

Influenza Surveillance Report

www.infectiousdisease.dhh.la.gov

Week 9: 2/24/19 - 3/2/19

Influenza activity remains elevated in Louisiana but decreased slightly this week. Outbreaks continue to be reported from schools and long-term care facilities. More than 25% of influenza tests reported by clinical labs are positive. Influenza A/H3 is now the dominant virus subtyped at the state public health laboratory, Influenza B activity remains low. 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.

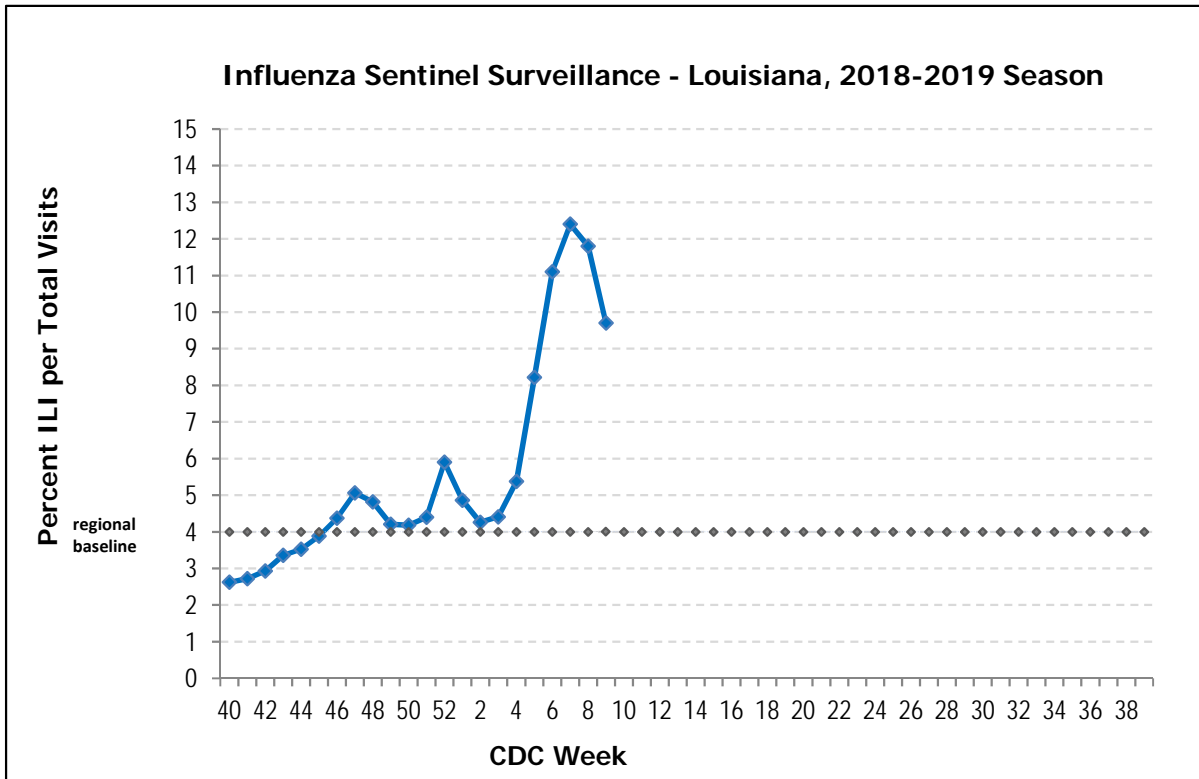


Laboratory testing: Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information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

