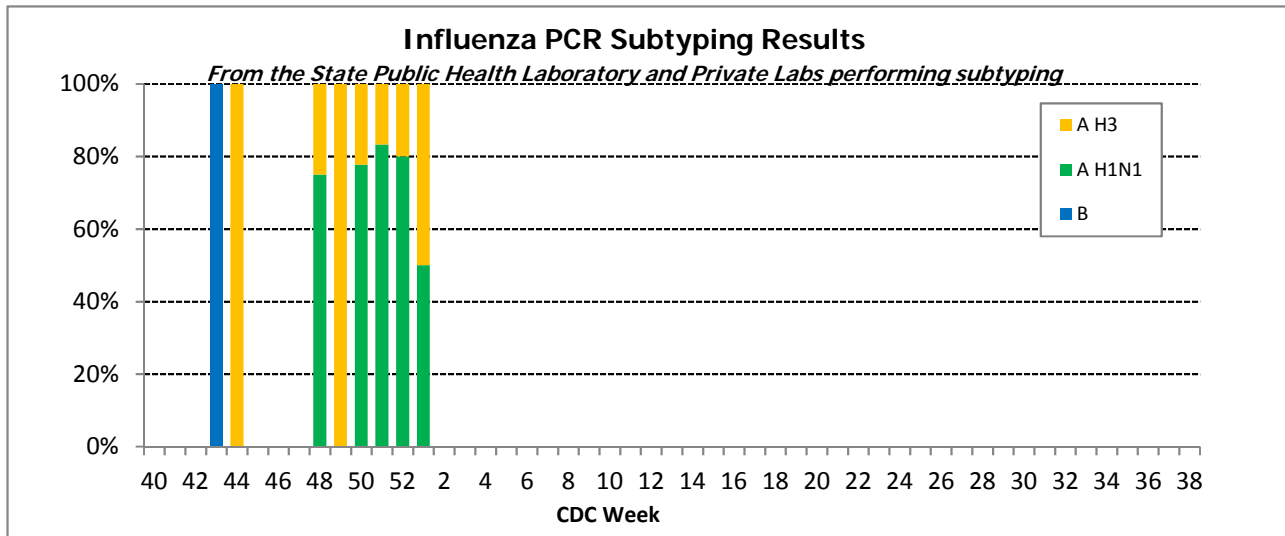
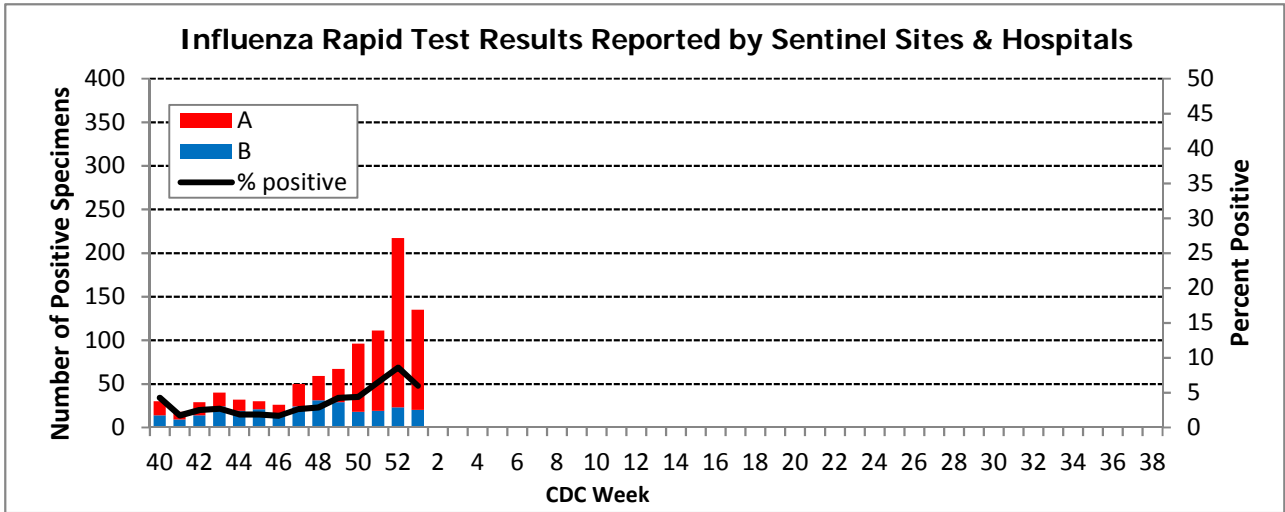


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.



