

# Influenza Surveillance Report

[www.infectiousdisease.dhh.la.gov](http://www.infectiousdisease.dhh.la.gov)

Week 49: 12/2/18 - 12/8/18

**Influenza activity remains near baseline in Louisiana. This week the state public health laboratory identified an influenza A/H1N1 infection in a surveillance sample. Rhino/Enteroviruses, RSV, and Metapneumovirus 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](mailto: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.

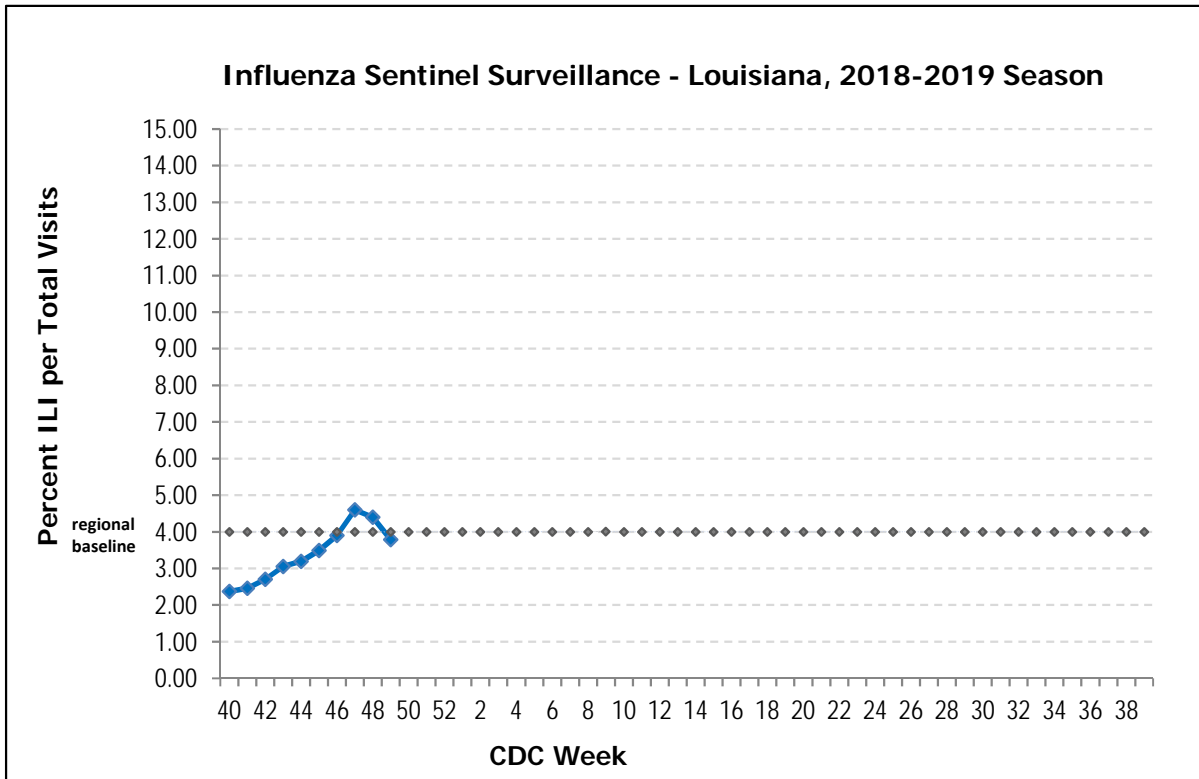


**Laboratory testing:** Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information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

