Influenza Surveillance Report

www.infectiousdisease.dhh.la.gov   **Week 52: 12/24/17-12/30/17**

Influenza activity continues to increase in Louisiana. Influenza A viruses represent 85% of positive samples tested at the State Laboratory (71% A/H3N2, 29% A/H1N1). The most commonly reported other respiratory viruses are Rhino/Enterovirus, RSV, and Coronavirus.

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.

Tracking Surveillance

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.
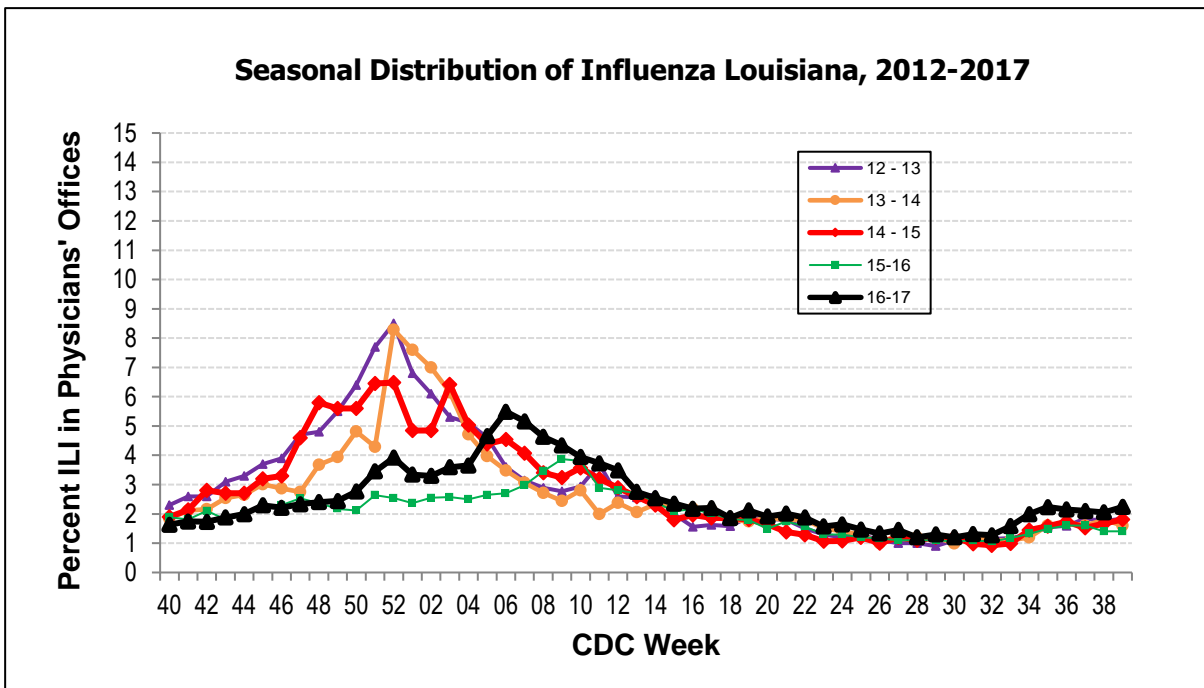
2017-2018 Season

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.