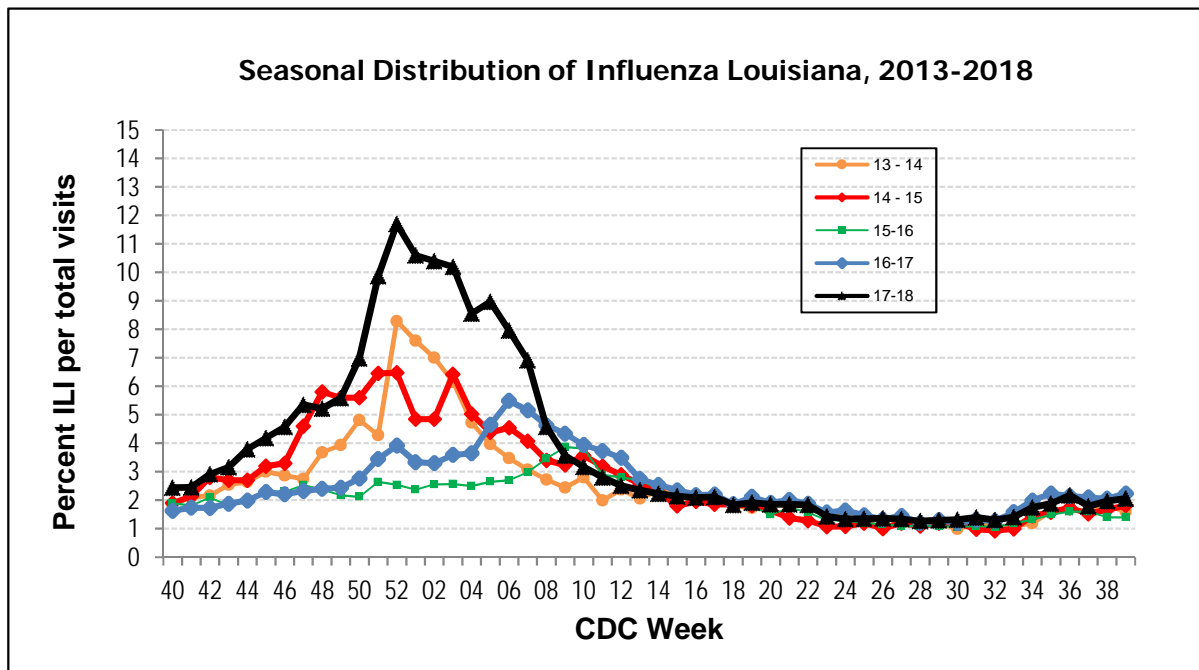
Page 2 : ILI Activity
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Page 4: Geographic Distribution
Page 5 & 6: Regional & National Data

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.

