Influenza Surveillance Report

www.infectiousdisease.dhh.la.gov **Week 47: 11/18/18 - 11/24/18**

Influenza activity continues to increase in Louisiana. The amount of influenza A positives being reported from clinical laboratories around the state is increasing. Rhino/Enteroviruses and RSV represent the majority (65%) 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.

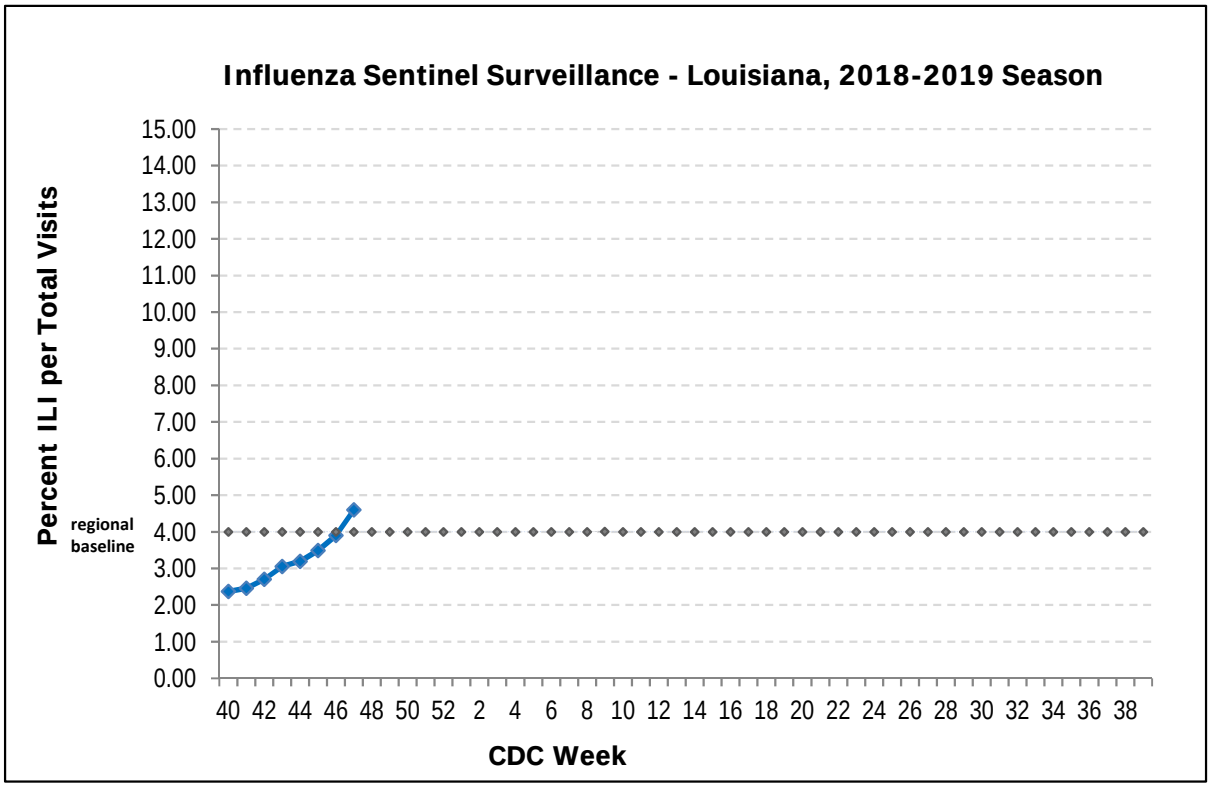
Taken together, ILI surveillance and laboratory surveillance provide a clear picture of the influenza activity occurring in Louisiana each week. If you have any questions about our surveillance system or would like more information, please contact Julie Hand at 504-568-8298 or julie.hand@la.gov.

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.

