

Influenza Surveillance Report

www.infectiousdisease.dhh.louisiana.gov

Week 41: 10/8/17-10/14/17

Influenza activity remains low in Louisiana. The most commonly reported other respiratory viruses are 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.

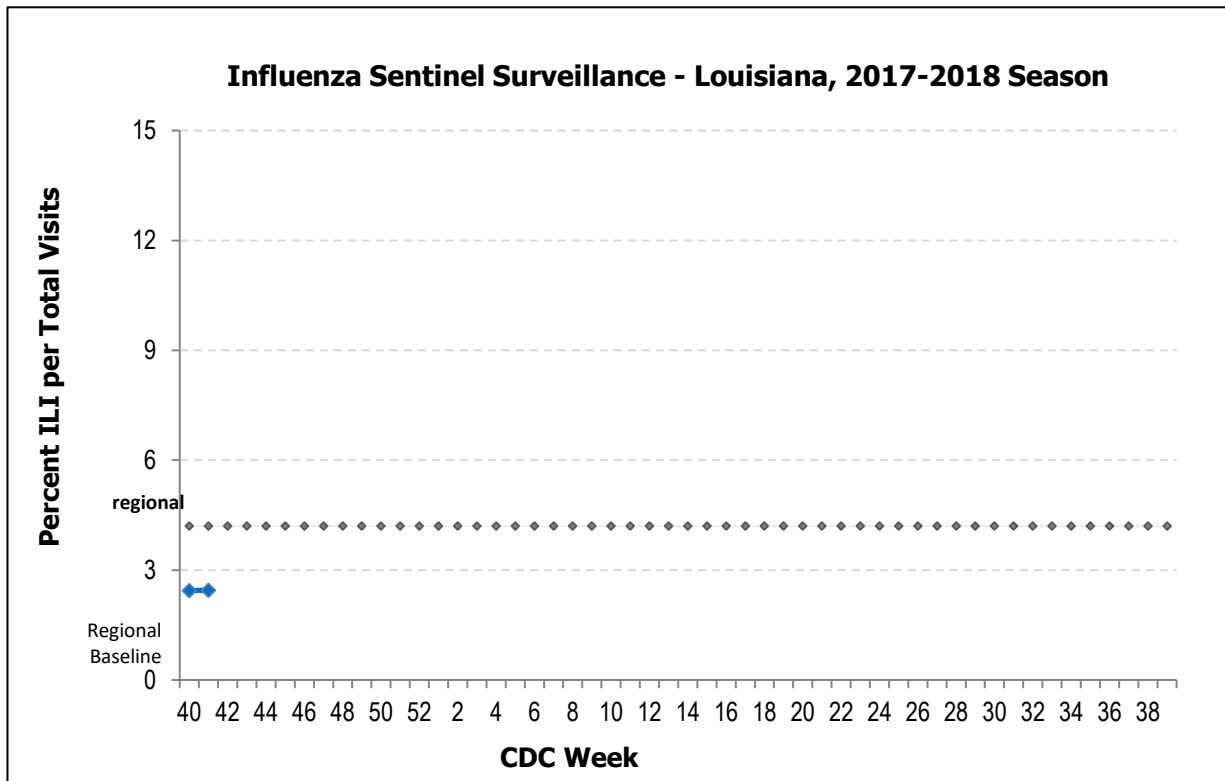


Laboratory testing: Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information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

