

Influenza Surveillance Report

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Week 6: 2/3/19 - 2/9/19

Influenza activity increased significantly again this week in Louisiana. Outbreaks continue to be reported from schools and long-term care facilities. For the second consecutive week, greater than 25% 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 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.



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

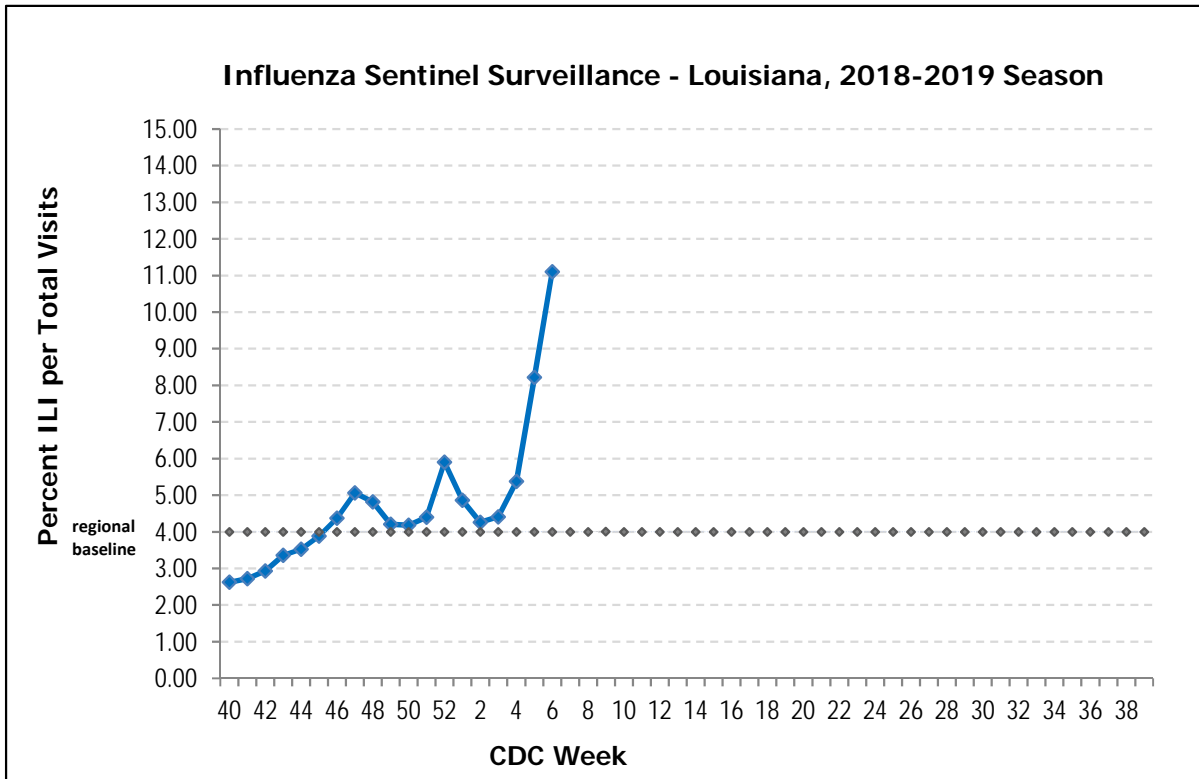
Page 3: Virologic Surveillance

Page 4: Geographic Distribution

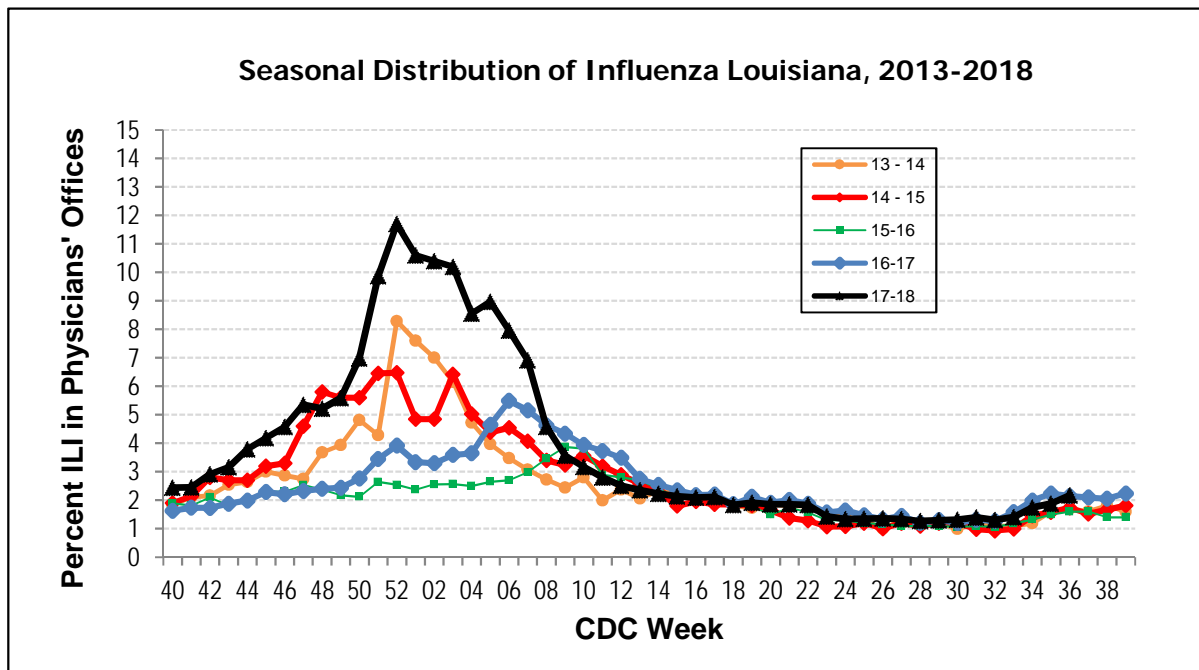
Page 5 & 6: Regional & National Data

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.