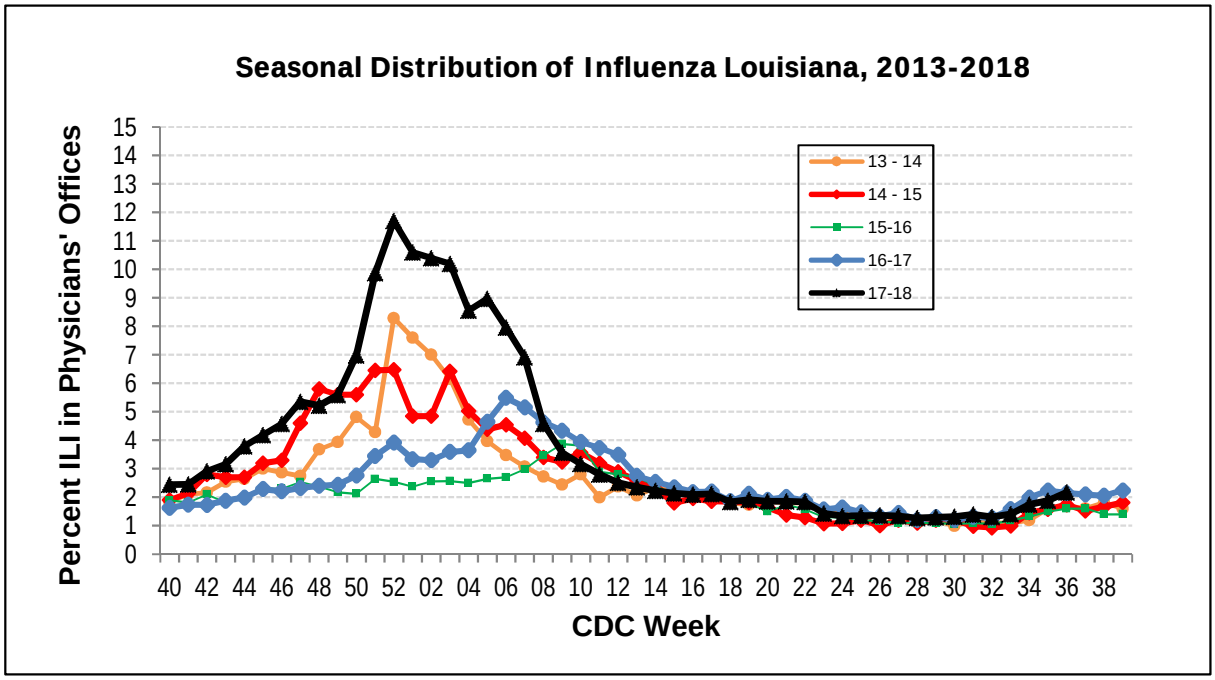
Laboratory testing: Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information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

2018-2019 Season

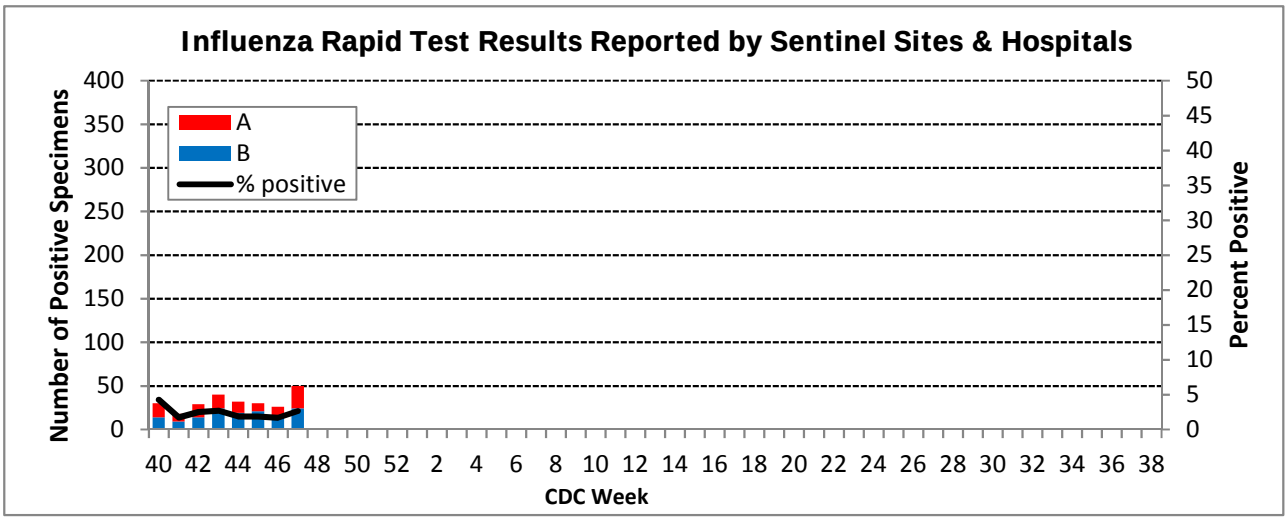
This graph shows the percentage of visits for ILI over the total number of visits for sentinel surveillance sites. This is the best approach to estimate the magnitude of influenza transmission. ILI counts do include some viral infections other than influenza, but experience over the last 50 years has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