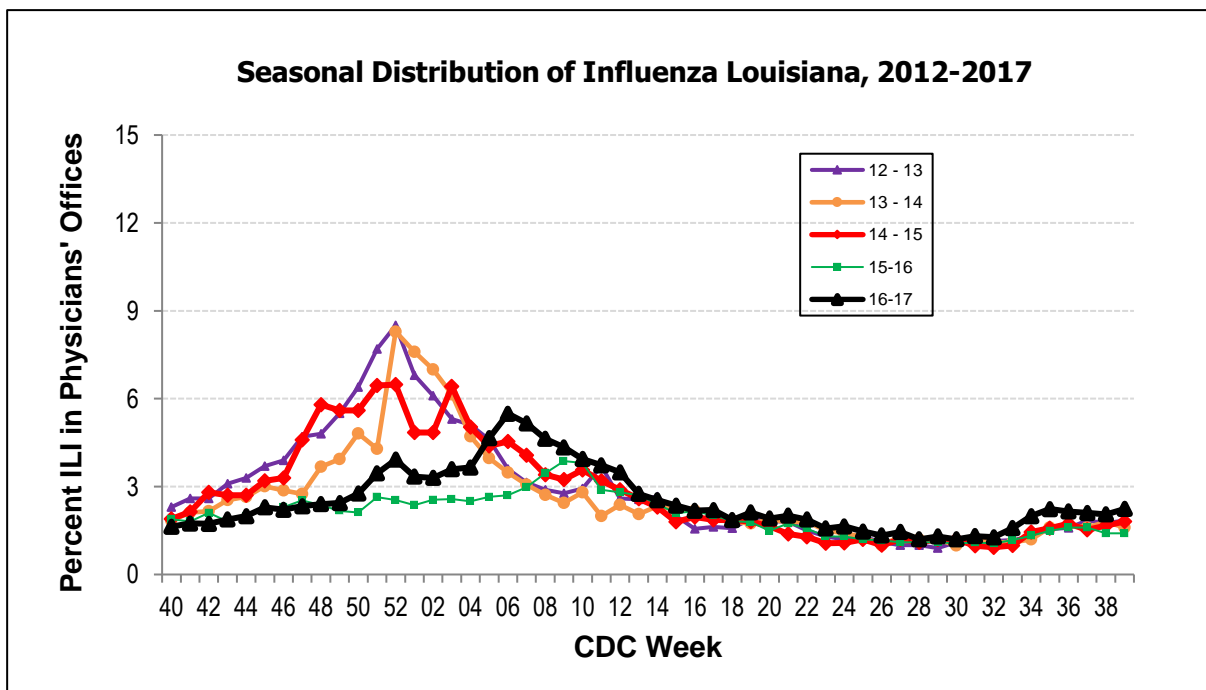
Page 2 : ILI Activity
Page 3: Virologic Surveillance
Page 4: Geographic Distribution
Page 5&6: Regional & National Data

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.

