

# Influenza Surveillance Report

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

Week 16: 4/14/19 - 4/20/19

Influenza activity decreased again this week in Louisiana. Influenza A/H3 has been the dominant virus in Louisiana since the beginning of February, Influenza B activity remains low. 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](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.

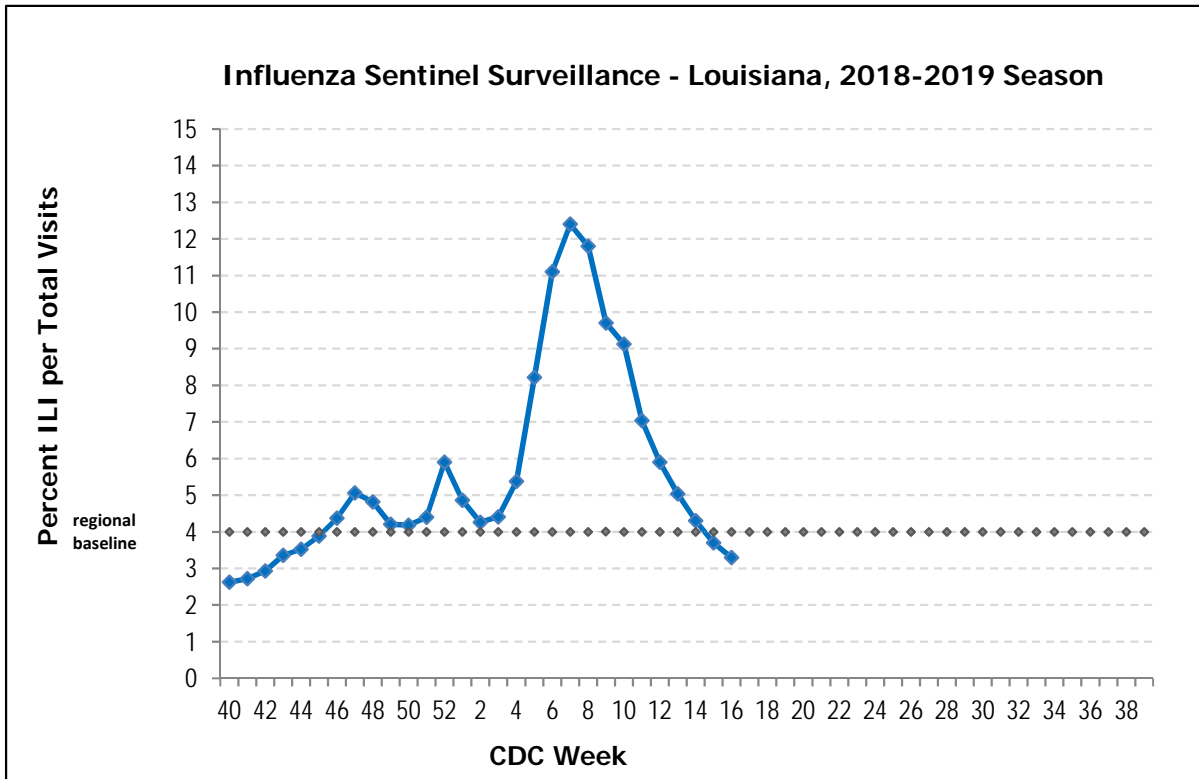


**Laboratory testing:** Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information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

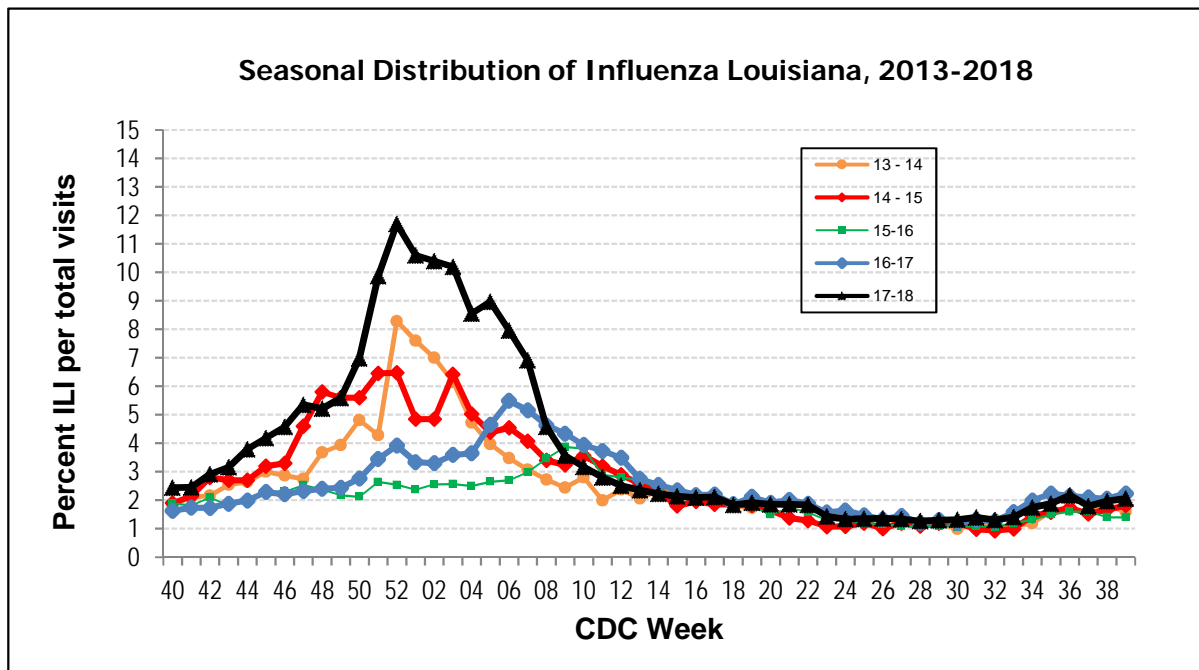
Page 2 : ILI Activity  
Page 3: Virologic Surveillance  
Page 4: Geographic Distribution  
Page 5 & 6: Regional & National Data