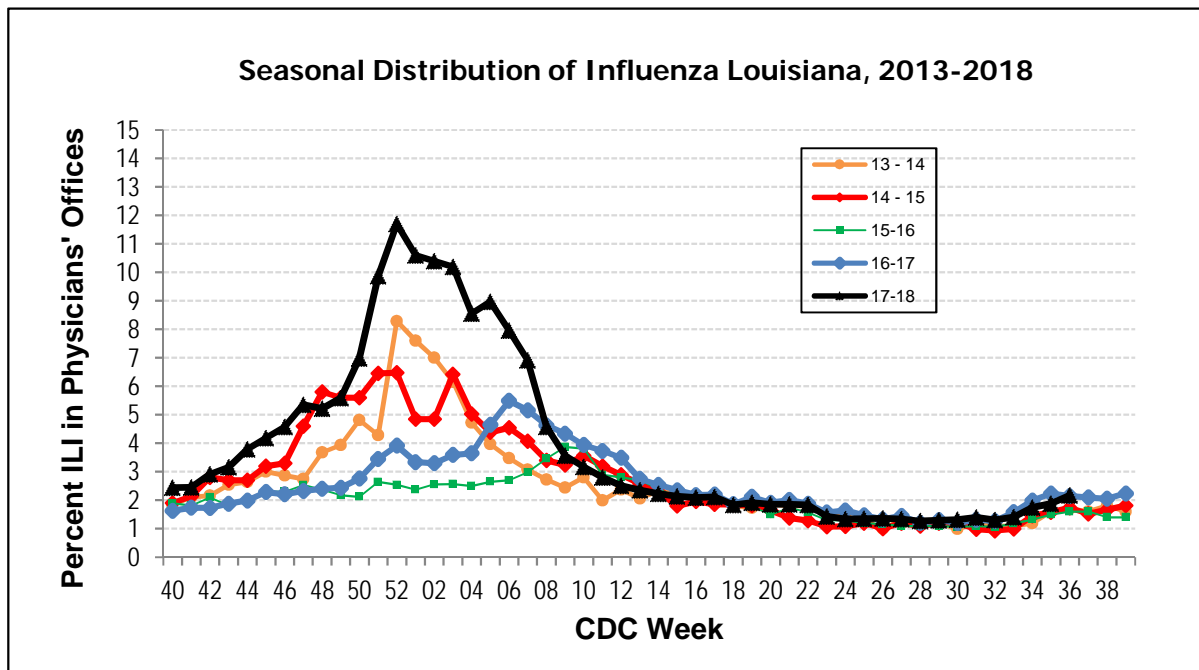
Page 2 : ILI Activity  
Page 3: Virologic Surveillance  
Page 4: Geographic Distribution  
Page 5 & 6: Regional & National Data