Influenza Sentinel Surveillance - Louisiana, 2017-2018 Season
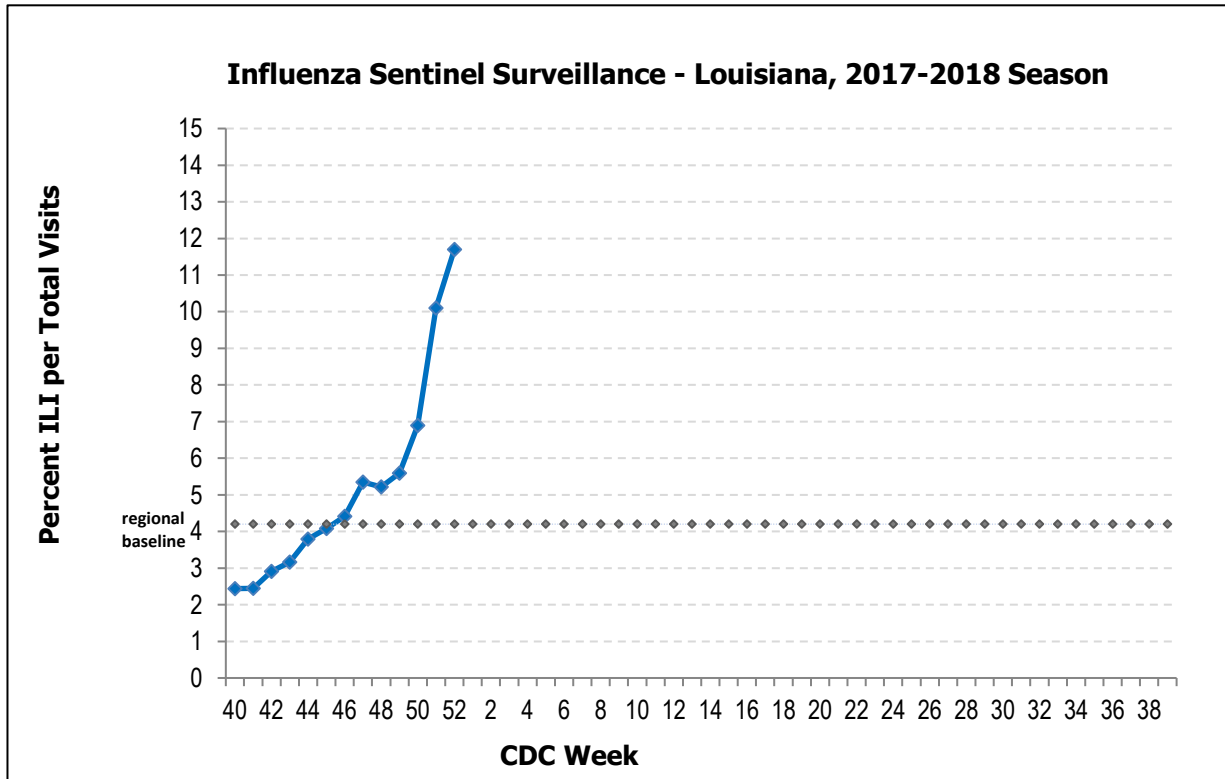
This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.

