Influenza Surveillance Report

www.infectiousdisease.dhh.la.gov **Week 45: 11/4/18 - 11/10/18**

Influenza activity continues to increase in Louisiana. Influenza B remains the predominant positive rapid result being reported from clinical laboratories around the state. Rhino/Enteroviruses and RSV represent 68% 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.

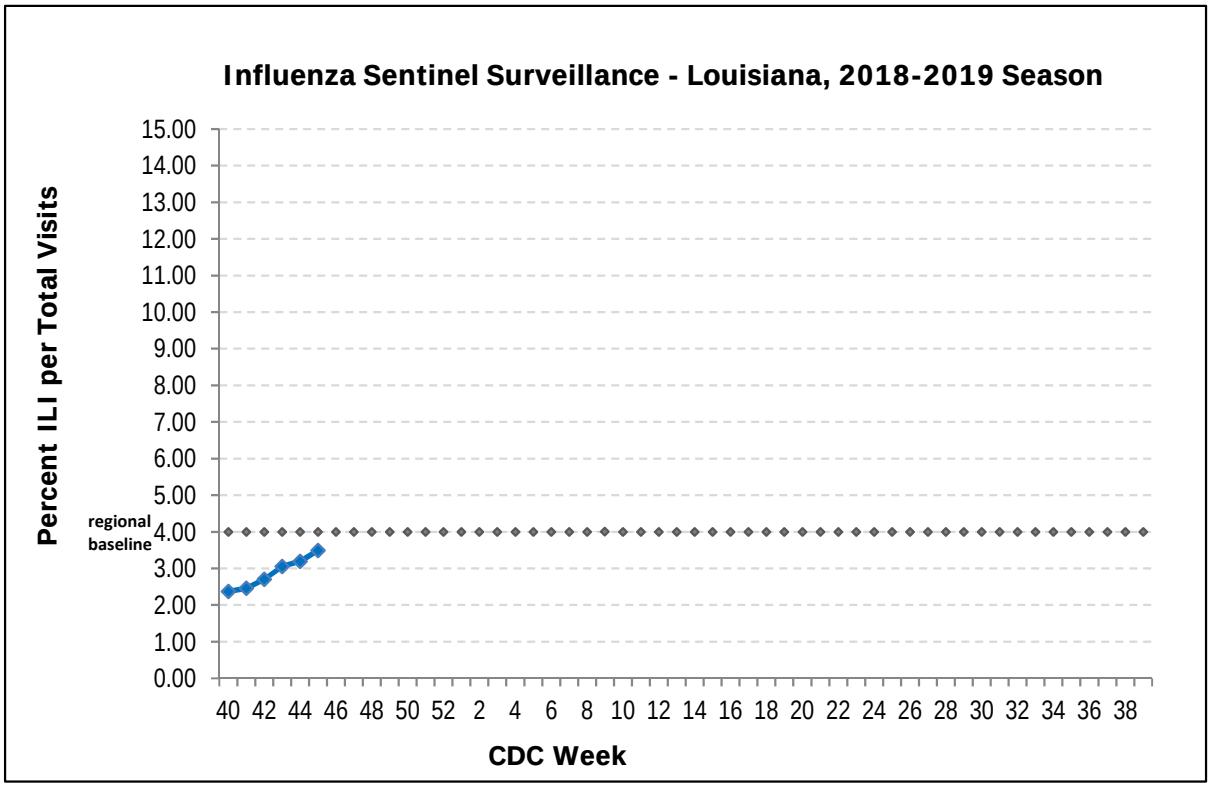
Taken together, ILI surveillance and laboratory surveillance provide a clear picture of the influenza activity occurring in Louisiana each week. If you have any questions about our surveillance system or would like more information, please contact Julie Hand at 504-568-8298 or julie.hand@la.gov.

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.

