

## Influenza Surveillance Report

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

Week 5: 1/27/19 - 2/2/19

Influenza activity increased significantly this week in Louisiana. Outbreaks continue to be reported from schools and long-term care facilities. The number of influenza tests reported by clinical labs nearly tripled this week and more than 25% of tests were reported positive. Influenza A/H1N1 remains the dominant virus subtyped at the state public health laboratory overall but influenza A/H3 was the most prevalent this week. Rhino/Enteroviruses 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

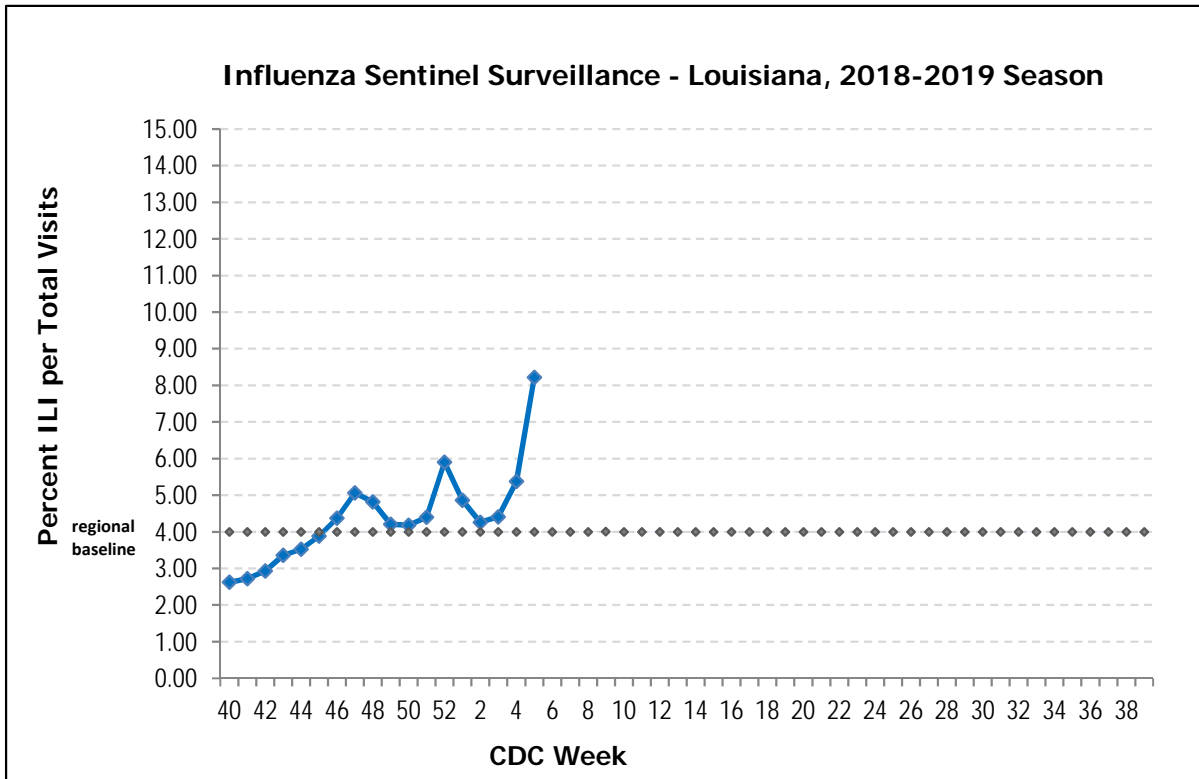