# 2018-2019 Season

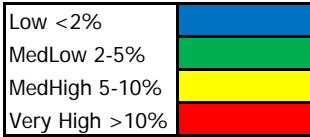
## Virologic Surveillance



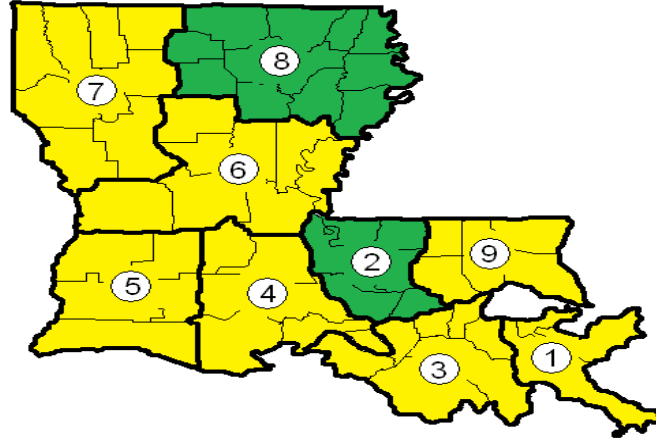
\*Based on results from the State Public Health Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 2 weeks.

## 2018-2019 Season

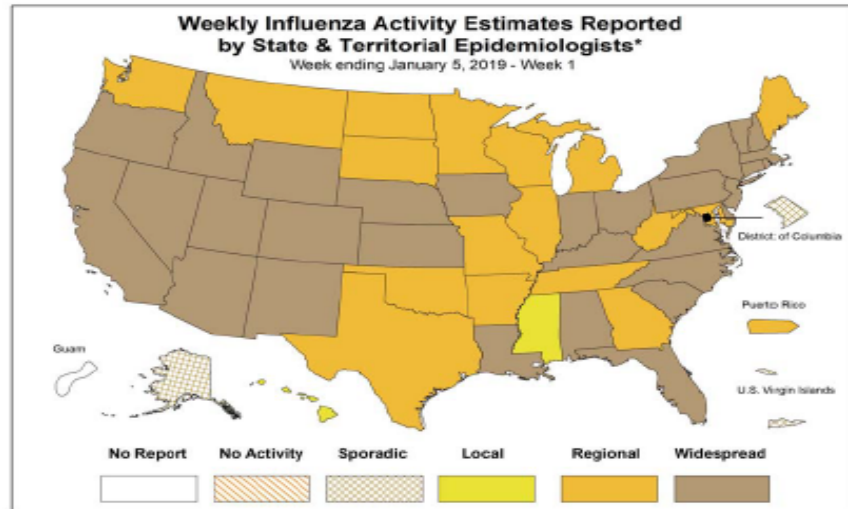
### Geographical Distribution of ILI\*



\* %ILI over the last 2 weeks based on sentinel surveillance data



### Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists



\* This map indicates geographic spread & does not measure the severity of influenza activity

### Influenza-Like Illness (ILI) Activity Level Indicator Determined by Data Reported to ILINet 2018-19 Influenza Season Week 1 ending Jan 05, 2019

### ILINet Activity Indicator Map



## 2018-2019 Season

### National Surveillance

Influenza activity remains elevated in the United States.

The proportion of outpatient visits for influenza-like illness (ILI) decreased from 4.0% to 3.5%, but remains above the national baseline of 2.2%.

The proportion of deaths attributed to pneumonia and influenza (P&I) was below the system-specific epidemic threshold.

Three influenza-associated pediatric deaths were reported to CDC in week 1.

### Clinical Laboratory Data

	Week 1	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	35,059	363,555
No. of positive specimens (%)	4,480 (12.7%)	26,430 (7.3%)
<i>Positive specimens by type</i>		
Influenza A	4,347 (97.5%)	24,867 (94.1%)
Influenza B	113 (2.5%)	1,563 (5.9%)

### Public Health Laboratory Data

	Week 1	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	833	18,125
No. of positive specimens*	444	5,131
<i>Positive specimens by type/subtype</i>		
Influenza A	440 (99.1%)	4,918 (95.8%)
(H1N1)pdm09	322 (82.6%)	3,772 (81.4%)
H3N2	68 (17.4%)	864 (18.6%)
Subtyping not performed	50	282
Influenza B	4 (0.9%)	213 (4.2%)
Yamagata lineage	0 (0%)	97 (58.8%)
Victoria lineage	2 (100%)	68 (41.2%)
Lineage not performed	2	48