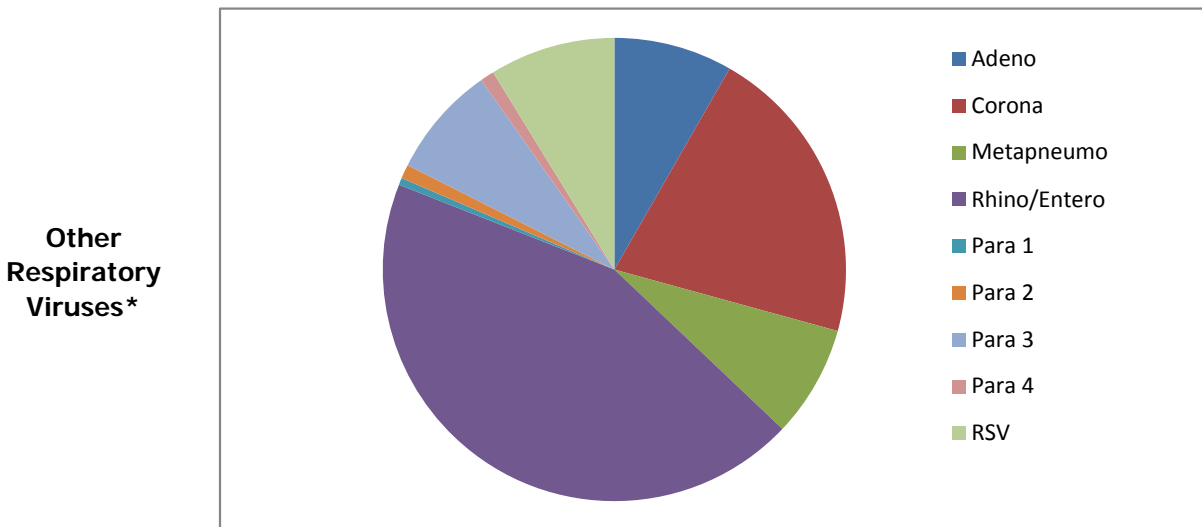
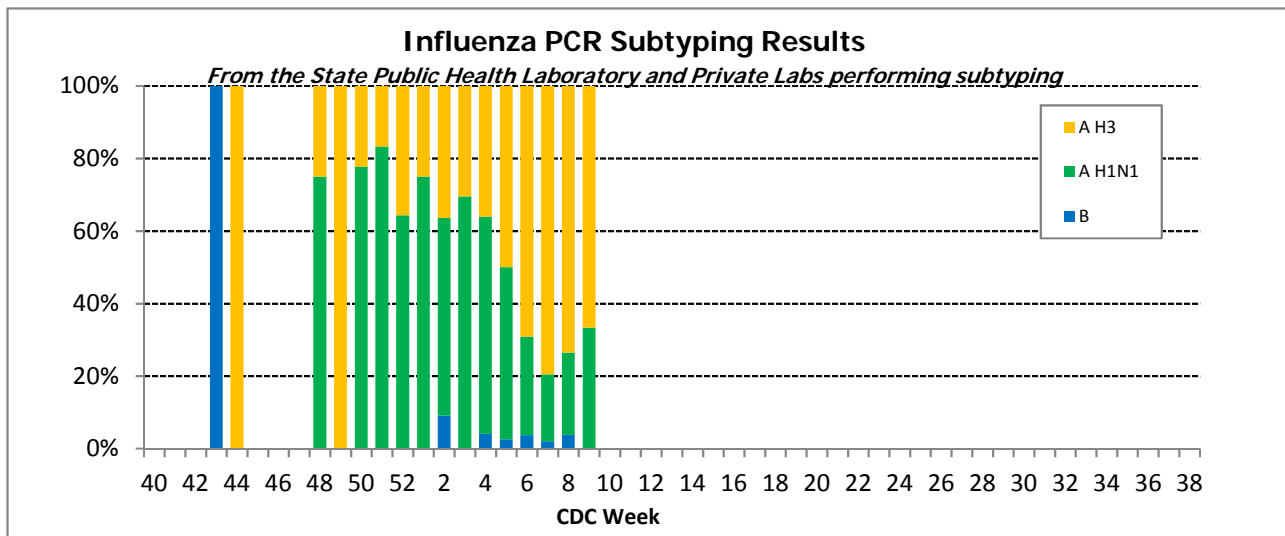
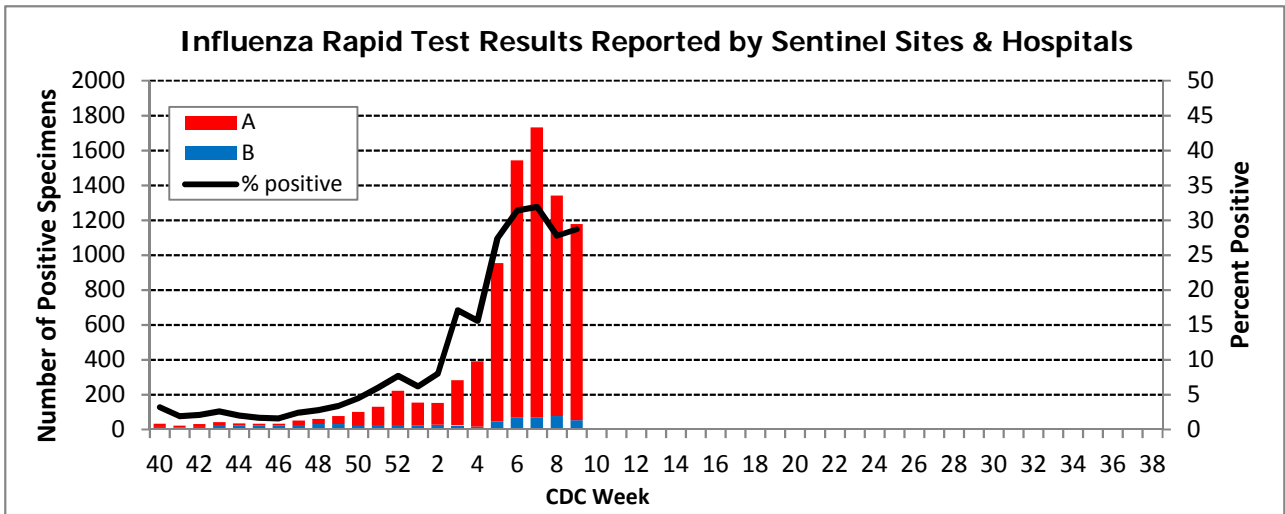


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.