Seasonal Distribution of Influenza Louisiana, 2012-2017

2017-2018 Season

Virologic Surveillance

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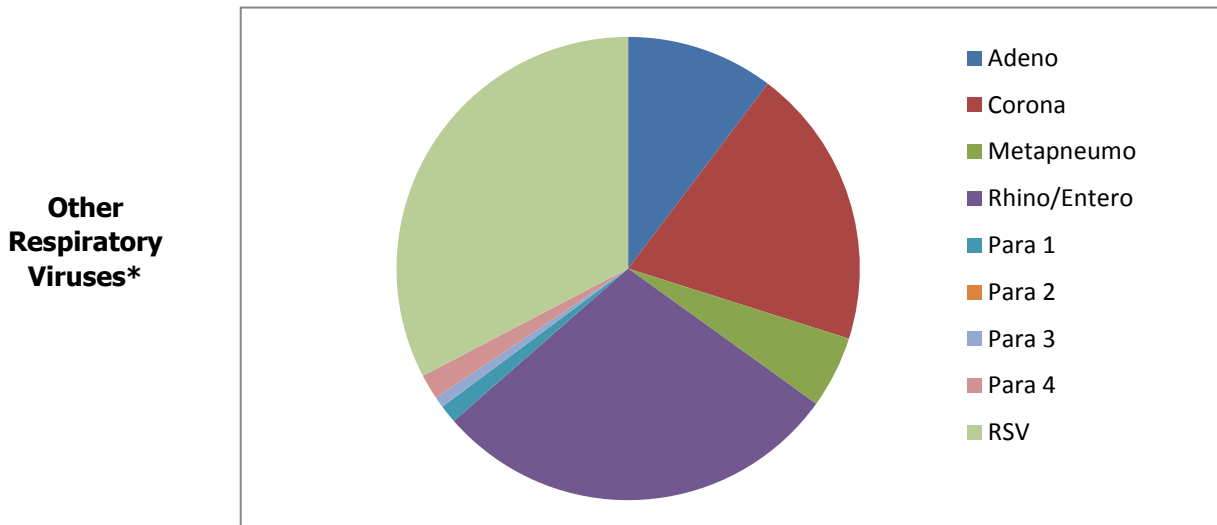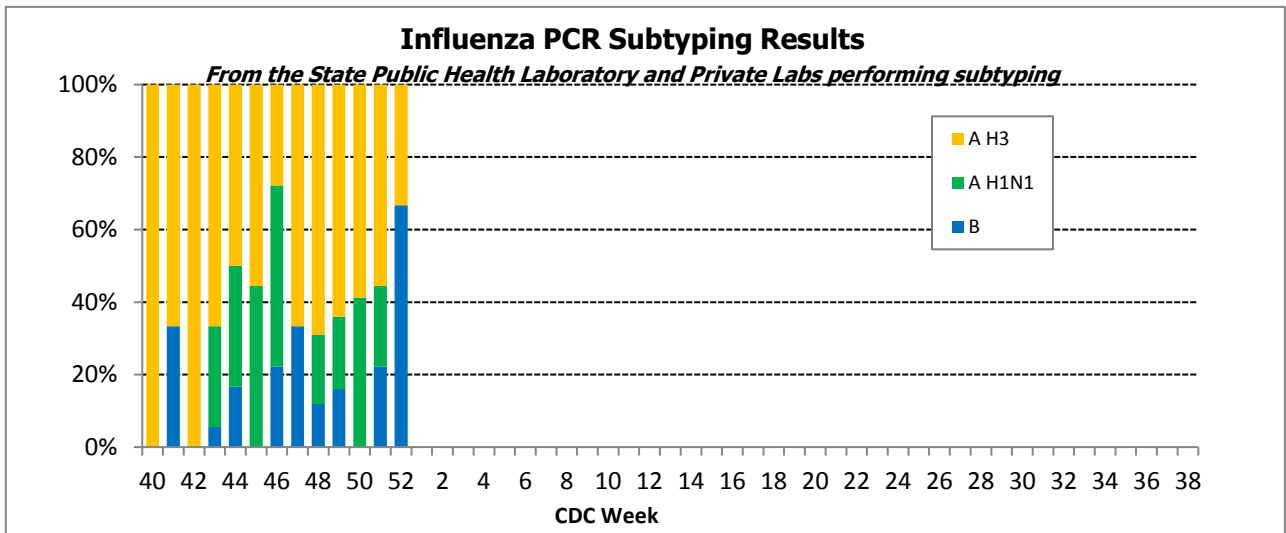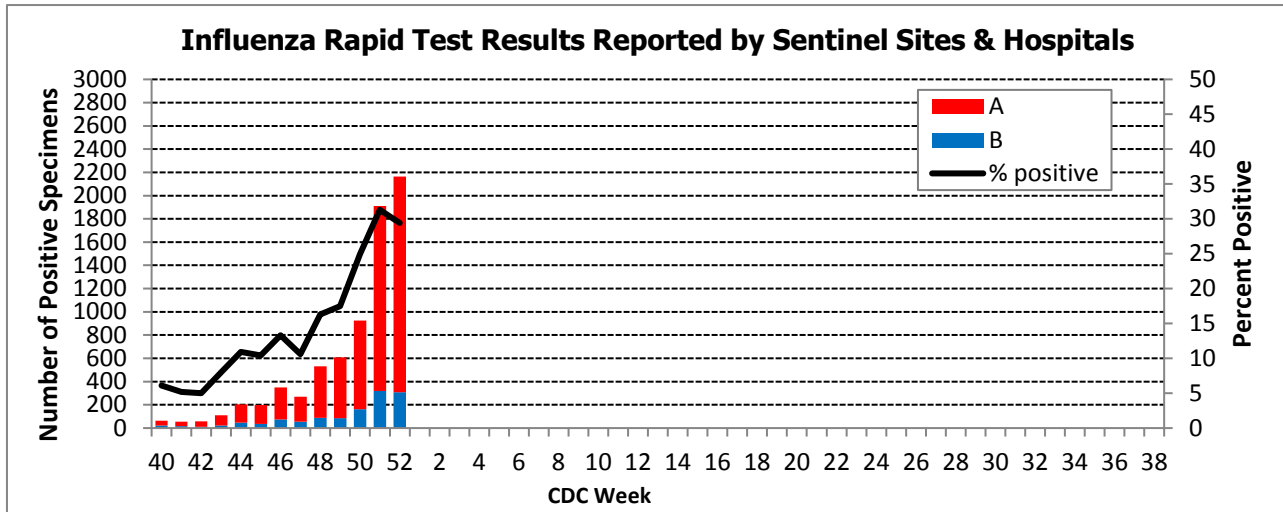
*Based on results from the State Public Heatlh Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 2 weeks.