Page 3: Virologic Surveillance

Page 4: Geographic Distribution

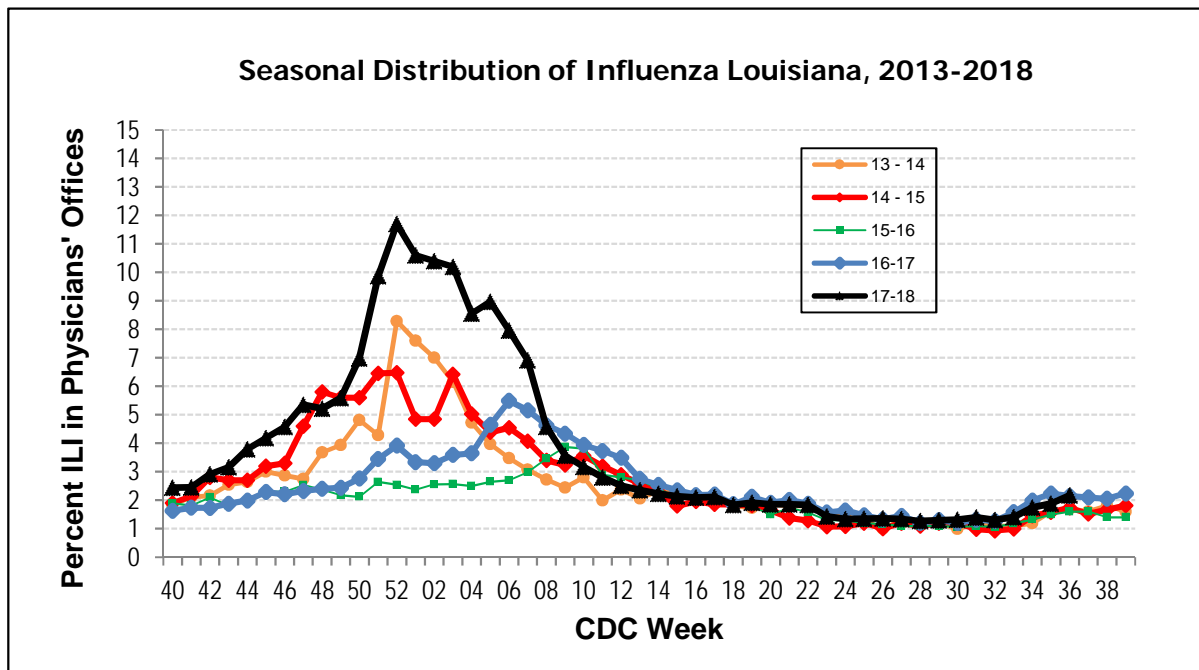
Page 5 & 6: Regional & National Data

## 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.

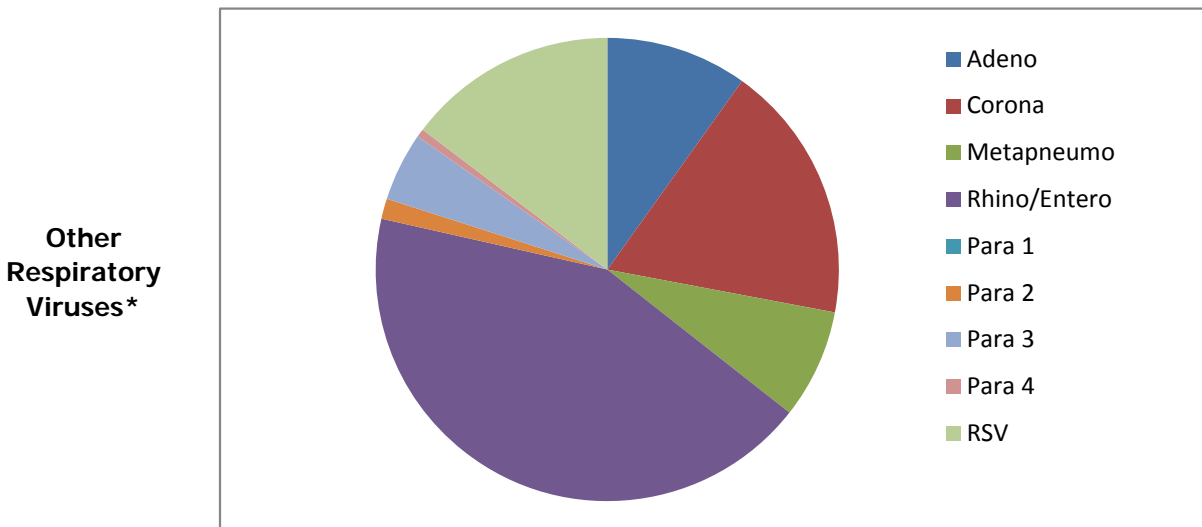
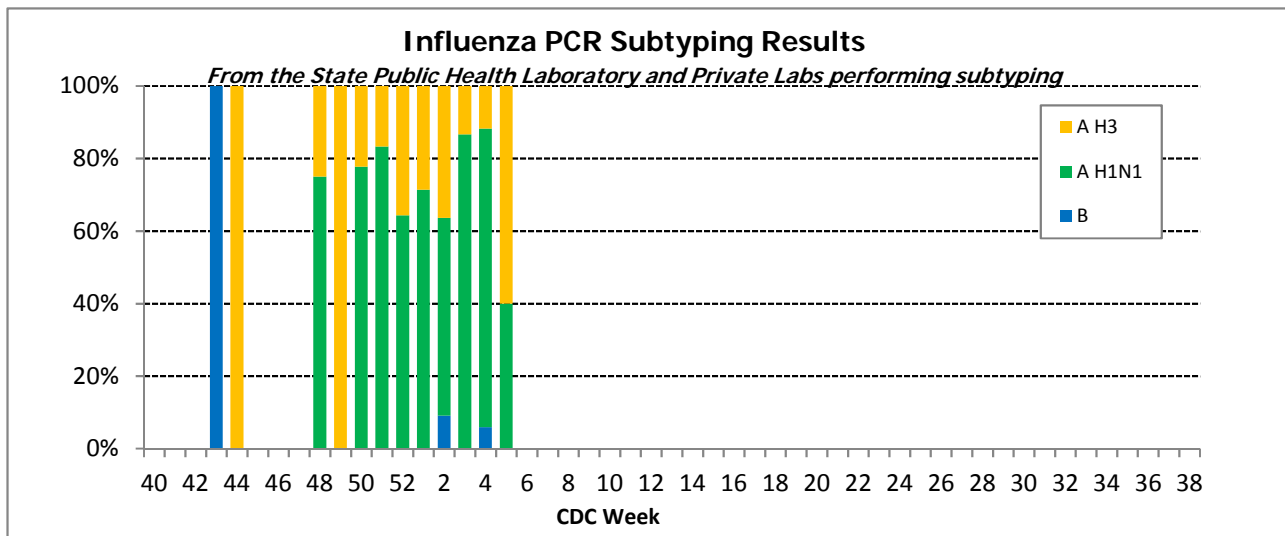
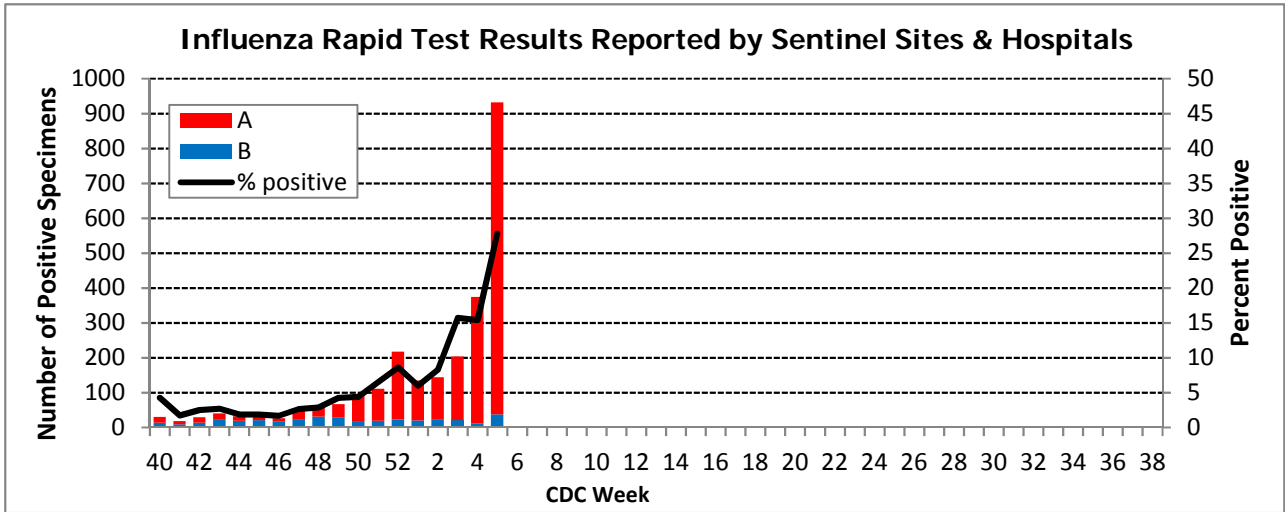