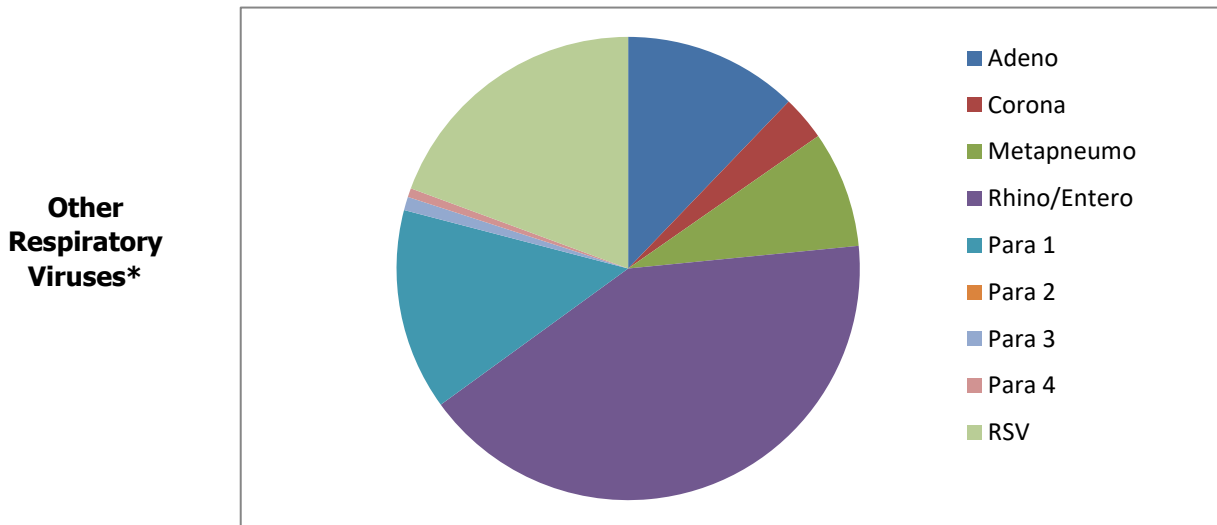
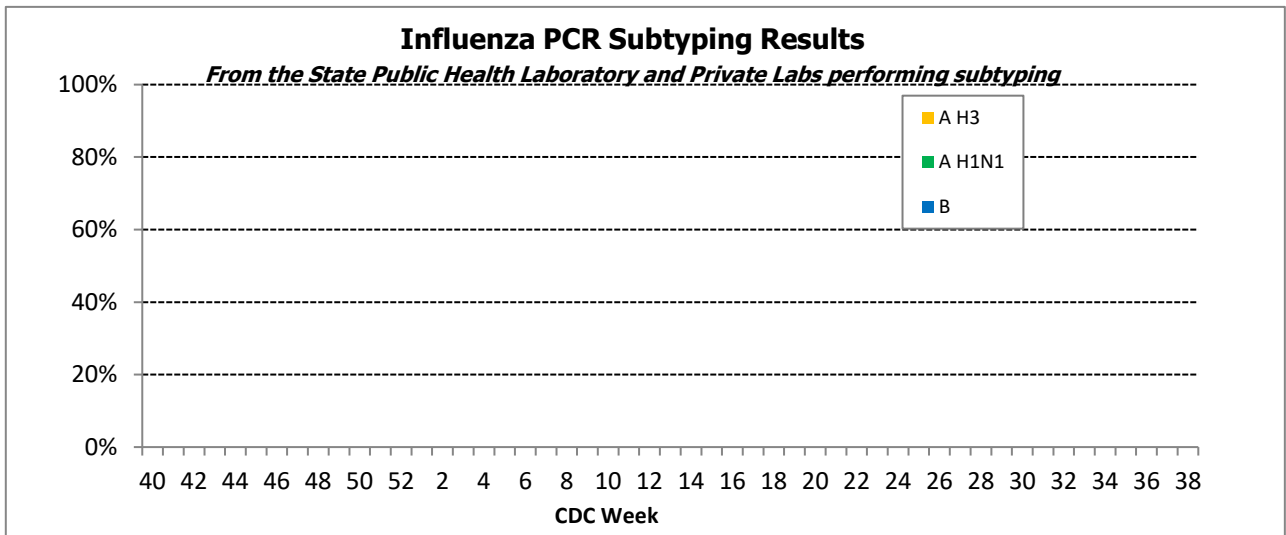
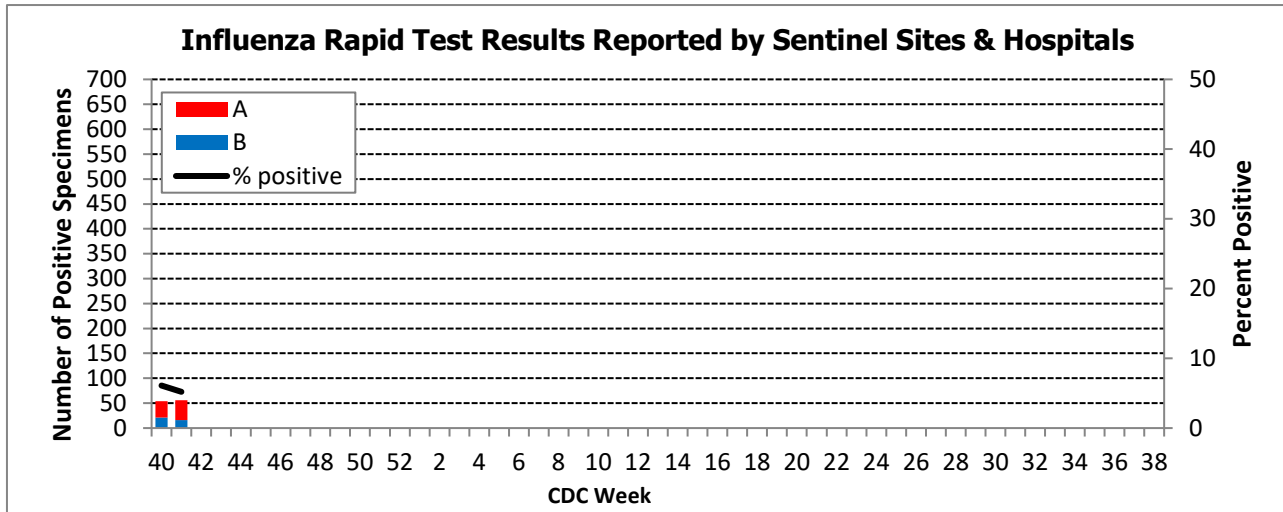


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.