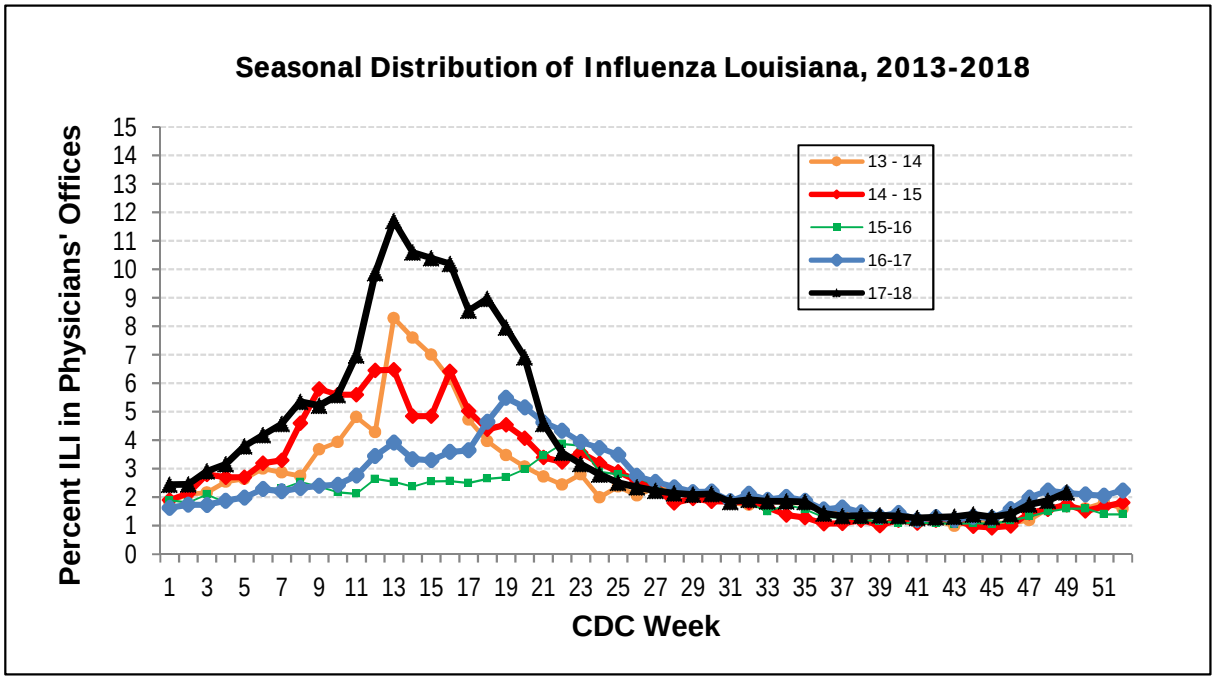
Laboratory testing: Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information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

2018-2019 Season

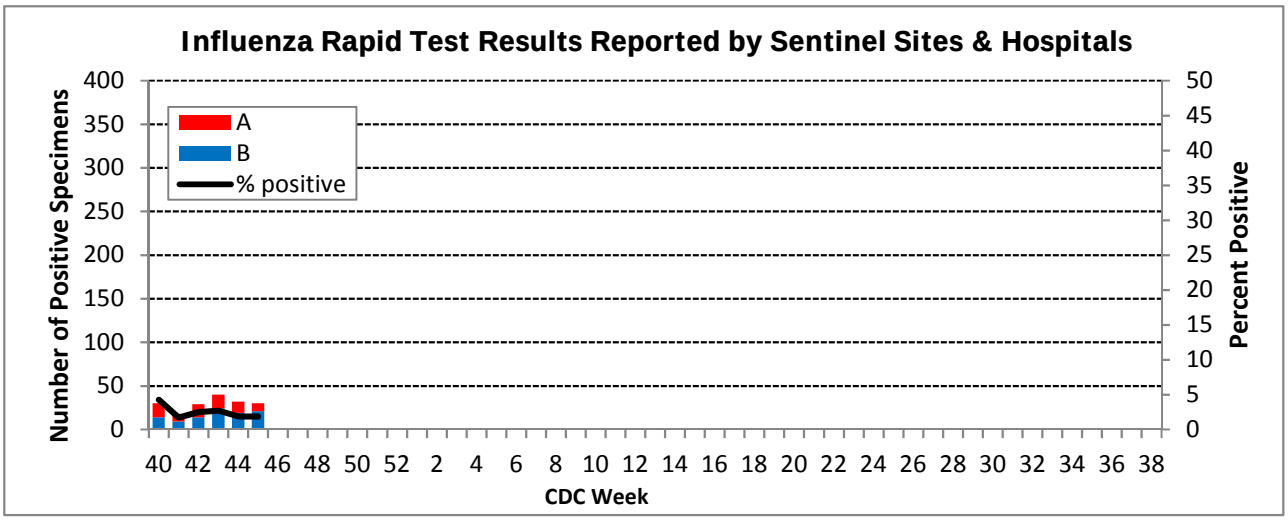
This graph shows the percentage of visits for ILI over the total number of visits for sentinel surveillance sites. This is the best approach to estimate the magnitude of influenza transmission. ILI counts do include some viral infections other than influenza, but experience over the last 50 years has 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.

