

Influenza Surveillance Report

www.infectiousdisease.dhh.la.gov

Week 47: 11/19/17-11/25/17

Influenza activity continues to increase in Louisiana. The majority of positive influenza specimens from the state public health laboratory are influenza A/H3. The most commonly reported other respiratory viruses are RSV and Rhino/Enterovirus.

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.

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.

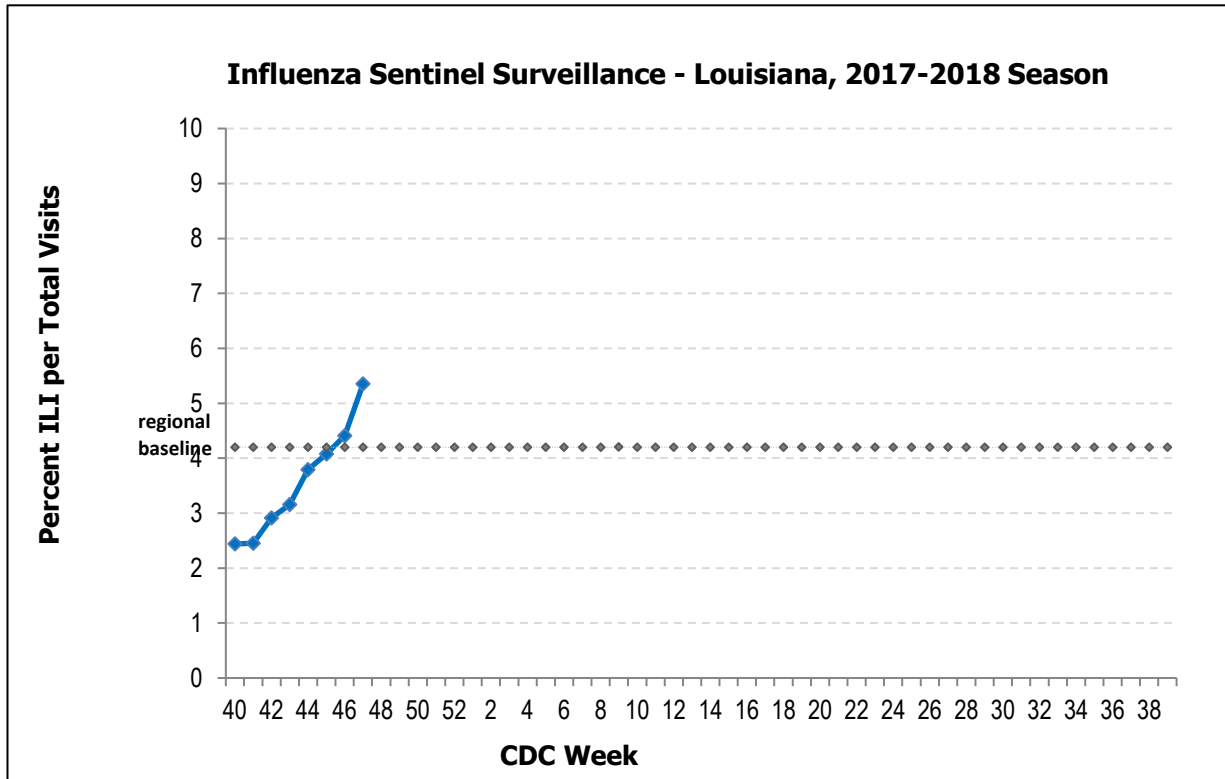


Laboratory testing: Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information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