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.



# 2018-2019 Season

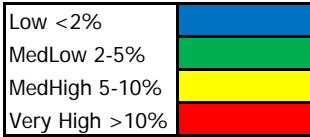
## Virologic Surveillance



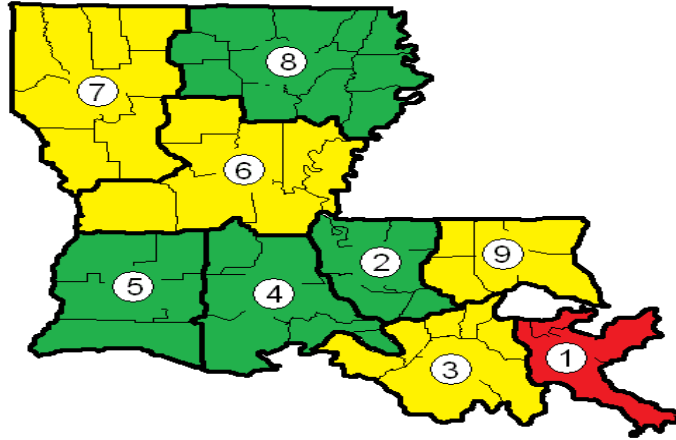
\*Based on results from the State Public Health Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 2 weeks.

## 2018-2019 Season

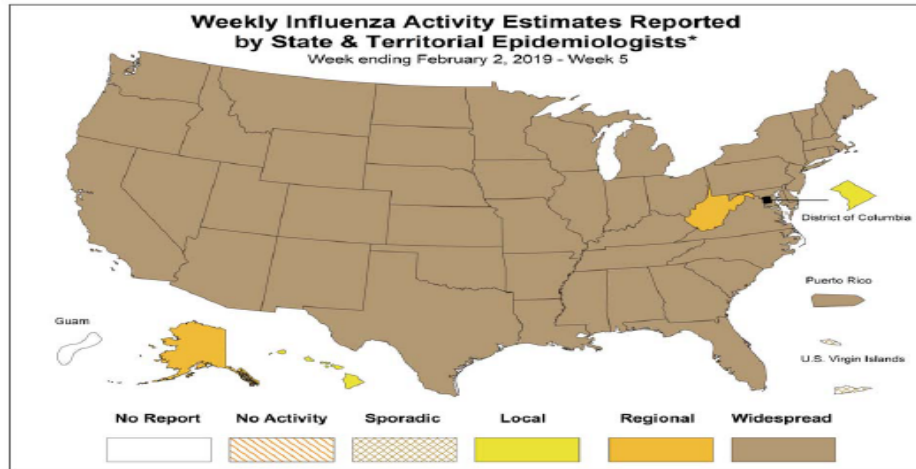
### Geographical Distribution of ILI\*



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



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



Influenza-Like Illness (ILI) Activity Level Indicator Determined by Data Reported to ILINet  
2018-19 Influenza Season Week 5 ending Feb 02, 2019

### ILINet Activity Indicator Map



## 2018-2019 Season

### National Surveillance

Influenza activity increased in the United States.

The proportion of outpatient visits for influenza-like illness (ILI) increased to 4.3%, which is 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.

Four influenza-associated pediatric deaths were reported to CDC during week 5.