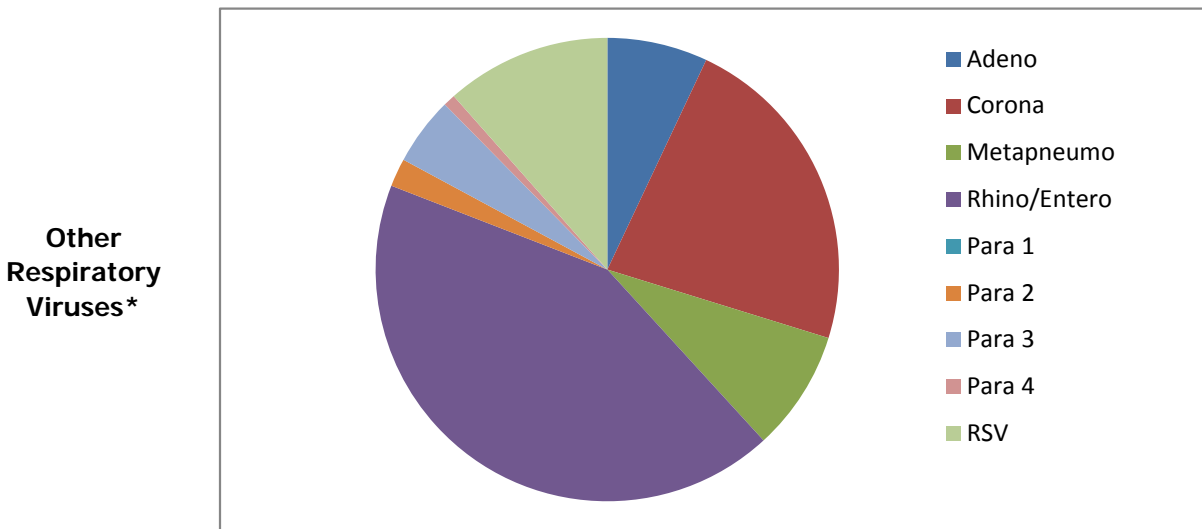
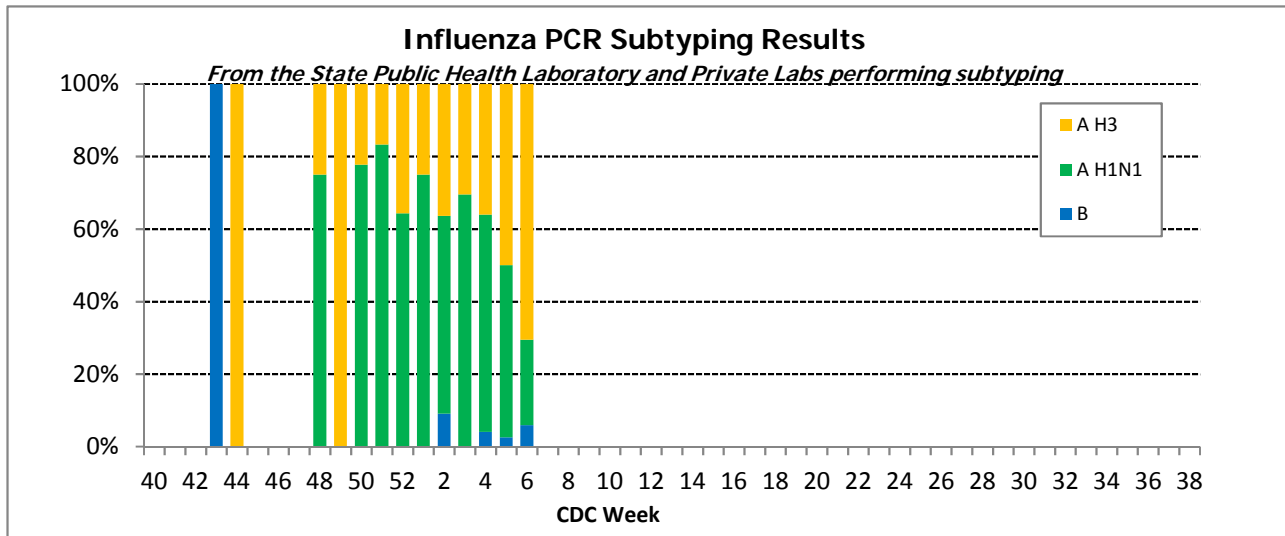