2018-2019 Season

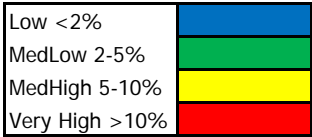
Virologic Surveillance



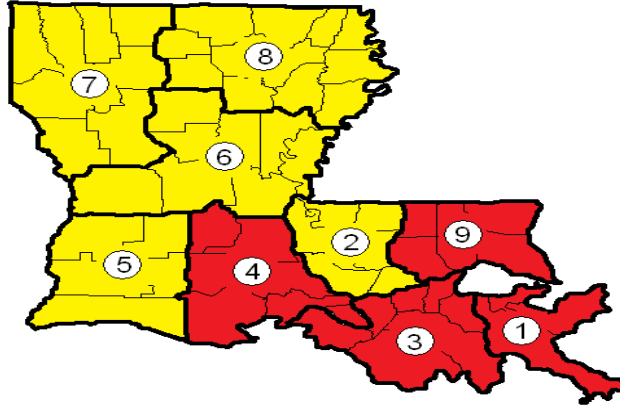
*Based on results from the State Public Health Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 2 weeks.

2018-2019 Season

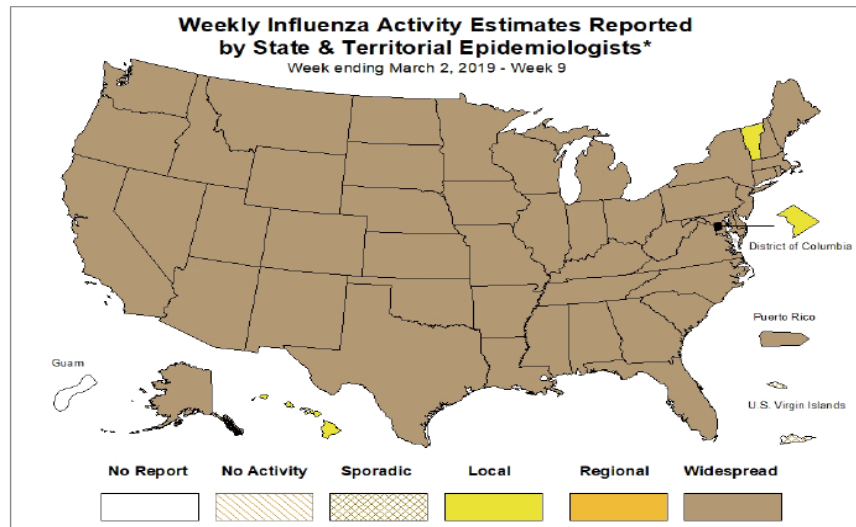
Geographical Distribution of ILI*



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

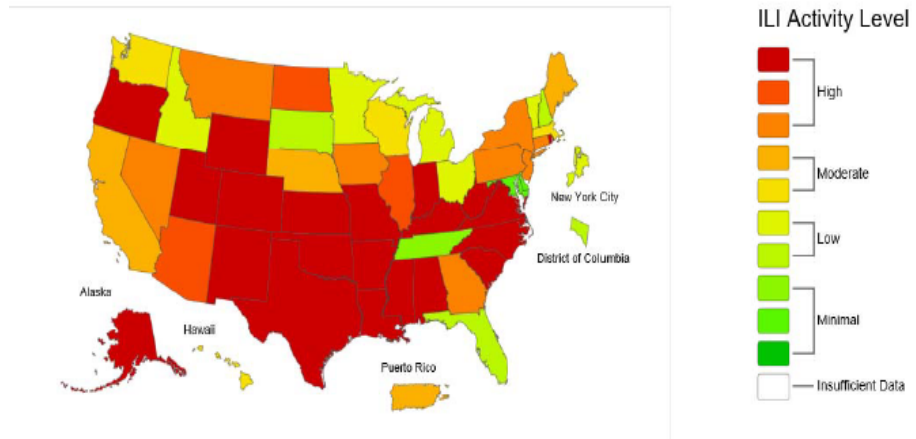


Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists



Influenza-Like Illness (ILI) Activity Level Indicator Determined by Data Reported to ILINet
2018-19 Influenza Season Week 9 ending Mar 02, 2019

ILINet Activity Indicator Map



2018-2019 Season

National Surveillance

Influenza activity remains elevated in the United States.

The proportion of outpatient visits for influenza-like illness (ILI) decreased slightly to 4.7%, 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.

Nine influenza-associated pediatric deaths were reported to CDC during week 9. Eight deaths occurred during the 2018-2019 season and one death occurred during the 2015-2016 season.