Geographical Distribution of ILI

%ILI*

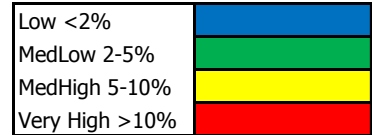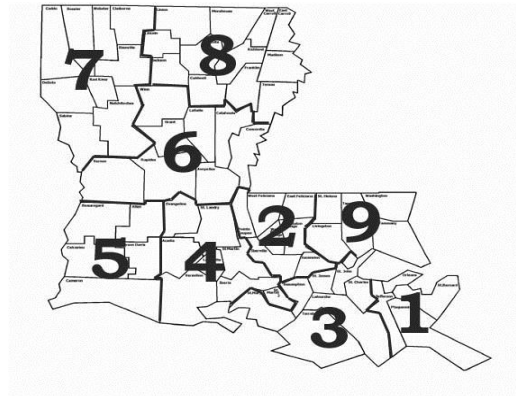|	
1	(yellow)
2	(yellow)
3	(yellow)
4	(red)
5	(red)
6	(red)
7	(red)
8	(yellow)
9	(red)

Low <2%	(blue)
MedLow 2-5%	(green)
MedHigh 5-10%	(yellow)
Very High >10%	(red)

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

Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists

Weekly Influenza Activity Estimates Reported by State & Territorial Epidemiologists*
Week ending December 30, 2017 – Week 52

No Report   No Activity   Sporadic   Local   Regional   Widespread
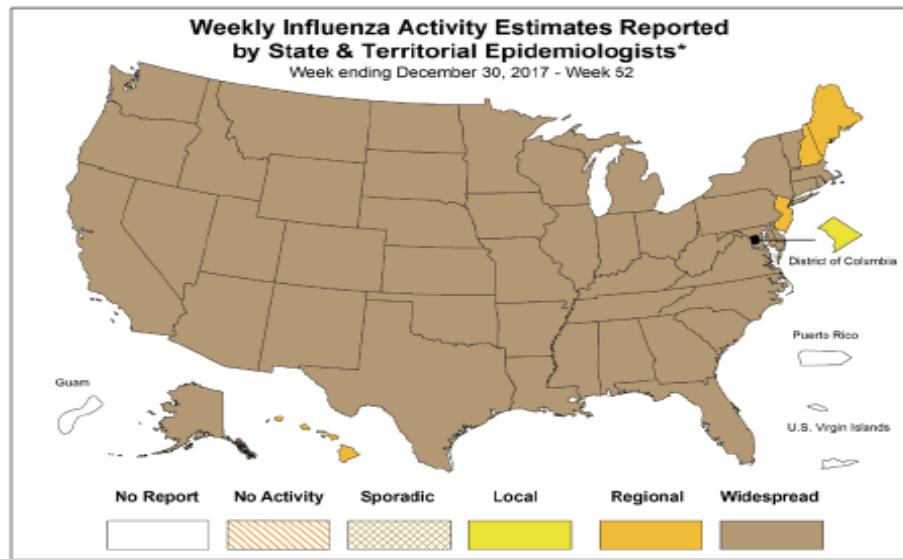
*   This map indicates geographic spread & does not measure the severity of influenza activity