### Clinical Laboratory Data

	Week 5	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	33,362	536,301
No. of positive specimens (%)	7,205 (21.6%)	54,381 (10.1%)
<i>Positive specimens by type</i>		
Influenza A	7,080 (98.3%)	52,028 (95.7%)
Influenza B	125 (1.7%)	2,353 (4.3%)

### Public Health Laboratory Data

	Week 5	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	1,442	30,344
No. of positive specimens*	843	12,200
<i>Positive specimens by type/subtype</i>		
Influenza A	829 (98.3%)	11,863 (97.2%)
(H1N1)pdm09	524 (65.0%)	9,023 (80.0%)
H3N2	282 (35.0%)	2,261 (20.0%)
Subtyping not performed	23	579
Influenza B	14 (1.7%)	337 (2.8%)
Yamagata lineage	2 (28.6%)	143 (57.4%)
Victoria lineage	5 (71.4%)	106 (42.6%)
Lineage not performed	7	88

### HHS Surveillance Region Data:

*U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet)  
2018-2019 Influenza Season  
HHS Region 6 (AR, LA, NM, OK, and TX) (Baseline: 4.0%)  
Data as of Friday, February 8, 2019*

CDC Week	# Sites Reporting	ILI 0-4 years	ILI 5-24 years	ILI 25-49 years	ILI 50-64 years	ILI 65 years and older	Total ILI	Total Patient Visits	% Unweighted ILI	% Weighted ILI
201902	290	1253	1255	1326	576	336	4746	112342	4.2	4.4
201903	290	1279	1814	1285	470	287	5135	110846	4.6	5.1
201904	285	1388	2523	1438	524	322	6195	110611	5.6	6.4
201905	199	807	2271	926	387	186	4577	68144	6.7	7.6

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
201902	8	209	0	81	15	0	1	0	2	23	4654	700	15.04	642	58
201903	9	206	0	57	25	0	2	1	1	22	4823	1017	21.09	978	39
201904	6	119	0	34	20	0	3	0	1	22	5610	1384	24.67	1321	63
201905	7	102	0	28	26	0	3	1	0	16	3680	1202	32.66	1178	24

## 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	823	2 (0.2%)	2 (0.2%)	823	0 (0%)	2 (0.2%)	823	0 (0%)	0 (0%)
A(H1N1)pdm09	481	2 (0.4%)	2 (0.4%)	481	0 (0%)	2 (0.4%)	481	0 (0%)	0 (0%)
A(H3N2)	254	0 (0%)	0 (0%)	254	0 (0%)	0 (0%)	254	0 (0%)	0 (0%)
B/Victoria	34	0 (0%)	0 (0%)	34	0 (0%)	0 (0%)	34	0 (0%)	0 (0%)
B/Yamagata	54	0 (0%)	0 (0%)	54	0 (0%)	0 (0%)	54	0 (0%)	0 (0%)

### Antigenic & Genetic Characterization:

CDC has antigenically or genetically characterized 769 influenza viruses collected September 30, 2018 – February 2, 2019, and submitted by U.S. laboratories, including 450 influenza A(H1N1)pdm09 viruses, 239 influenza A(H3N2) viruses, and 80 influenza B viruses.

#### Influenza A Viruses

- A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 450 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. One hundred ninety-four A(H1N1)pdm09 viruses were antigenically characterized, and 191 (98.5%) 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 239 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=55), subclade 3C.2a1 (n=98) or clade 3C.3a (n=86). One hundred forty-five A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and 102 (70.3%) 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 reference virus representing the A(H3N2) component of 2018-19 Northern Hemisphere influenza vaccines. Forty-three viruses (29.7%) reacted poorly (at titers that were 8-fold or greater reduced compared with that of the homologous virus A/Singapore/INFIMH-16-0019/2016) and of those, 42 (97.7%) belonged to clade 3C.3a.

#### Influenza B Viruses

- B/Victoria:** Phylogenetic analysis of 30 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). Twenty-one B/Victoria lineage viruses were antigenically characterized and 15 (71.4%) were antigenically similar with ferret antisera raised against cell-propagated B/Colorado/06/2017-like V1A.1 reference virus. Six (28.6%) 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 50 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.