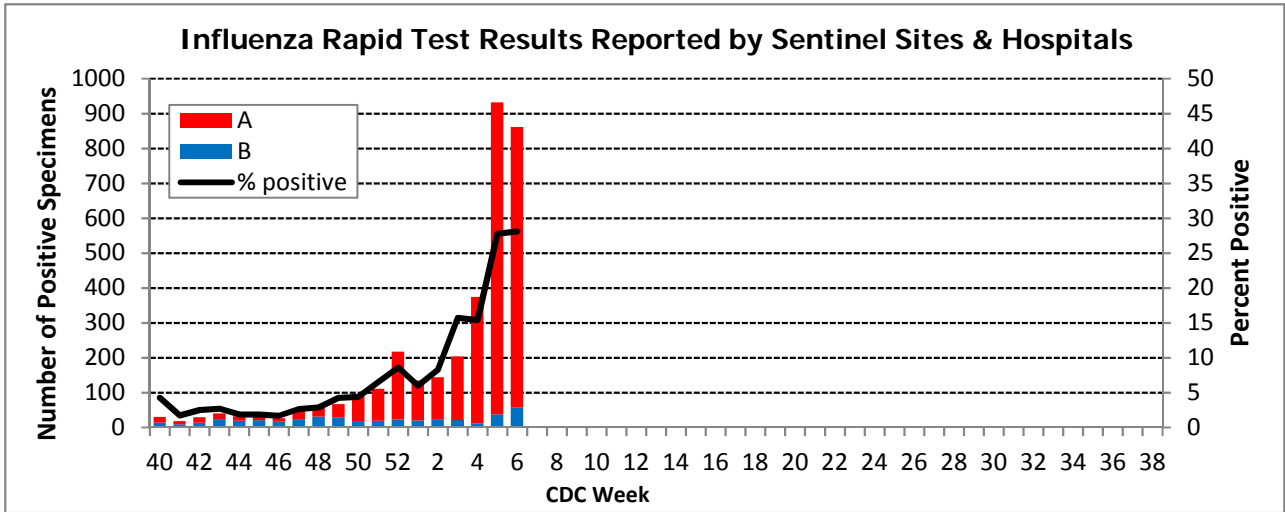


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.



