Influenza Surveillance Report

Week 7: 2/10/19 - 2/16/19

Influenza activity continues to increase in Louisiana. Outbreaks continue to be reported from schools and long-term care facilities. More than 30% of influenza tests reported by clinical labs are positive. Influenza A/H1N1 remains the dominant virus subtyped at the state public health laboratory overall but influenza A/H3 activity continues to increase. Rhino/Enteroviruses and Coronaviruses represent the majority 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.

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.

2018-2019 Season

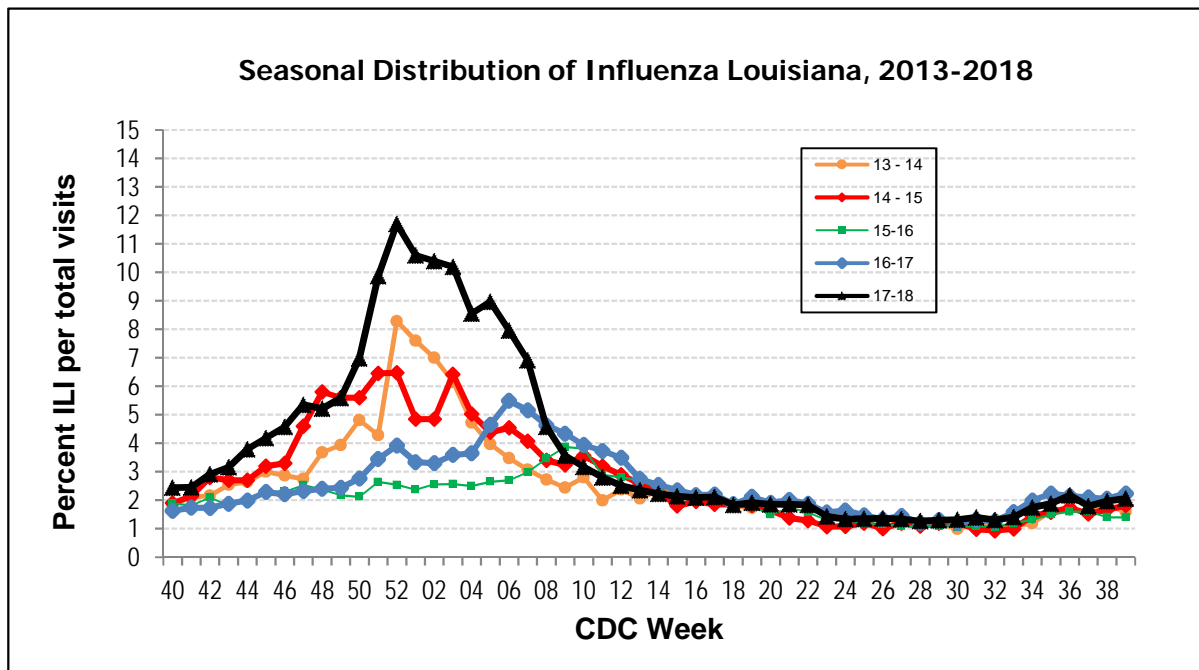This graph shows the percentage of visits for ILI over the total number of visits for sentinel surveillance sites. This is the best approach to estimate the magnitude of influenza transmission. ILI counts do include some viral infections other than influenza, but experience over the last 50 years has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