Clinical Laboratory Data

	Week 9	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	36,193	738,333
No. of positive specimens (%)	9,434 (26.1%)	105,413 (14.3%)
Positive specimens by type		
Influenza A	9,171 (97.2%)	101,414 (96.2%)
Influenza B	263 (2.8%)	3,999 (3.8%)

Public Health Laboratory Data

	Week 9	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	1,995	48,972
No. of positive specimens*	1,209	23,837
Positive specimens by type/subtype		
Influenza A	1,186 (98.1%)	23,284 (97.7%)
(H1N1)pdm09	429 (38.0%)	15,432 (69.6%)
H3N2	699 (62.0%)	6,725 (30.4%)
Subtyping not performed	58	1,127
Influenza B	23 (1.9%)	553 (2.3%)
Yamagata lineage	2 (15.4%)	205 (52.3%)
Victoria lineage	11 (84.6%)	187 (47.7%)
Lineage not performed	10	161

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, March 8, 2019*

CDC Week	# Sites Reporting	ILI 0-4 years	ILI 5-24 years	ILI 25-49 years	ILI 50-64 years	ILI 65	Total ILI	Total Patient Visits	% Unweighted ILI	% Weighted ILI
						years and older				
201906	295	2389	5628	2362	829	432	11640	121369	9.6	9.9
201907	293	2678	5867	2629	887	490	12551	120778	10.4	10.2
201908	287	2394	5285	2524	877	526	11606	116879	9.9	9.4
201909	274	2048	4417	2278	797	485	10025	111674	9.0	9.3

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

CDC Week	Public Health Labs	Public Health Specimens Tested	AUNK	AH1N1 pdm09	AH3N2	AH3N2v	B	BVlc	BYam	Clinical Labs	Clinical Specimens Tested	Clinical Flu Positive	% Positive	A	B
201906	9	416	0	69	124	0	4	0	0	24	9507	3164	33.28	3052	112
201907	10	392	0	53	136	0	2	3	0	22	6096	1972	32.35	1912	60
201908	8	392	3	51	148	0	5	2	0	22	5644	1635	28.97	1585	50
201909	9	190	0	21	89	0	4	0	0	19	5047	1373	27.20	1317	56

2018-2019 Season

Antiviral Resistance:

Assessment of Virus Susceptibility to Neuraminidase Inhibitors Using Next-Generation Sequencing Analysis and/or Neuraminidase Inhibition Assay

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	1,396	2 (0.1%)	2 (0.1%)	1,396	0 (0%)	2 (0.1%)	1,396	0 (0%)	0 (0%)
A(H1N1)pdm09	755	2 (0.3%)	2 (0.3%)	755	0 (0%)	2 (0.3%)	755	0 (0%)	0 (0%)
A(H3N2)	482	0 (0%)	0 (0%)	482	0 (0%)	0 (0%)	482	0 (0%)	0 (0%)
B/Victoria	64	0 (0%)	0 (0%)	64	0 (0%)	0 (0%)	64	0 (0%)	0 (0%)
B/Yamagata	95	0 (0%)	0 (0%)	95	0 (0%)	0 (0%)	95	0 (0%)	0 (0%)

Antigenic & Genetic Characterization:

CDC has antigenically or genetically characterized 1,416 influenza viruses collected September 30, 2018 – March 2, 2019, and submitted by U.S. laboratories, including 762 influenza A(H1N1)pdm09 viruses, 490 influenza A(H3N2) viruses, and 164 influenza B viruses.

Influenza A Viruses

- A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 762 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Two hundred sixty-four A(H1N1)pdm09 viruses were antigenically characterized, and 260 (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 490 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=64), subclade 3C.2a1 (n=135) or clade 3C.3a (n=291). Two hundred twenty-four A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and 138 (61.6%) 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. Eighty-six (38.4%) 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, 85 (98.8%) belonged to clade 3C.3a.

Influenza B Viruses

- B/Victoria:** Phylogenetic analysis of 67 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). Fifty-four B/Victoria lineage viruses were antigenically characterized and 44 (81.5%) were antigenically similar with ferret antisera raised against cell-propagated B/Colorado/06/2017-like V1A.1 reference virus. Ten (18.5%) reacted poorly (at titers that were 8-fold or greater reduced compared with the homologous virus titer) and belonged to clade V1A or genetic subclade V1A-3Del.
- B/Yamagata:** Phylogenetic analysis of 97 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 75 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.