### HHS Surveillance Region Data:

<i>U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet) 2017-2018 Influenza Season</i>										
<i>HHS Region 6 (AR, LA, NM, OK, and TX) (Baseline: 4.0%) Data as of Friday, January 11, 2019</i>										
						ILI 65		Total	%	%
CDC Week	# Sites Reporting	ILI 0-4 years	ILI 5-24 years	ILI 25-49 years	ILI 50-64 years	and older	Total ILI	Patient Visits	Unweighted ILI	Weighted ILI
201850	284	1309	1303	828	283	193	3916	107339	3.6	3.9
201851	271	1437	1429	1013	412	267	4558	103354	4.4	4.6
201852	261	1764	1495	1422	560	406	5647	96145	5.9	6.0
201901	264	1426	1117	1458	626	405	5032	101098	5.0	4.9

#### Region 6 (AR, LA, NM, OK, TX)

CDC Week	Public Health Labs	Public Health Specimens Tested	AUNK	AH1N1 pdm09	AH3N2	AH3N2v	B	BVic	BYam	Clinical Labs	Clinical Specimens Tested	Clinical Flu Positive	% Positive	A	B
201850	8	194	1	79	6	0	0	1	1	22	3438	345	10.03	322	23
201851	9	123	0	65	3	0	0	0	0	23	5134	843	16.42	811	32
201852	8	24	0	0	7	0	1	1	0	22	4941	963	19.49	918	45
201901	5	25	0	4	4	0	0	0	0	20	4050	563	13.90	533	30

## 2018-2019 Season

### Antiviral Resistance:

Type/Subtype or Lineage	Inhibition of Neuraminidase Activity by Antiviral Drug								
	Oseltamivir			Peramivir			Zanamivir		
	Virus Tested (n)	Reduced, Number (%)	Highly Reduced, Number (%)	Virus Tested (n)	Reduced, Number (%)	Highly Reduced, Number (%)	Virus Tested (n)	Reduced, Number (%)	Highly Reduced, Number (%)
Total Viruses	496	0 (0%)	0 (0%)	496	0 (0%)	0 (0%)	496	0 (0%)	0 (0%)
A(H1N1)pdm09	302	0 (0%)	0 (0%)	302	0 (0%)	0 (0%)	302	0 (0%)	0 (0%)
A(H3N2)	141	0 (0%)	0 (0%)	141	0 (0%)	0 (0%)	141	0 (0%)	0 (0%)
B/Victoria	15	0 (0%)	0 (0%)	15	0 (0%)	0 (0%)	15	0 (0%)	0 (0%)
B/Yamagata	38	0 (0%)	0 (0%)	38	0 (0%)	0 (0%)	38	0 (0%)	0 (0%)

### Antigenic & Genetic Characterization:

CDC has antigenically or genetically characterized 444 influenza viruses collected September 30, 2018 – January 5, 2019, and submitted by U.S. laboratories, including 270 influenza A(H1N1)pdm09 viruses, 127 influenza A(H3N2) viruses, and 47 influenza B viruses.

#### Influenza A Viruses

- A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 270 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Seventy-nine A(H1N1)pdm09 viruses were antigenically characterized, and 78 (98.7%) 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 127 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=43), subclade 3C.2a1 (n=61) or clade 3C.3a (n=23). Six A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and all 6 (100%) A(H3N2) viruses tested were well-inhibited (reacting at titers that were within 4-fold 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.

#### Influenza B Viruses

- B/Victoria:** Phylogenetic analysis of 13 B/Victoria-lineage viruses indicate that all HA genes belonged to genetic clade V1A, however genetic subclades which are antigenically distinct have emerged. Genetic subclades which are antigenically distinct include viruses with a two amino acid deletion (162-163) in the HA protein (V1A.1, previously abbreviated as V1A-2Del) and viruses with a three amino acid deletion (162-164) in the HA protein (abbreviated as V1A-3Del). Eight B/Victoria lineage viruses were antigenically characterized and 4 (50%) were antigenically similar with ferret antisera raised against cell-propagated B/Colorado/06/2017-like V1A.1 reference virus. Four (50%) reacted poorly (at titers that were 8-fold or greater reduced compared with the homologous virus titer) and belonged to clade V1A.
- B/Yamagata:** Phylogenetic analysis of 34 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 33 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.