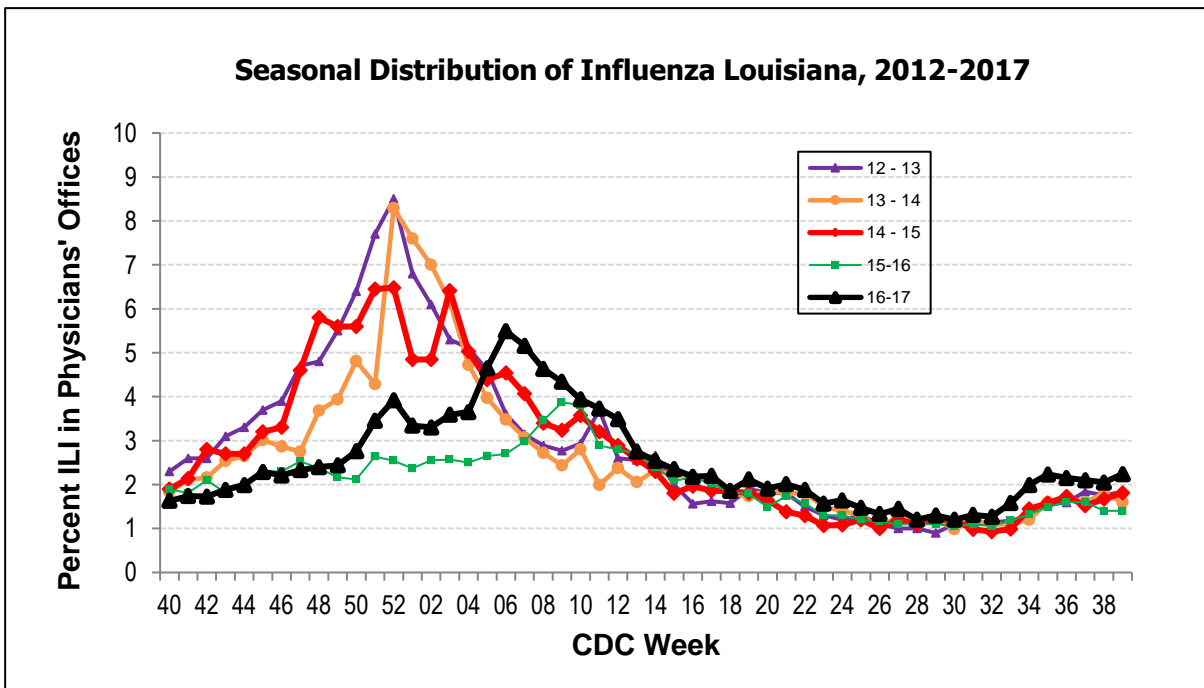
Page 2 : ILI Activity
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Page 5 & 6: Regional & National Data

2017-2018 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.