2017-2018 Season

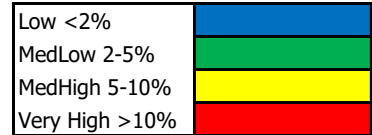
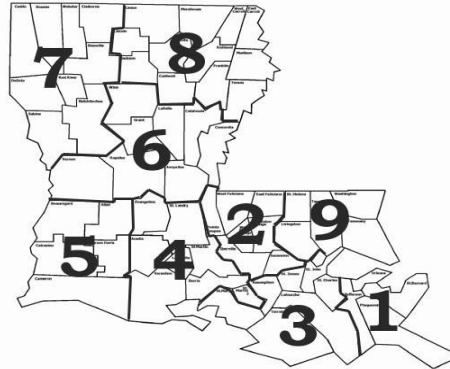
Virologic Surveillance



*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.

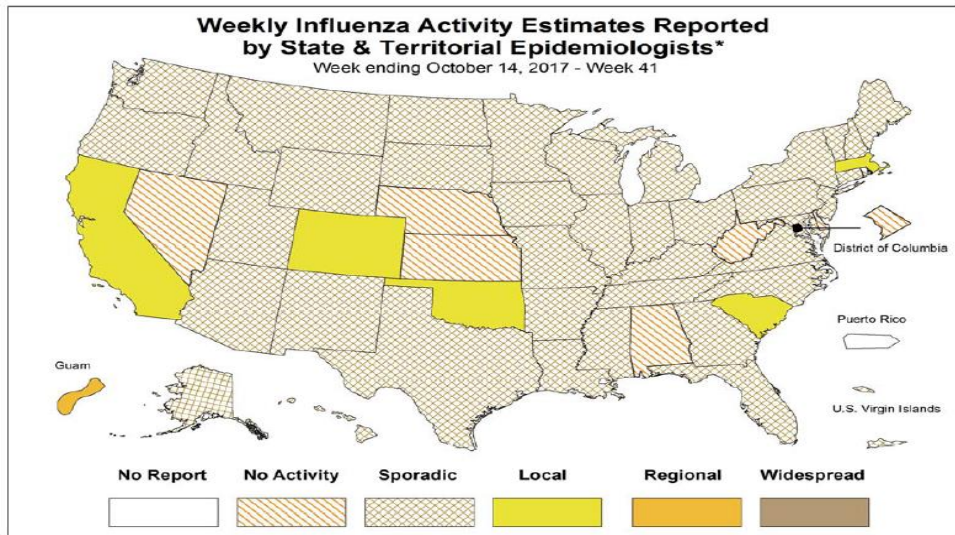
2017-2018 Season

Geographical Distribution of ILI



* %ILI over the last 4 weeks based on sentinel surveillance data

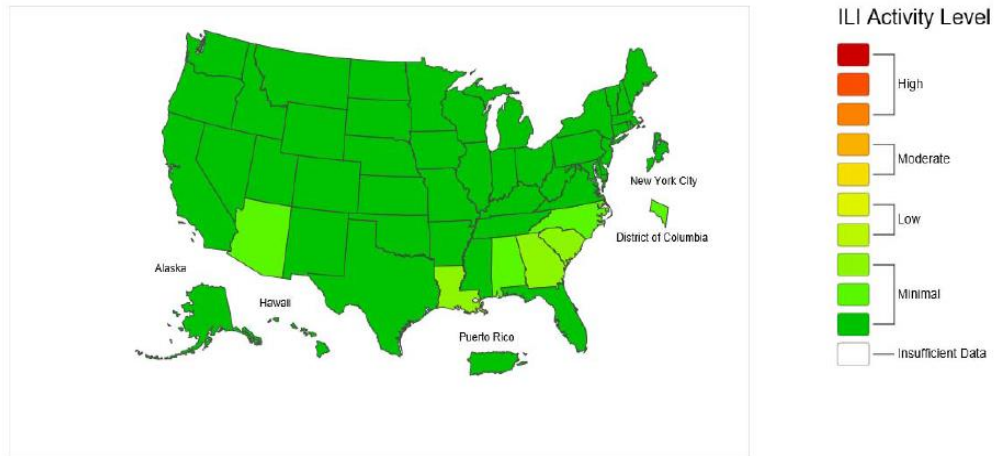
Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists