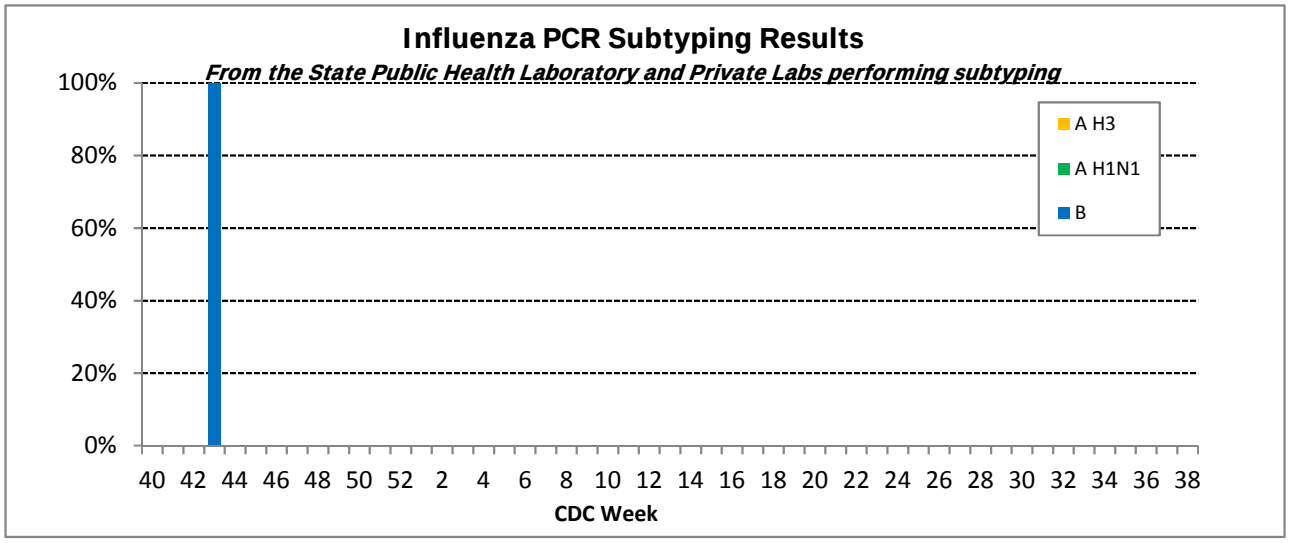


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.