## 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.

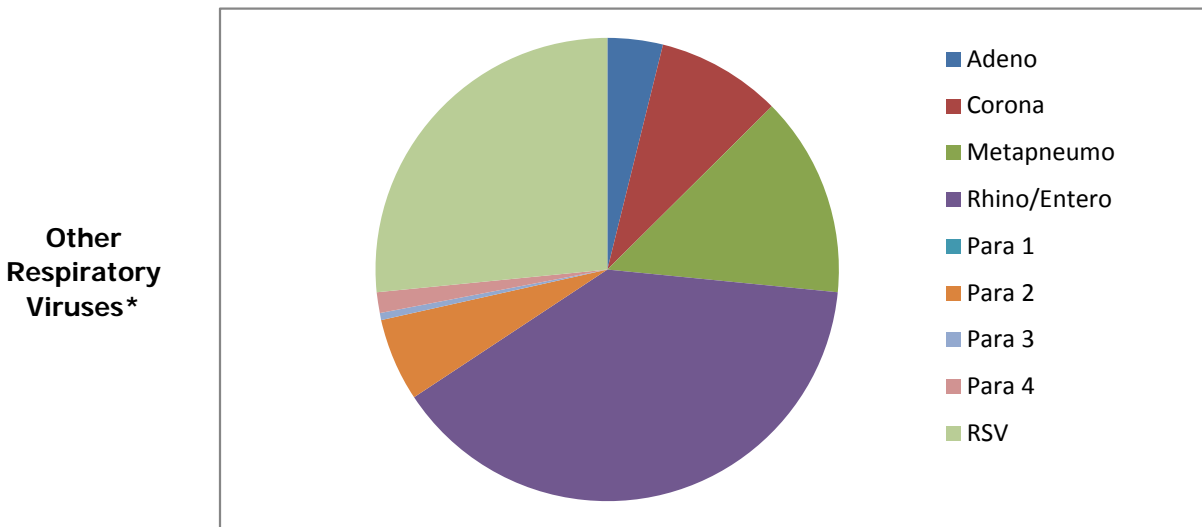
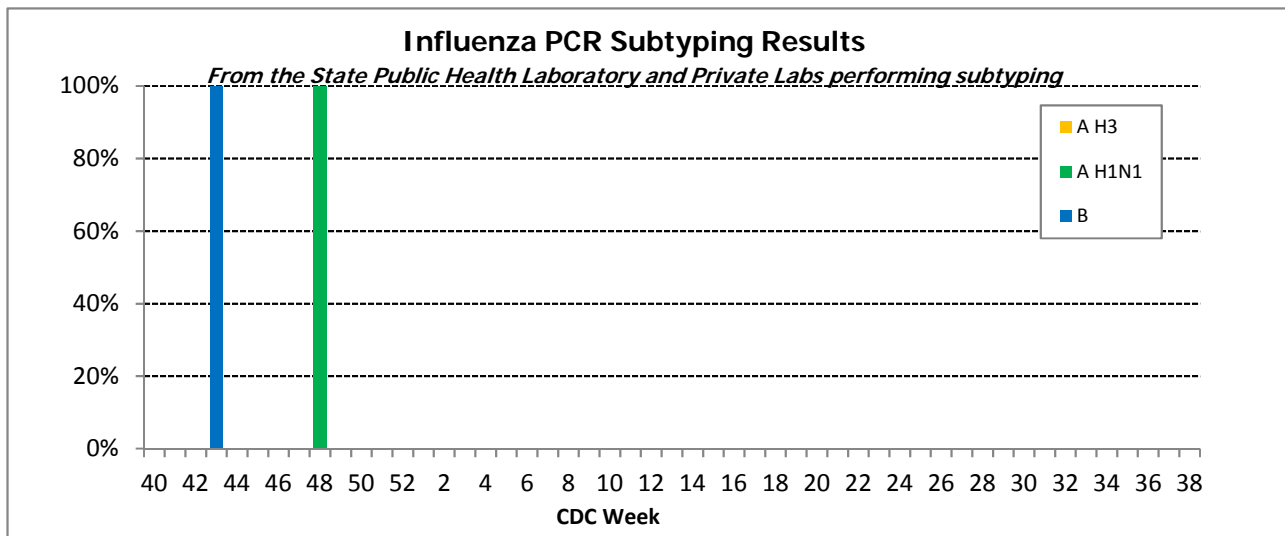
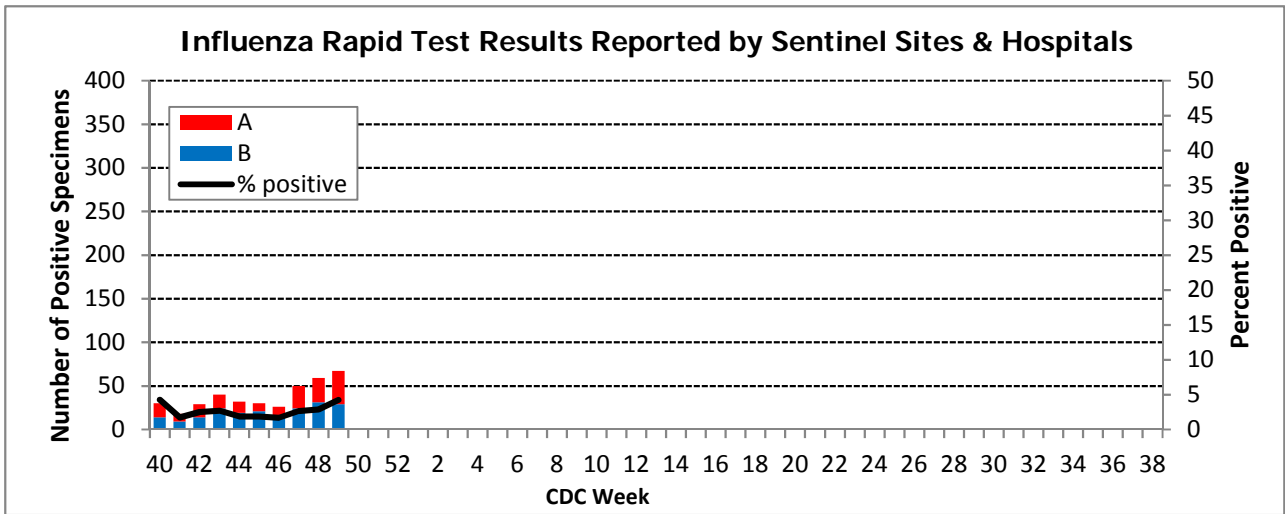


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.