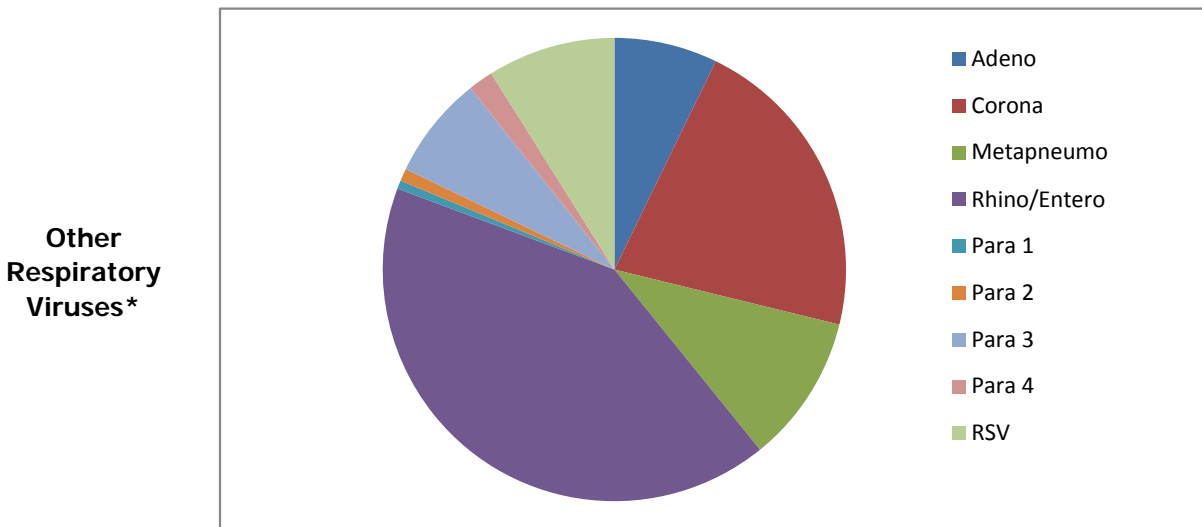**Influenza Sentinel Surveillance - Louisiana, 2018-2019 Season**
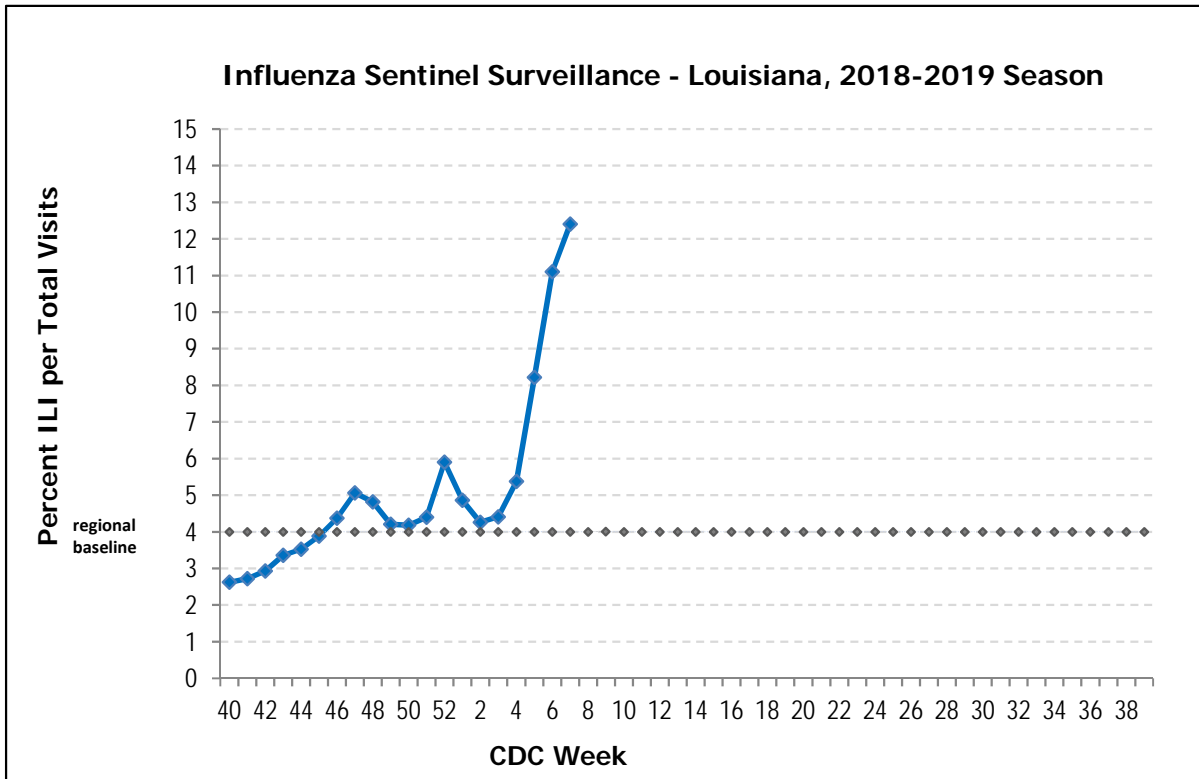