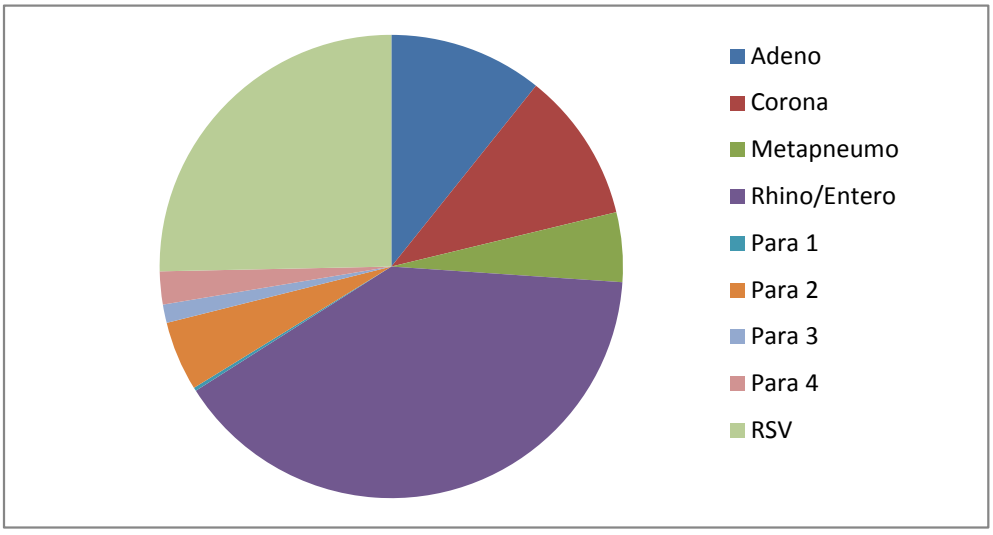


Virologic Surveillance





Other Respiratory Viruses*

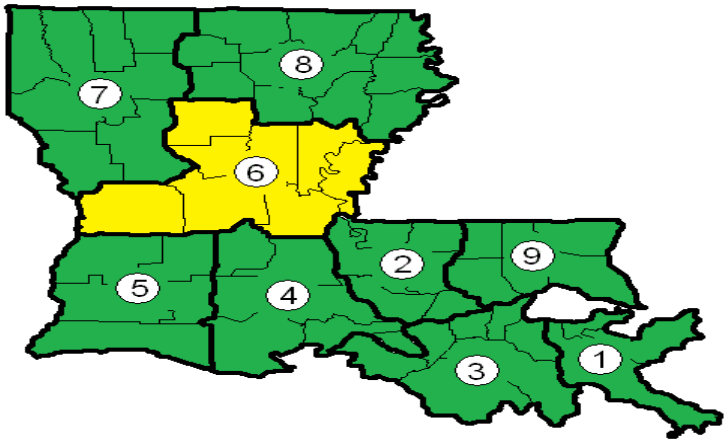


*Based on results from the State Public Heatlh Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 2 weeks.