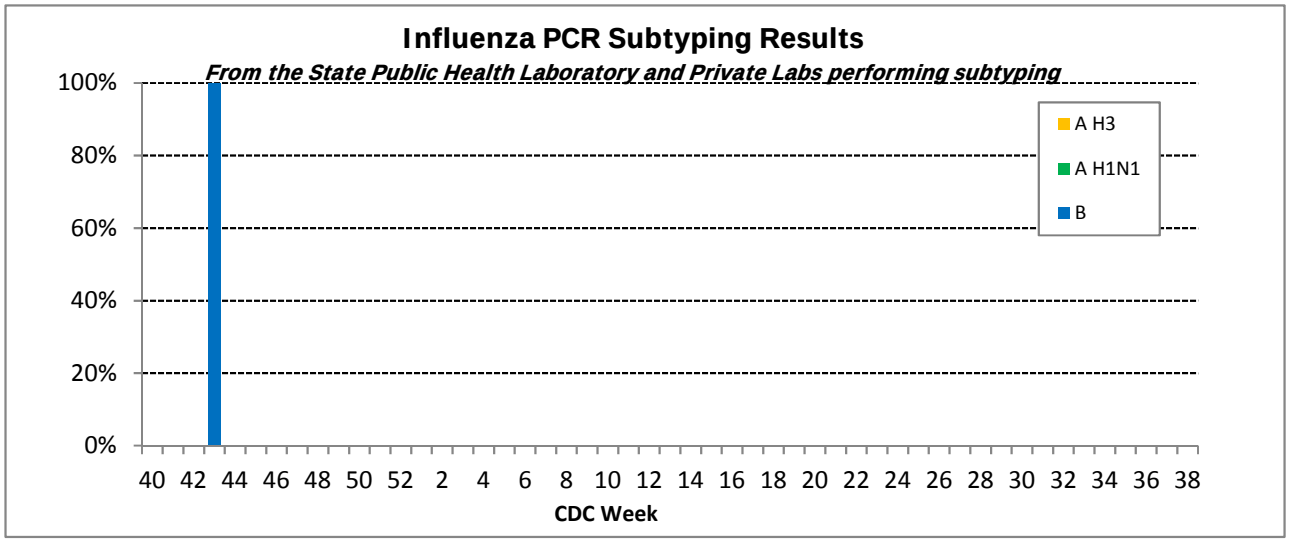


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.