2018-2019 Season

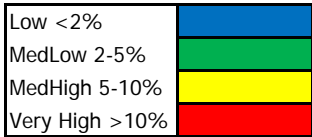
Virologic Surveillance



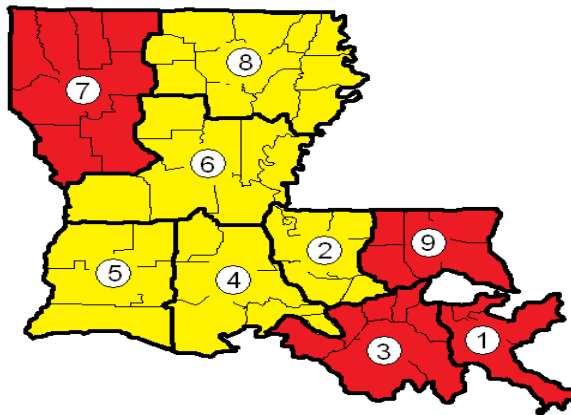
*Based on results from the State Public Health Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 2 weeks.

2018-2019 Season

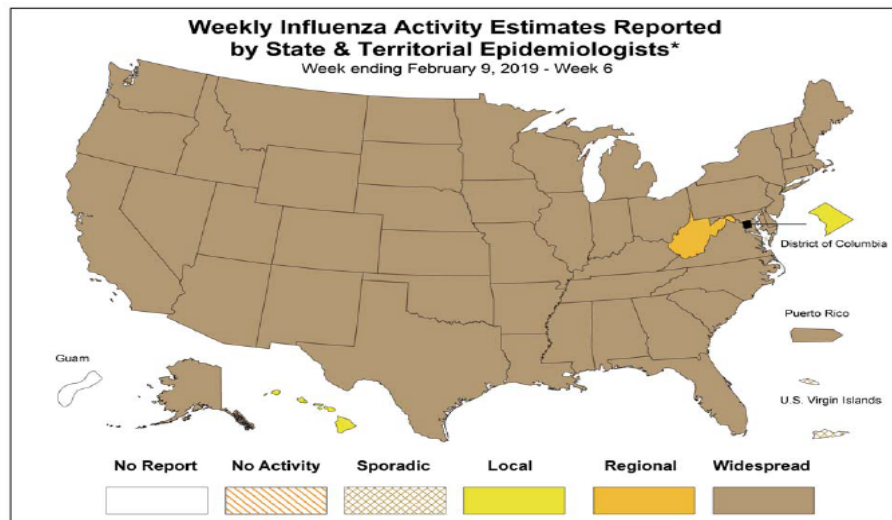
Geographical Distribution of ILI*



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

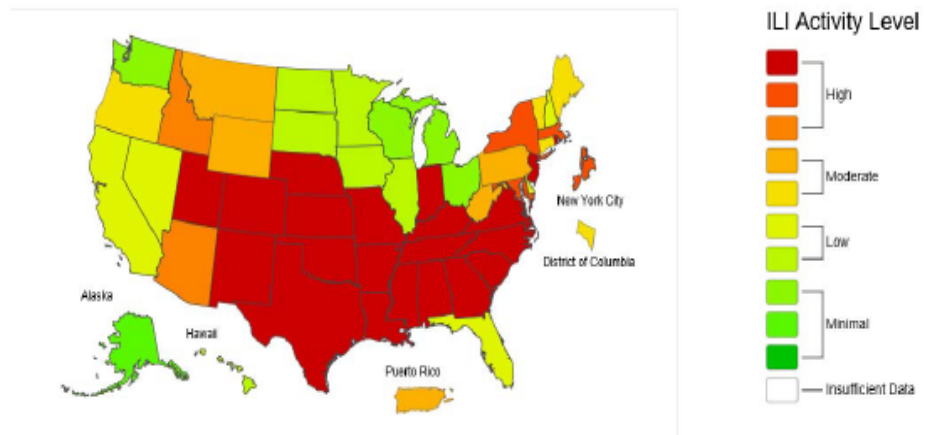


Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists



Influenza-Like Illness (ILI) Activity Level Indicator Determined by Data Reported to ILINet 2018-19 Influenza Season Week 6 ending Feb 09, 2019

ILINet Activity Indicator Map



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 4.8%, 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.