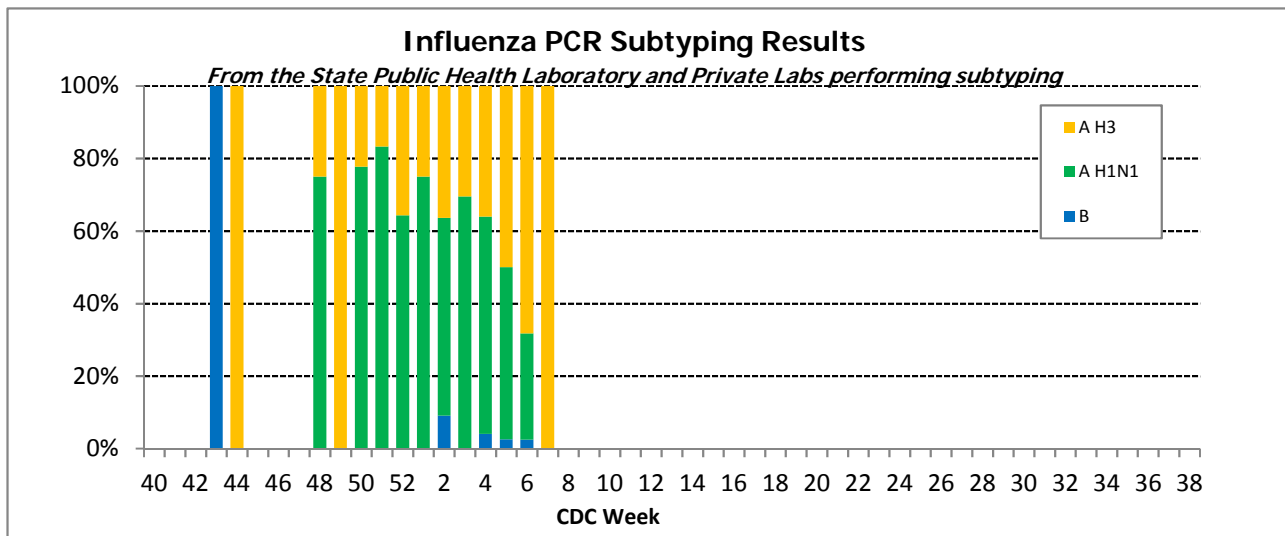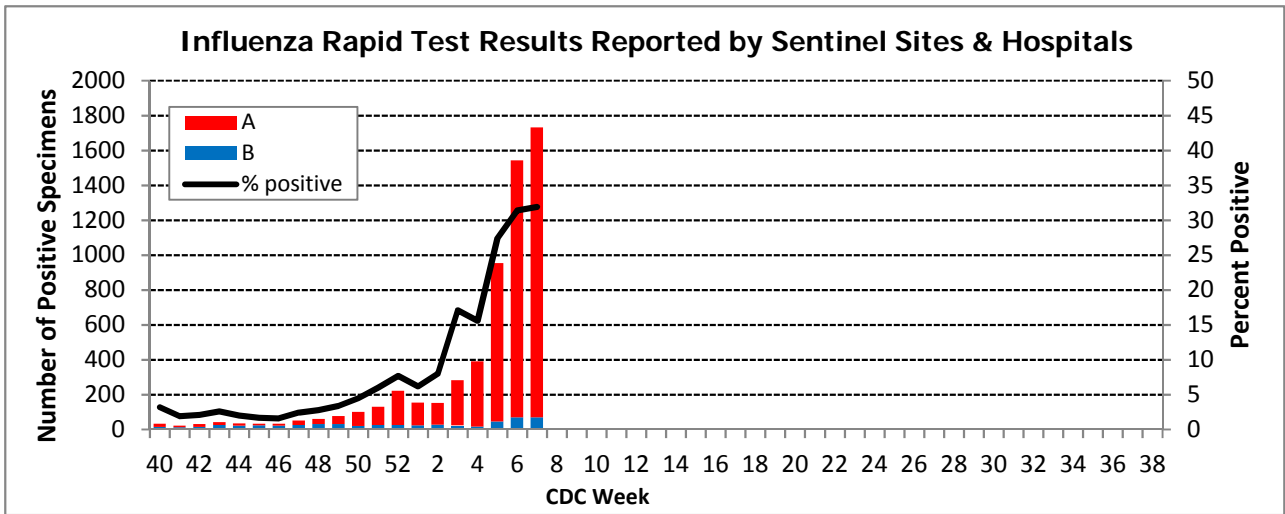
This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.