ILINet Activity Indicator Map

Influenza-Like Illness (ILI) Activity Level Indicator Determined by Data Reported to ILINet
2017-18 Influenza Season Week 52 ending Dec 30, 2017

ILI Activity Level
High
Moderate
Low
Minimal
Insufficient Data

National Surveillance

During week 52, influenza activity increased sharply in the United States.

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

One influenza-associated pediatric death was reported.

The proportion of outpatient visits for influenza-like illness (ILI) was 5.8%, which is above the national baseline of 2.2%.

Clinical Laboratory Data

	Week 52	Data Cumulative since October 1, 2017 (Week 40)
No. of specimens tested	36,226	311,593
No. of positive specimens (%)	9,228 (25.5%)	32,826 (10.5%)
Positive specimens by type		
Influenza A	7,818 (84.7%)	27,241 (83.0%)
Influenza B	1,410 (15.3%)	5,585 (17.0%)

Public Health Laboratory Data

	Week 52	Data Cumulative since October 1, 2017 (Week 40)
No. of specimens tested	1,801	22,827
No. of positive specimens*	923	8,893
Positive specimens by type/subtype		
Influenza A	784 (84.9%)	7,754 (87.2%)
(H1N1)pdm09	60 (7.7%)	644 (8.3%)
H3N2	682 (87.0%)	7,012 (90.4%)
Subtyping not performed	42 (5.4%)	98 (1.3%)
Influenza B	139 (15.1%)	1,139 (12.8%)
Yamagata lineage	81 (58.3%)	748 (65.7%)
Victoria lineage	9 (6.5%)	76 (6.7%)
Lineage not performed	49 (35.3%)	315 (27.7%)

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, January 5, 2018

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
201749	273	1258	1616	1143	496	329	4842	107244	4.5	5.2
201750	269	1656	2776	1876	785	491	7584	114132	6.6	8.1
201751	253	2135	3762	2936	1315	765	10913	115358	9.5	12.1
201752	190	2258	2200	2356	1014	745	8573	85890	10.0	11.3

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

CDC Week	Public Health Labs	Public Health Specimens Tested	AUNK	AH1N1pdm09	AH3N2	AH3N2v	B	BVic	BYam	Clinical Labs	Clinical Specimens Tested	Clinical Flu Positive	% Positive	A	B
201749	8	159	3	11	43	0	6	0	2	24	4062	573	14.11	472	101
201750	9	198	1	20	47	0	1	0	11	24	4552	988	21.70	907	81
201751	9	217	1	14	106	0	12	0	13	22	6379	1957	30.68	1802	155
201752	5	44	0	0	16	0	3	0	9	15	5550	1869	33.68	1656	213

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	111	1 (0.9)	99	0 (0.0)	111	1 (0.9)
Influenza A (H3N2)	462	0 (0.0)	462	0 (0.0)	375	0 (0.0)
Influenza B	127	0 (0.0)	127	0 (0.0)	127	0 (0.0)

Antigenic & Genetic Charactization:

Influenza A Viruses

- **A(H1N1)pdm09:** Phylogenetic analysis of the HA genes from 100 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Sixty-seven 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 410 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=326), subclade 3C.2a1 (n=80) or clade 3C.3a (n=4). One hundred sixty one influenza A(H3N2) viruses were antigenically characterized, and 159 (99.2%) 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 20 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). Four (57.1%) 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. Three (42.9%) B/Victoria lineage viruses 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 these viruses had the V1A-2Del HA.

- **B/Yamagata:** Phylogenetic analysis of 156 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 71 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.