Six influenza-associated pediatric deaths were reported to CDC during week 6.

Clinical Laboratory Data

	Week 6	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	38,350	587,279
No. of positive specimens (%)	9,428 (24.6%)	67,119 (11.4%)
Positive specimens by type		
Influenza A	9,218 (97.8%)	64,385 (95.9%)
Influenza B	210 (2.2%)	2,734 (4.1%)

Public Health Laboratory Data

	Week 6	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	1,731	33,772
No. of positive specimens*	1,046	14,439
Positive specimens by type/subtype		
Influenza A	1,029 (98.4%)	14,056 (97.3%)
(H1N1)pdm09	649 (64.5%)	10,545 (78.5%)
H3N2	357 (35.5%)	2,887 (21.5%)
Subtyping not performed	23	624
Influenza B	17 (1.6%)	383 (2.7%)
Yamagata lineage	2 (20.0%)	161 (56.1%)
Victoria lineage	8 (80.0%)	126 (43.9%)
Lineage not performed	7	96

HHS Surveillance Region Data:

*U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet)
2018-2019 Influenza Season
HHS Region 6 (AR, LA, NM, OK, and TX) (Baseline: 4.0%)
Data as of Friday, February 15, 2019*

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
201903	290	1278	1815	1285	470	287	5135	110863	4.6	5.1
201904	291	1389	2531	1443	526	325	6214	111239	5.6	6.4
201905	284	1751	3949	1801	687	330	8518	115525	7.4	8.0
201906	279	2359	5507	2323	808	420	11417	118393	9.6	9.8

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
201903	9	206	0	57	25	0	2	1	1	22	4823	1017	21.09	978	39
201904	6	121	0	36	20	0	3	0	1	22	5610	1384	24.67	1321	63
201905	7	118	0	34	29	0	3	2	0	20	6977	2178	31.22	2100	78
201906	6	145	0	28	47	0	3	0	0	17	5285	1782	33.72	1754	28

2018-2019 Season

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	992	2 (0.2%)	2 (0.2%)	992	0 (0%)	2 (0.2%)	992	0 (0%)	0 (0%)
A(H1N1)pdm09	565	2 (0.4%)	2 (0.4%)	565	0 (0%)	2 (0.4%)	565	0 (0%)	0 (0%)
A(H3N2)	319	0 (0%)	0 (0%)	319	0 (0%)	0 (0%)	319	0 (0%)	0 (0%)
B/Victoria	38	0 (0%)	0 (0%)	38	0 (0%)	0 (0%)	38	0 (0%)	0 (0%)
B/Yamagata	70	0 (0%)	0 (0%)	70	0 (0%)	0 (0%)	70	0 (0%)	0 (0%)

Antigenic & Genetic Characterization:

CDC has antigenically or genetically characterized 968 influenza viruses collected September 30, 2018 – February 9, 2019, and submitted by U.S. laboratories, including 554 influenza A(H1N1)pdm09 viruses, 308 influenza A(H3N2) viruses, and 106 influenza B viruses.

Influenza A Viruses

- A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 554 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. One hundred ninety four A(H1N1)pdm09 viruses were antigenically characterized, and 191 (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 308 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=61), subclade 3C.2a1 (n=109) or clade 3C.3a (n=138). 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 40 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). Twenty-one B/Victoria lineage viruses were antigenically characterized and 15 (71.4%) were antigenically similar with ferret antisera raised against cell-propagated B/Colorado/06/2017-like V1A.1 reference virus. Six (28.6%) 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 66 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.