# 2018-2019 Season

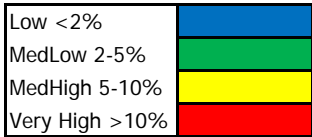
## Virologic Surveillance



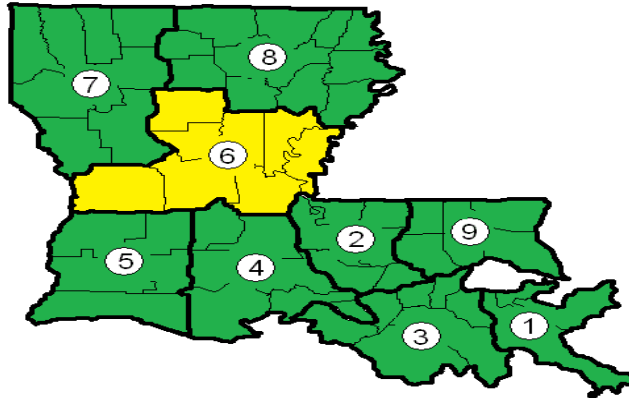
\*Based on results from the State Public Health Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 2 weeks.

## 2018-2019 Season

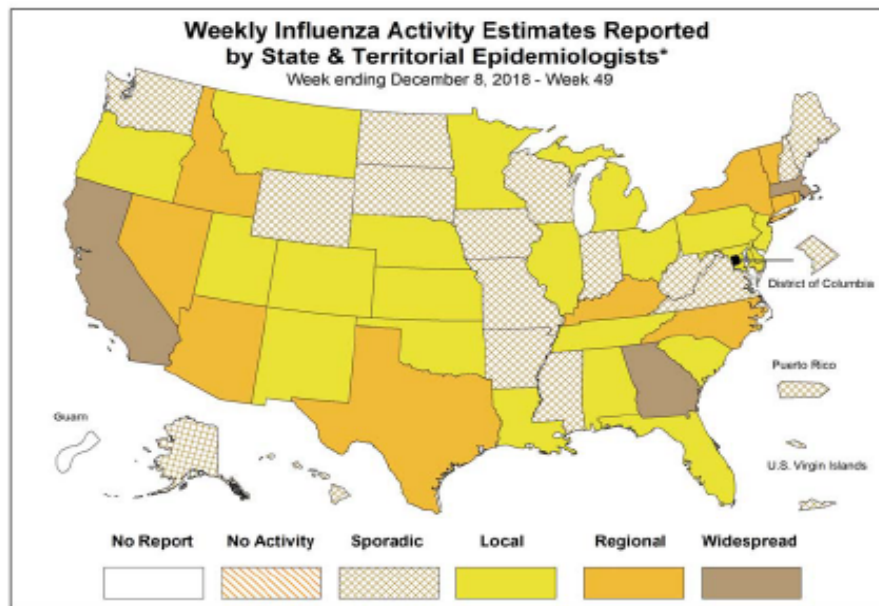
### Geographical Distribution of ILI\*



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



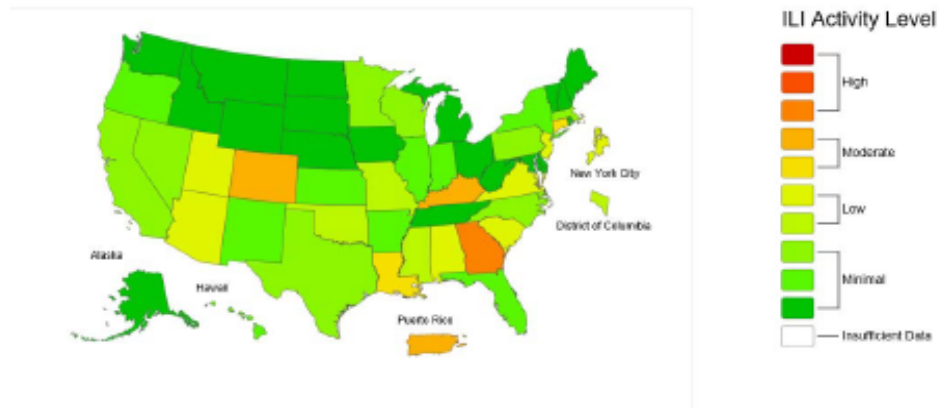
### Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists



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

### Influenza-Like Illness (ILI) Activity Level Indicator Determined by Data Reported to ILINet 2018-19 Influenza Season Week 49 ending Dec 08, 2018

### ILINet Activity Indicator Map



## 2018-2019 Season

### National Surveillance

Influenza activity in the United States remained slightly elevated.