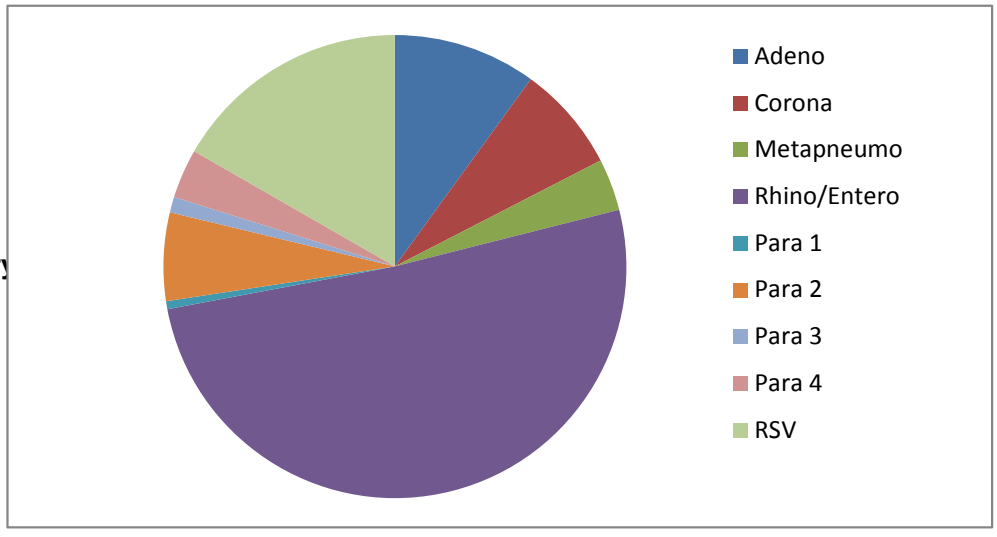


Virologic Surveillance





Other Respiratory Viruses*

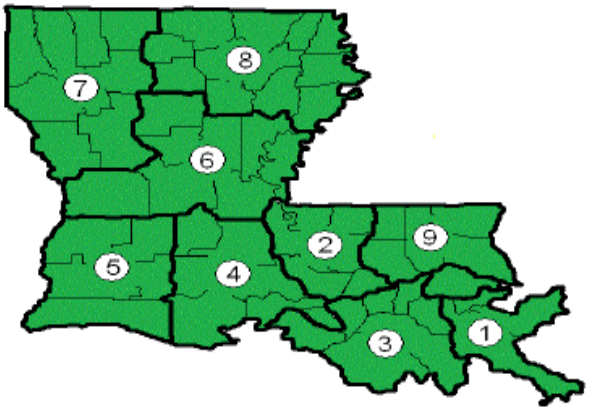


*Based on results from the State Public Heatlh Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 4 weeks.

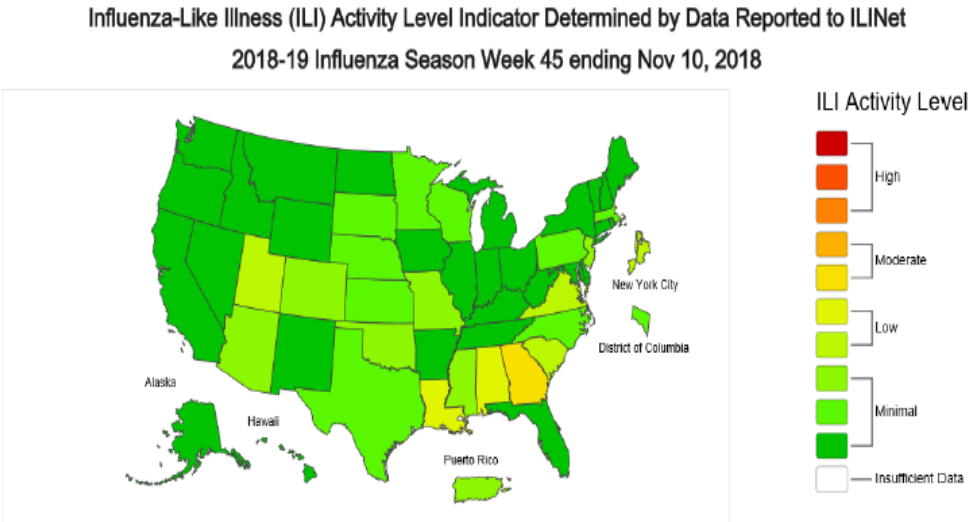
Geographical Distribution of ILI*

Low <2%	
MedLow 2-5%	
MedHigh 5-10%	
Very High >10%	

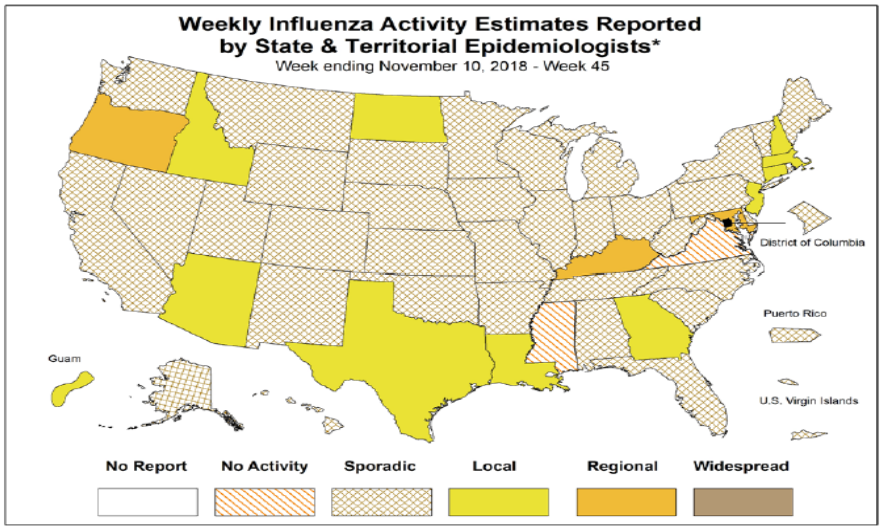
** %ILI over the last 4 weeks based on sentinel surveillance data*



Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists



ILINet Activity Indicator Map



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

National Surveillance

Influenza activity in the United States remains low, although small increases in activity were reported.