Seasonal Distribution of Influenza Louisiana, 2013-2018

2018-2019 Season

Virologic Surveillance

Influenza Rapid Test Results Reported by Sentinel Sites & Hospitals

Influenza PCR Subtyping Results
From the State Public Health Laboratory and Private Labs performing subtyping

Other Respiratory Viruses*
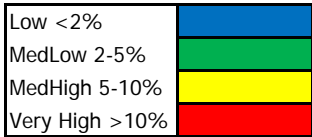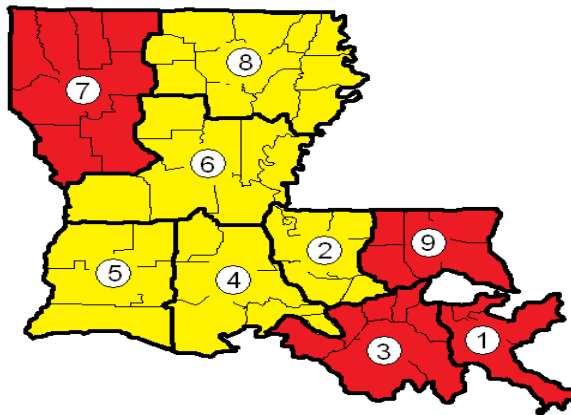

*Based on results from the State Public Heatlh Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 2 weeks.

Geographical Distribution of ILI*

Low <2%	(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 February 16, 2019 - Week 7

No Report No Activity Sporadic Local Regional Widespread

ILINet Activity Indicator Map
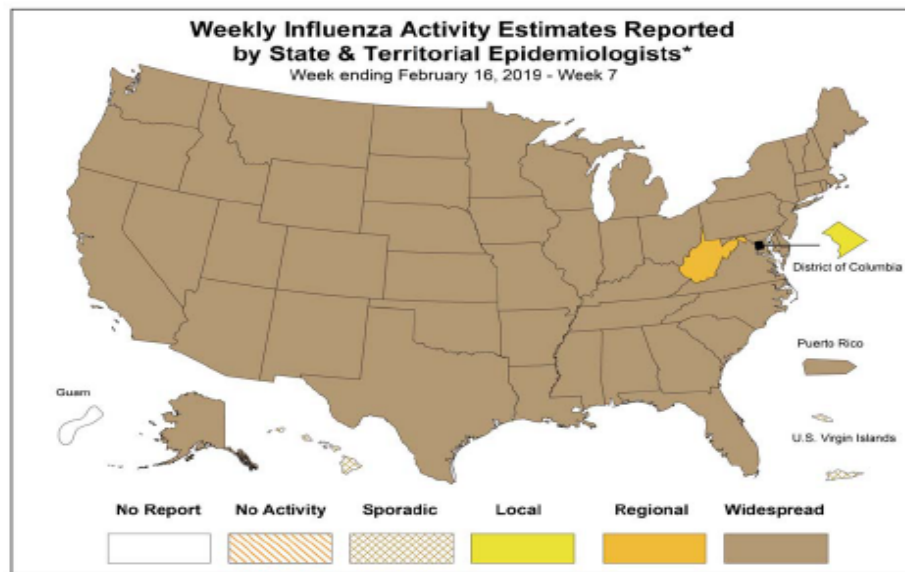
Influenza-Like Illness (ILI) Activity Level Indicator Determined by Data Reported to ILINet
2018-19 Influenza Season Week 7 ending Feb 16, 2019

ILI Activity Level: High, Moderate, Low, Minimal, Insufficient Data
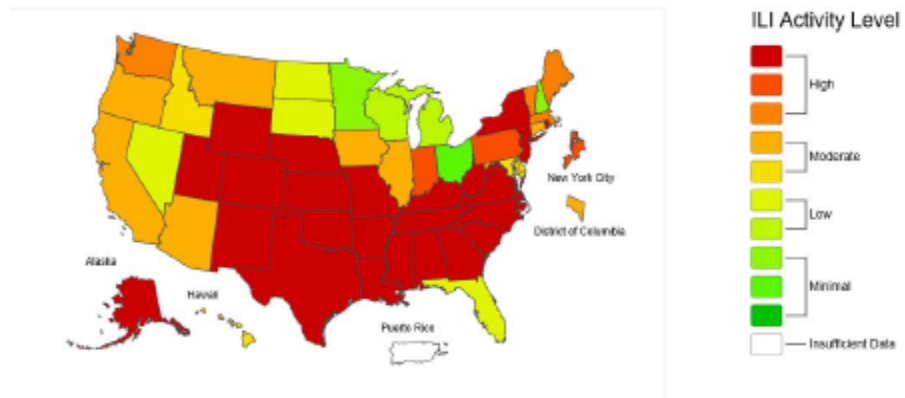
2018-2019 Season

National Surveillance

Influenza activity continues to increase in the United States.

The proportion of outpatient visits for influenza-like illness (ILI) increased to 5.1%, 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.