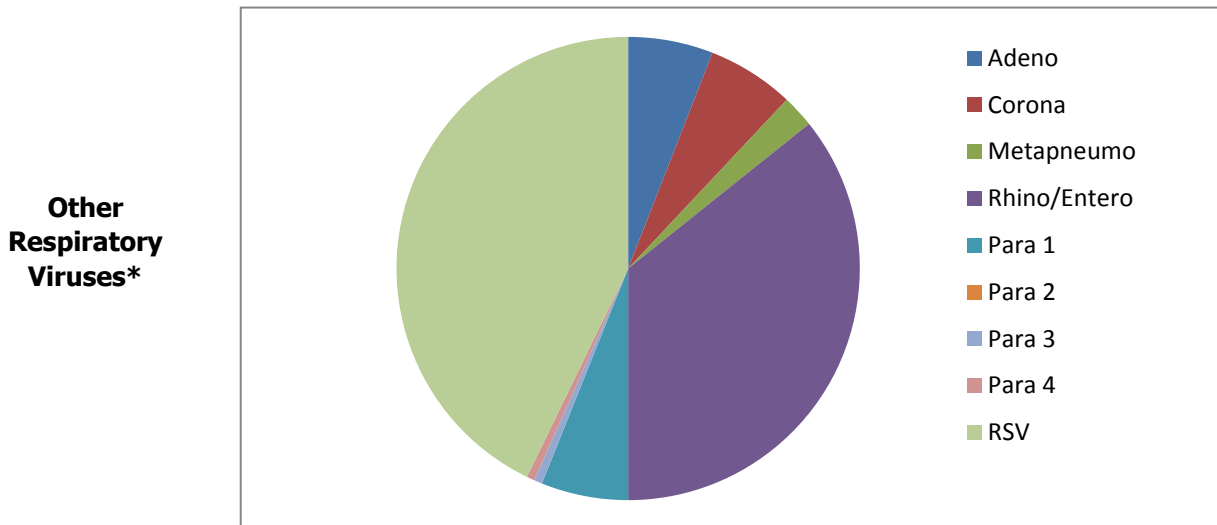
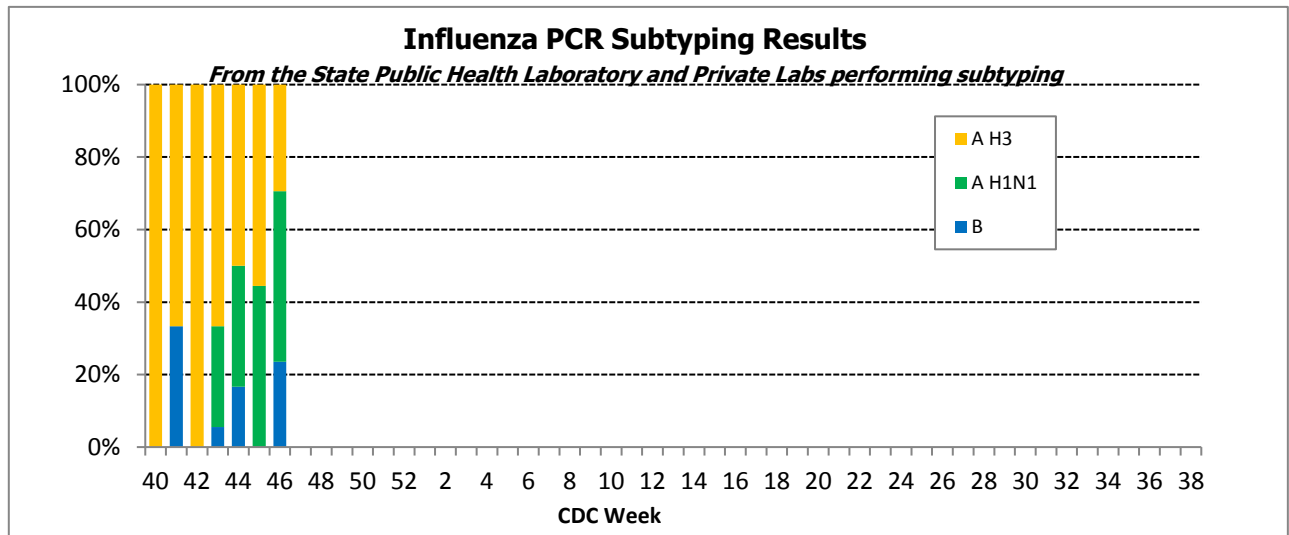
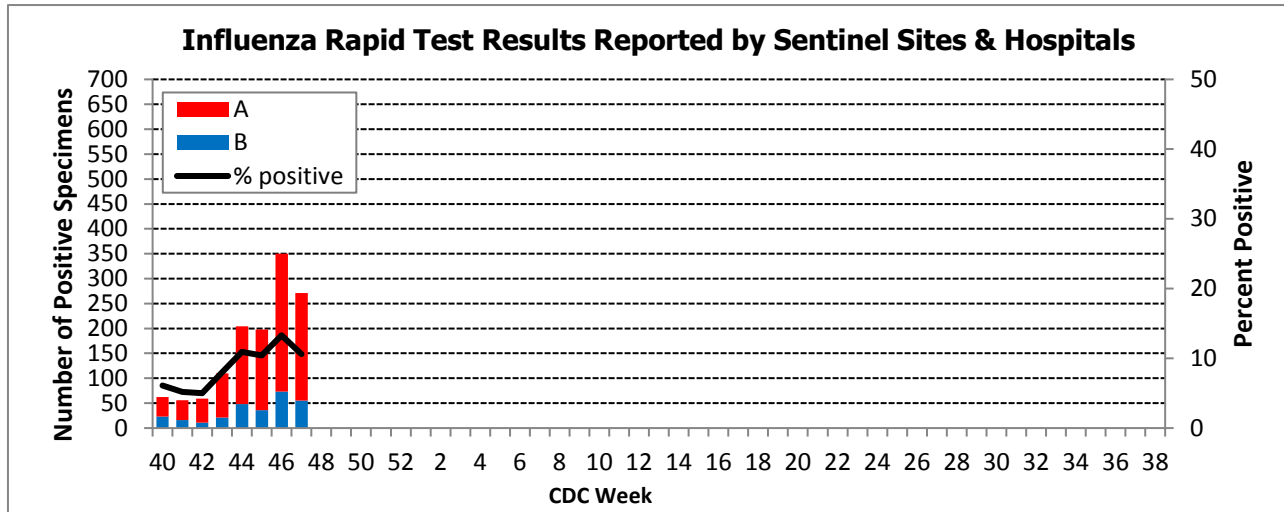


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.