The proportion of outpatient visits for influenza-like illness (ILI) remained at 2.2%, which is at the national baseline of 2.2%.

The proportion of deaths attributed to pneumonia and influenza (P&I) was below the system-specific epidemic threshold.

One influenza-associated pediatric death was reported to CDC for week 49.

### Clinical Laboratory Data

	Week 49	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	18,518	209,570
No. of positive specimens (%)	665 (3.6%)	5,801 (2.8%)
<i>Positive specimens by type</i>		
Influenza A	613 (92.2%)	4,989 (86.0%)
Influenza B	52 (7.8%)	812 (14.0%)

### Public Health Laboratory Data

	Week 49	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	772	9,063
No. of positive specimens*	207	1,424
<i>Positive specimens by type/subtype</i>		
<b>Influenza A</b>	<b>196 (94.7%)</b>	<b>1,313 (92.2%)</b>
(H1N1)pdm09	148 (80.9%)	1,000 (81.3%)
H3N2	35 (19.1%)	230 (18.7%)
Subtyping not performed	13	83
<b>Influenza B</b>	<b>11 (5.3%)</b>	<b>111 (7.8%)</b>
Yamagata lineage	4 (66.7%)	62 (72.9%)
Victoria lineage	2 (33.3%)	23 (27.1%)
Lineage not performed	5	26

### HHS Surveillance Region Data:

<i>U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet) 2017-2018 Influenza Season</i>										
<i>HHS Region 6 (AR, LA, NM, OK, and TX) (Baseline: 4.0%) Data as of Friday, December 14, 2018</i>										
						ILI 65		Total	%	%
CDC	# Sites	ILI 0-4	ILI 5-24	ILI 25-49	ILI 50-64	and	Total	Patient	Unweighted	Weighted
Week	Reporting	years	years	years	years	older	ILI	Visits	ILI	ILI
201846	289	1245	1079	732	261	182	3499	109941	3.2	3.1
201847	283	1309	906	787	320	201	3523	97407	3.6	3.5
201848	285	1354	1095	927	416	253	4045	118801	3.4	3.4
201849	242	1104	937	702	284	181	3208	96718	3.3	3.2

#### 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
201846	7	68	0	8	2	0	0	0	0	23	3122	54	1.73	36	18
201847	4	33	0	8	3	0	0	0	1	23	3309	104	3.14	91	13
201848	7	45	0	11	6	0	0	0	1	20	2698	65	2.41	60	5
201849	6	38	0	9	6	0	1	0	0	19	2165	115	5.31	108	7

## 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	190	0 (0%)	0 (0%)	190	0 (0%)	0 (0%)	190	0 (0%)	0 (0%)
A(H1N1)pdm09	116	0 (0%)	0 (0%)	116	0 (0%)	0 (0%)	116	0 (0%)	0 (0%)
A(H3N2)	49	0 (0%)	0 (0%)	49	0 (0%)	0 (0%)	49	0 (0%)	0 (0%)
B/Victoria	7	0 (0%)	0 (0%)	7	0 (0%)	0 (0%)	7	0 (0%)	0 (0%)
B/Yamagata	18	0 (0%)	0 (0%)	18	0 (0%)	0 (0%)	18	0 (0%)	0 (0%)

### Antigenic & Genetic Characterization:

CDC has antigenically or genetically characterized 166 influenza viruses collected September 30, 2018 – December 8, 2018, and submitted by U.S. laboratories, including 97 influenza A(H1N1)pdm09 viruses, 45 influenza A(H3N2) viruses, and 24 influenza B viruses.

#### Influenza A Viruses

- A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 97 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Sixty-eight A(H1N1)pdm09 viruses were antigenically characterized, and all 68 (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 45 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=19), subclade 3C.2a1 (n=24) or clade 3C.3a (n=2). Six A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and all 6 (100%) 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 7 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). Three B/Victoria lineage viruses were antigenically characterized and all 3 (100%) 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 V1A.1 reference virus, and belonged to clade V1A.
- B/Yamagata:** Phylogenetic analysis of 17 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 16 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.