Seven influenza-associated pediatric deaths were reported to CDC during week 7.

Clinical Laboratory Data

	Week 7	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	38,208	639,225
No. of positive specimens (%)	10,210 (26.7%)	80,755 (12.6%)
Positive specimens by type		
Influenza A	9,936 (97.3%)	77,625 (96.1%)
Influenza B	274 (2.7%)	3,130 (3.9%)

Public Health Laboratory Data

	Week 7	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	1,792	40,074
No. of positive specimens*	1,075	18,076
Positive specimens by type/subtype		
Influenza A	1,058 (98.4%)	17,636 (97.6%)
(H1N1)pdm09	529 (53.1%)	12,720 (75.4%)
H3N2	467 (46.9%)	4,142 (24.6%)
Subtyping not performed	62	774
Influenza B	17 (1.6%)	440 (2.4%)
Yamagata lineage	3 (30.0%)	178 (55.3%)
Victoria lineage	7 (70.0%)	144 (44.7%)
Lineage not performed	7	118

HHS Surveillance Region Data:

Updated data tables for HHS region not available at time of report distribution.

All 5 jurisdictions (AR, LA, NM, OK, and TX) in region reporting elevated activity.

More than 30% of tests from clinical laboratories are positive.

Influenza A/H3 viruses are the predominant viruses being reported by public health laboratories in the most recent weeks.

Antiviral Resistance:

Type/Subtype or Lineage	Inhibition of Neuraminidase Activity by Antiviral Drug								
	Oseltamivir			Peramivir			Zanamivir		
	Virus Tested (n)	Reduced, Number (%)	Highly Reduced, Number (%)	Virus Tested (n)	Reduced, Number (%)	Highly Reduced, Number (%)	Virus Tested (n)	Reduced, Number (%)	Highly Reduced, Number (%)
Total Viruses	1,115	2 (0.2%)	2 (0.2%)	1,115	0 (0%)	2 (0.2%)	1,115	0 (0%)	0 (0%)
A(H1N1)pdm09	619	2 (0.3%)	2 (0.3%)	619	0 (0%)	2 (0.3%)	619	0 (0%)	0 (0%)
A(H3N2)	375	0 (0%)	0 (0%)	375	0 (0%)	0 (0%)	375	0 (0%)	0 (0%)
B/Victoria	46	0 (0%)	0 (0%)	46	0 (0%)	0 (0%)	46	0 (0%)	0 (0%)
B/Yamagata	75	0 (0%)	0 (0%)	75	0 (0%)	0 (0%)	75	0 (0%)	0 (0%)

Antigenic & Genetic Charactization:

CDC has antigenically or genetically characterized 1,129 influenza viruses collected September 30, 2018 – February 16, 2019, and submitted by U.S. laboratories, including 626 influenza A(H1N1)pdm09 viruses, 381 influenza A(H3N2) viruses, and 122 influenza B viruses.

Influenza A Viruses

- **A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 626 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Two hundred sixty-three A(H1N1)pdm09 viruses were antigenically characterized, and 259 (98.5%) 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 381 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=62), subclade 3C.2a1 (n=122) or clade 3C.3a (n=197). One hundred ninety-four A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and 128 (66%) 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 reference virus representing the A(H3N2) component of 2018-19 Northern Hemisphere influenza vaccines. Sixty-six (34%) viruses reacted poorly (at titers that were 8-fold or greater reduced compared with that of the homologous virus A/Singapore/INFIMH-16-0019/2016) and of those, 65 (98.5%) belonged to clade 3C.3a.

Influenza B Viruses

- **B/Victoria:** Phylogenetic analysis of 48 B/Victoria-lineage viruses indicate that all HA genes belonged to genetic clade V1A, however genetic subclades which are antigenically distinct have emerged. Genetic subclades which are antigenically distinct include viruses with a two amino acid deletion (162-163) in the HA protein (V1A.1, previously abbreviated as V1A-2Del) and viruses with a three amino acid deletion (162-164) in the HA protein (abbreviated as V1A-3Del). Forty B/Victoria lineage viruses were antigenically characterized and 33 (82.5%) were antigenically similar with ferret antisera raised against cell-propagated B/Colorado/06/2017-like V1A.1 reference virus. Seven (17.5%) reacted poorly (at titers that were 8-fold or greater reduced compared with the homologous virus titer) and belonged to clade V1A.

- **B/Yamagata:** Phylogenetic analysis of 74 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 53 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.