2017-2018 Season

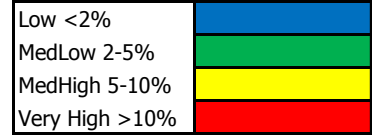
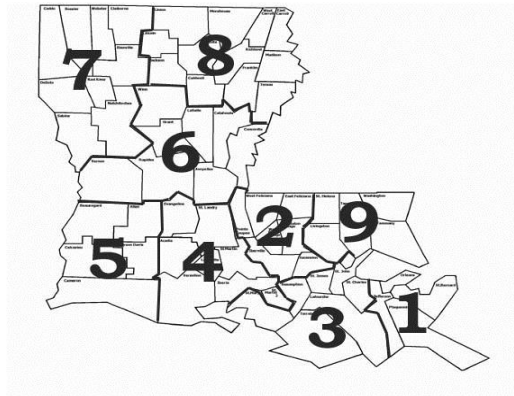
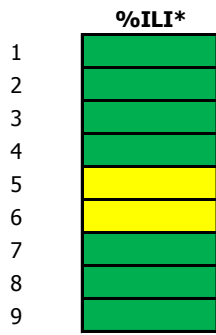
Virologic Surveillance



*Based on results from the State Public Health Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 4 weeks.

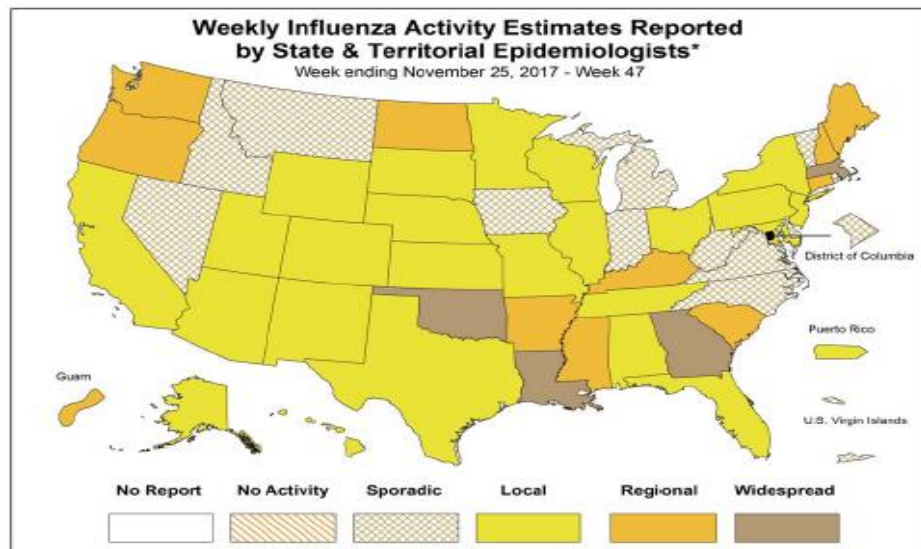
2017-2018 Season

Geographical Distribution of ILI



** %ILI over the last 4 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 2017-18 Influenza Season Week 47 ending Nov 25, 2017

ILINet Activity Indicator Map



2017-2018 Season

National Surveillance

During week 47, influenza activity increased in the United States.

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

No influenza-associated pediatric deaths were reported.

The proportion of outpatient visits for influenza-like illness (ILI) was 2.3%, which is above the national baseline of 2.2%.

Clinical Laboratory Data

	Week 47	Data Cumulative since October 1, 2017 (Week 40)
No. of specimens tested	14,626	135,202
No. of positive specimens (%)	1,051 (7.2%)	5,070 (3.7%)
<i>Positive specimens by type</i>		
Influenza A	795 (75.6%)	3,723 (73.4%)
Influenza B	256 (24.4%)	1,347 (26.6%)

Public Health Laboratory Data

	Week 47	Data Cumulative since October 1, 2017 (Week 40)
No. of specimens tested	642	8,778
No. of positive specimens*	210	1,970
<i>Positive specimens by type/subtype</i>		
Influenza A	186 (88.6%)	1,714 (87.0%)
(H1N1)pdm09	18 (9.7%)	169 (9.9%)
H3N2	168 (90.3%)	1,527 (89.1%)
Subtyping not performed	0 (0%)	18 (1.1%)
Influenza B	24 (11.4%)	255 (13.0%)
Yamagata lineage	20 (83.3%)	159 (62.4%)
Victoria lineage	0 (0%)	11 (4.3%)
Lineage not performed	4 (16.7%)	85 (33.3%)

HHS Surveillance Region Data:

**U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet) 2017-2018 Influenza Season
HHS Region 6 (AR, LA, NM, OK, and TX) (Baseline: 4.2%) Data as of Friday, December 1, 2017**

						ILI 65 years and older	Total ILI	Total Patient Visits	% Unweighted ILI	% Weighted ILI
CDC Week	# Sites Reporting	ILI 0-4 years	ILI 5-24 years	ILI 25-49 years	ILI 50-64 years					
201744	242	985	1098	570	239	190	3082	104384	3.0	2.9
201745	270	1118	1238	757	299	173	3585	109156	3.3	3.3
201746	269	1265	1523	901	370	244	4303	123441	3.5	4.0
201747	258	1321	1083	847	347	252	3850	91439	4.2	4.2

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

CDC Week	Public Health Labs	Public Health Specimens Tested	AUNK_POS	AH1N1 pdm09	AH3N2	AH3N2v	B	BVic	BYam	Clinical Labs	Clinical Specimens Tested	Clinical Flu Positive	% Positive	A	B
201744	7	97	0	5	23	0	3	0	2	26	3399	180	5.30	125	55
201745	8	103	0	7	35	0	1	0	0	25	2870	170	5.92	148	22
201746	8	169	0	18	30	0	6	1	4	23	3176	223	7.02	193	30
201747	7	36	0	8	7	0	1	0	1	18	2141	199	9.29	168	31

2017-2018 Season

Antiviral Resistance:

Neuraminidase Inhibitor Resistance Testing Results on Samples Collected Since October 1, 2017

	Oseltamivir		Zanamivir		Peramivir	
	Virus Samples tested (n)	Resistant Viruses, Number (%)	Virus Samples tested (n)	Resistant Viruses, Number (%)	Virus Samples tested (n)	Resistant Viruses, Number (%)
Influenza A (H1N1)pdm09	38	0 (0.0)	37	0 (0.0)	38	0 (0.0)
Influenza A (H3N2)	186	0 (0.0)	186	0 (0.0)	164	0 (0.0)
Influenza B	46	0 (0.0)	46	0 (0.0)	46	0 (0.0)

Antigenic & Genetic Characterization:

CDC has antigenically or genetically characterized 244 influenza viruses collected during October 1 – November 25, 2017, and submitted by U.S. laboratories, including 33 influenza A(H1N1)pdm09 viruses, 166 influenza A(H3N2) viruses, and 45 influenza B viruses.

Influenza A Viruses

- A(H1N1)pdm09:** Phylogenetic analysis of the HA genes from 33 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. 13 A(H1N1)pdm09 viruses were antigenically characterized, and all were antigenically similar (analyzed using HI with ferret antisera) to the reference 6B.1 virus A/Michigan/45/2015, representing the recommended influenza A(H1N1)pdm09 reference virus for the 2017–18 Northern Hemisphere influenza vaccines.
- A(H3N2):** Phylogenetic analysis of the HA genes from 166 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=128) or subclade 3C.2a1 (n=38). 12 influenza A(H3N2) viruses were antigenically characterized, and 11 (92%) 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/Michigan/15/2014 (3C.2a), a cell propagated A/Hong Kong/4801/2014-like reference virus representing the A(H3N2) component of 2017–18 Northern Hemisphere influenza vaccines.

Influenza B Viruses

- B/Victoria:** Phylogenetic analysis of two B/Victoria-lineage viruses indicate that all HA genes belonged to genetic clade V1A, the same genetic clade as the vaccine reference virus, B/Brisbane/60/2008. However, a small number of viruses identified in 2017 had a 6-nucleotide deletion (encoding amino acids 162 and 163) in the HA (abbreviated as V1A-2Del). One (50%) of two B/Victoria lineage viruses were well-inhibited by ferret antisera raised against cell-propagated B/Brisbane/60/2008 reference virus, representing a recommended B virus component of 2017–18 Northern Hemisphere influenza vaccines. One 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/Brisbane/60/2008, and this virus had the two amino acid deletion in the HA of the V1A-2Del viruses.
- B/Yamagata:** Phylogenetic analysis of 43 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 14 influenza B/Yamagata-lineage viruses were antigenically characterized, and all were antigenically similar to cell propagated B/Phuket/3073/2013, the reference vaccine virus representing the influenza B/Yamagata-lineage component of the 2017–18 Northern Hemisphere quadrivalent vaccines.