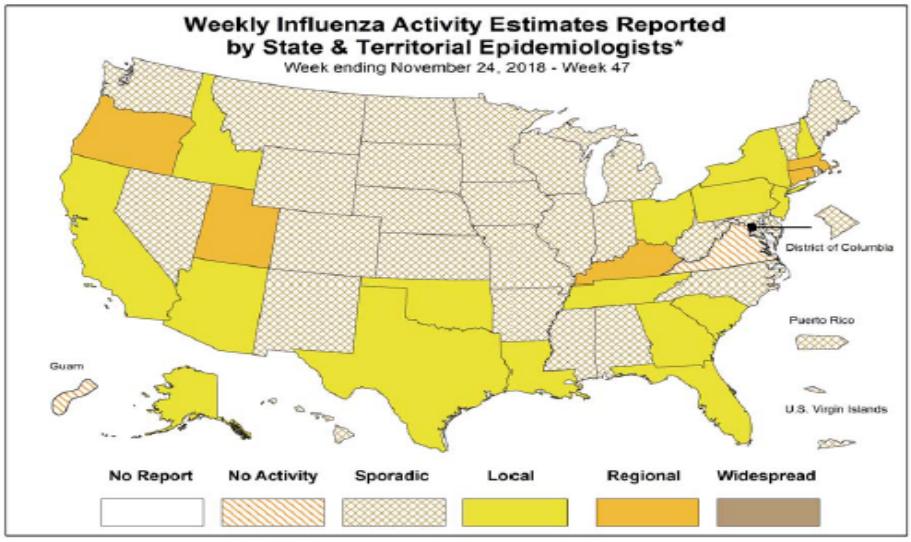
Geographical Distribution of ILI*

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

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

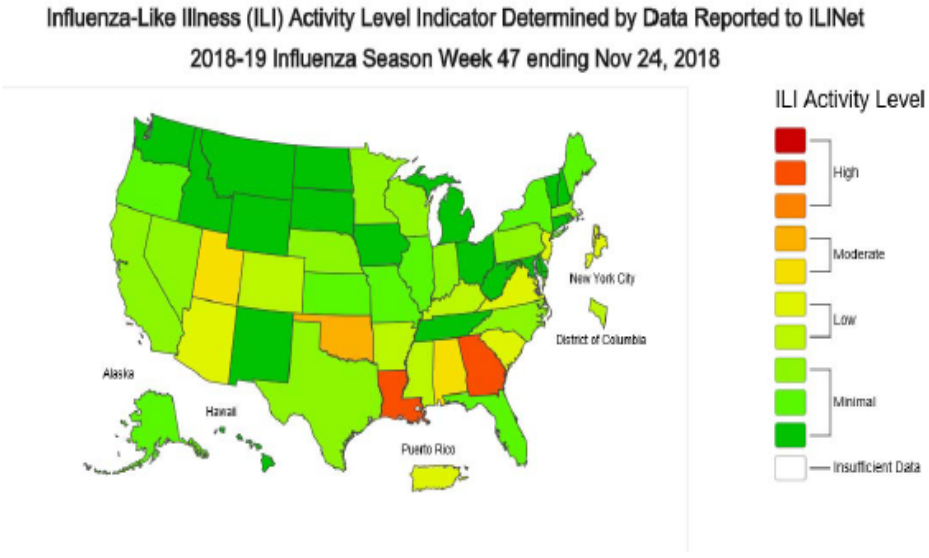


Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists



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

ILINet Activity Indicator Map



National Surveillance

Influenza activity in the United States increased slightly.

The proportion of outpatient visits for influenza-like illness (ILI) increased to 2.3%, 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.

Two influenza-associated pediatric deaths was reported to CDC for week 47.

Clinical Laboratory Data

	Week 47	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	16,648	153,017
No. of positive specimens (%)	397 (2.4%)	3,249 (2.1%)
Positive specimens by type		
Influenza A	372 (93.7%)	2,657 (81.8%)
Influenza B	25 (6.3%)	592 (18.2%)

Public Health Laboratory Data

	Week 47	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	374	6,567
No. of positive specimens*	88	776
Positive specimens by type/subtype		
Influenza A	84 (95.5%)	689 (88.8%)
(H1N1)pdm09	60 (83.3%)	497 (79.4%)
H3N2	12 (16.7%)	129 (20.6%)
Subtyping not performed	12	63
Influenza B	4 (4.5%)	87 (11.2%)
Yamagata lineage	3 (100%)	51 (75.0%)
Victoria lineage	0 (0%)	17 (25.0%)
Lineage not performed	1	19

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 30, 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
201844	285	1011	965	660	215	155	3006	113177	2.7	2.8
201845	288	1046	1093	682	218	162	3201	113737	2.8	2.9
201846	283	1245	1079	731	260	182	3497	109236	3.2	3.2
201847	268	1291	886	777	316	196	3466	96044	3.6	3.5

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
201844	9	60	0	4	3	0	0	0	0	24	2849	50	1.76	29	21
201845	8	124	0	12	0	0	0	1	0	24	3014	45	1.49	30	15
201846	7	68	0	8	2	0	0	0	0	22	2587	34	1.31	28	6
201847	3	15	0	2	3	0	0	0	0	21	2650	87	3.28	80	7

Antiviral Resistance:

Antiviral Resistance: During May 20-November 24, 2018, 173 specimens (72 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.

Antigenic & Genetic Charactization:

CDC has antigenically or genetically characterized 338 influenza viruses collected May 20, 2018 – November 24, 2018, and submitted by U.S. laboratories, including 166 influenza A(H1N1)pdm09 viruses, 106 influenza A(H3N2) viruses, and 66 influenza B viruses.

Influenza A Viruses

- **A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 166 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Eighty-eight A(H1N1)pdm09 viruses were antigenically characterized, and all 88 (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 106 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=41), subclade 3C.2a1 (n=61) or clade 3C.3a (n=4). Seventy influenza A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and 65 (92.9%) 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 14 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 (69.2%) 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. Four (30.8%) 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/Colorado/06/2017-like reference virus, and belonged to clade V1A.

- **B/Yamagata:** Phylogenetic analysis of 52 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 48 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.