* 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 2017-18 Influenza Season Week 41 ending Oct 14, 2017

ILINet Activity Indicator Map



2017-2018 Season

National Surveillance

During week 41, influenza activity was low 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 1.3%, which is below the national baseline of 2.2%.

Clinical Laboratory Data

	Week 41	Cumulative
Specimens tested	12,290	25,777
Positive specimens	270 (2.2%)	596 (2.3%)
<i>Positive specimens by type</i>		
Influenza A	185 (68.5%)	404 (67.8%)
Influenza B	85 (31.5%)	192 (32.2%)

Public Health Laboratory Data

	Week 41	Cumulative
Specimens tested	504	1,142
Positive specimens	96	213
<i>Positive specimens by type/subtype</i>		
Influenza A	82 (85.4%)	185 (86.9%)
A (2009 H1N1)	3 (3.7%)	14 (7.6%)
A (H3)	67 (81.7%)	158 (85.4%)
A (subtyping not performed)	12 (14.6%)	13 (7.0%)
Influenza B	10 (14.6%)	28 (13.1%)
Yamagata lineage	6 (42.9%)	14 (50.0%)
Victoria lineage	1 (7.1%)	1 (3.6%)
Lineage not performed	7 (50.0%.%)	13 (46.4%)

HHS Surveillance Region Data:

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
201740	8	65	0	0	4	0	0	0	0	23	2166	68	3.14	47	21
201741	6	65	0	0	10	0	1	0	1	20	1925	47	2.44	34	13
Total	0	130	0	0	14	0	1	0	1	.	4091	115	2.81	81	34

**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, October 20, 2017**

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
201740	271	705	705	385	176	126	2097	108415	1.9	1.9
201741	242	746	662	462	156	137	2163	96742	2.2	2.2
<i>Totals</i>							4260	205157		

2017-2018 Season

Antiviral Resistance: No antiviral resistance data are available for specimens collected after 10/1/17.

Antigenic Characterization:

During May 21 – October 14, 2017, 1,898 influenza positive specimens were collected and reported by public health laboratories in the United States (Figure, left). CDC genetically characterized 390 influenza viruses [52 influenza A(H1N1)pdm09, 232 influenza A(H3N2), and 106 influenza B viruses] collected by U.S. laboratories.

Influenza A Viruses

- **A(H1N1)pdm09 [52]:** The HA gene segment of all influenza A(H1N1)pdm09 viruses analyzed showed that one virus belonged to clade 6B, with the remainder belonging to 6B.1, the same genetic clade as the vaccine reference virus, A/Michigan/45/2015.
- **A(H3N2) [232]:** Phylogenetic analysis of the HA genes indicate that multiple clades/subclades are circulating. The HA genes show extensive diversity and belong to clades 3C.2a, subclade 3C.2a1 or 3C.3a, with 3C.2a predominating. The vaccine reference virus, A/Hong Kong/4801/2014, belongs to the genetic clade 3C.2a.

Influenza B Viruses

- **B/Victoria [31]:** The HA of influenza B/Victoria-lineage viruses all belonged to genetic group V1A, the same genetic clade as the vaccine reference virus, B/Brisbane/60/2008.
 - Two subgroups of viruses within V1A have been detected with a double or triple deletion of amino acids in the HA. The majority of the double deletion viruses were identified in the United States, while no triple deletion viruses have been identified in the United States.
- **B/Yamagata [75]:** The HA of influenza B/Yamagata-lineage viruses analyzed all belonged to genetic group Y3, the same genetic clade as the vaccine reference virus, B/Phuket/3073/2013.