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 to CDC for week 45.

The proportion of outpatient visits for influenza-like illness (ILI) increased slightly to 1.9%, which is below the national baseline of 2.2%.

Clinical Laboratory Data

	Week 45	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	16,335	109,195
No. of positive specimens (%)	189 (1.2%)	2,063 (1.9%)
Positive specimens by type		
Influenza A	152 (80.4%)	1,600 (77.6%)
Influenza B	37 (19.6%)	463 (22.4%)

Public Health Laboratory Data

	Week 45	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	620	4,665
No. of positive specimens*	94	491
Positive specimens by type/subtype		
Influenza A	84 (89.4%)	413 (84.1%)
(H1N1)pdm09	57 (90.5%)	283 (78.2%)
H3N2	6 (9.5%)	79 (21.8%)
Subtyping not performed	21	51
Influenza B	10 (10.6%)	78 (15.9%)
Yamagata lineage	4 (57.1%)	45 (73.8%)
Victoria lineage	3 (42.9%)	16 (26.2%)
Lineage not performed	3	17

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: 4.0%) Data as of Friday, November 16, 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*
201842	290	741	787	536	184	138	2386	109749	2.2	2.1
201843	286	820	932	628	202	133	2715	113587	2.4	2.4
201844	280	1002	956	648	215	154	2975	112271	2.6	2.8
201845	276	1031	1075	668	212	158	3144	111966	2.8	2.8

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
201842	9	70	0	1	0	0	0	0	0	24	2250	37	1.64	19	18
201843	7	71	0	8	2	0	0	0	0	24	2436	33	1.35	19	14
201844	9	38	0	4	1	0	0	0	0	24	2849	50	1.76	29	21
201845	8	96	0	11	0	0	0	1	0	21	2761	44	1.59	29	15

Antiviral Resistance:

Antiviral Resistance: During May 20-November 10, 2018, 171 specimens (70 influenza A(H1N1)pdm09, 57 influenza A(H3N2), and 44 influenza B viruses) collected in the United States were tested for susceptibility to the neuraminidase inhibitors (oseltamivir, zanamivir, and peramivir). All tested viruses were sensitive to all three recommended antiviral medications.

While all of the recently circulating influenza viruses are susceptible to the neuraminidase inhibitor antiviral medications oseltamivir, zanamivir, and peramivir; rare sporadic instances of oseltamivir-resistant and peramivir-resistant influenza A(H1N1)pdm09 viruses and oseltamivir-resistant influenza A(H3N2) viruses have been detected worldwide. Antiviral treatment as early as possible is recommended for patients with confirmed or suspected influenza who have severe, complicated, or progressive illness; who require hospitalization; or who are at high risk for serious influenza-related complications. Additional information on recommendations for treatment and chemoprophylaxis of influenza virus infection with antiviral agents is available at: http://www.cdc.gov/flu/antivirals/index.htm.

Antigenic & Genetic Charactization:

Influenza A Viruses

- **A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 111 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Eighty-six A(H1N1)pdm09 viruses were antigenically characterized, and all 86 (100%) 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 79 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=28), subclade 3C.2a1 (n=48) or clade 3C.3a (n=3). Fifty-eight influenza A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and 53 (91.4%) 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 11 B/Victoria-lineage viruses indicate that all HA genes belonged to genetic clade V1A, however genetic subclades which are antigenically distinct have emerged. The majority of recent B/Victoria-lineage viruses belonged to a subclade of viruses with a 6-nucleotide deletion (encoding amino acids 162 and 163) in the HA (V1A.1, previously abbreviated as V1A-2Del). In addition, a small number of B/Victoria-lineage viruses have a three amino acid deletion (162-164) in the HA protein (abbreviated as V1A-3Del). Nine (81.8%) B/Victoria lineage viruses were well-inhibited by ferret antisera raised against cell-propagated B/Colorado/06/2017-like (V1A.1) reference virus, representing the B/Victoria lineage component of 2018-19 Northern Hemisphere influenza vaccines. Two (18.2%) 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/Colorado/06/2017-like reference virus, and belonged to clade V1A.

- **B/Yamagata:** Phylogenetic analysis of 44 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 39 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.