## 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.

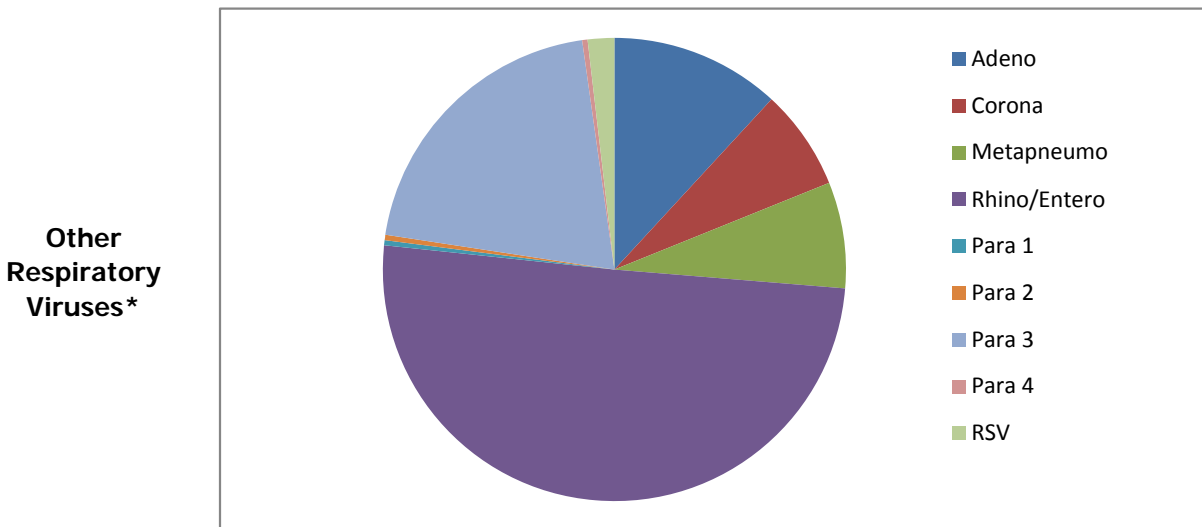
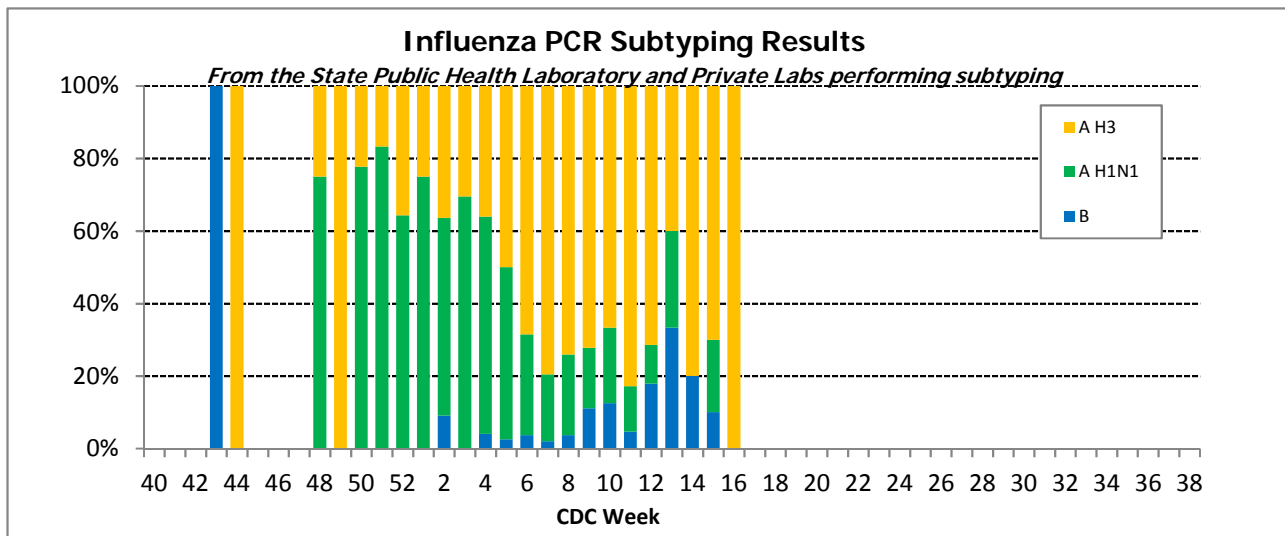
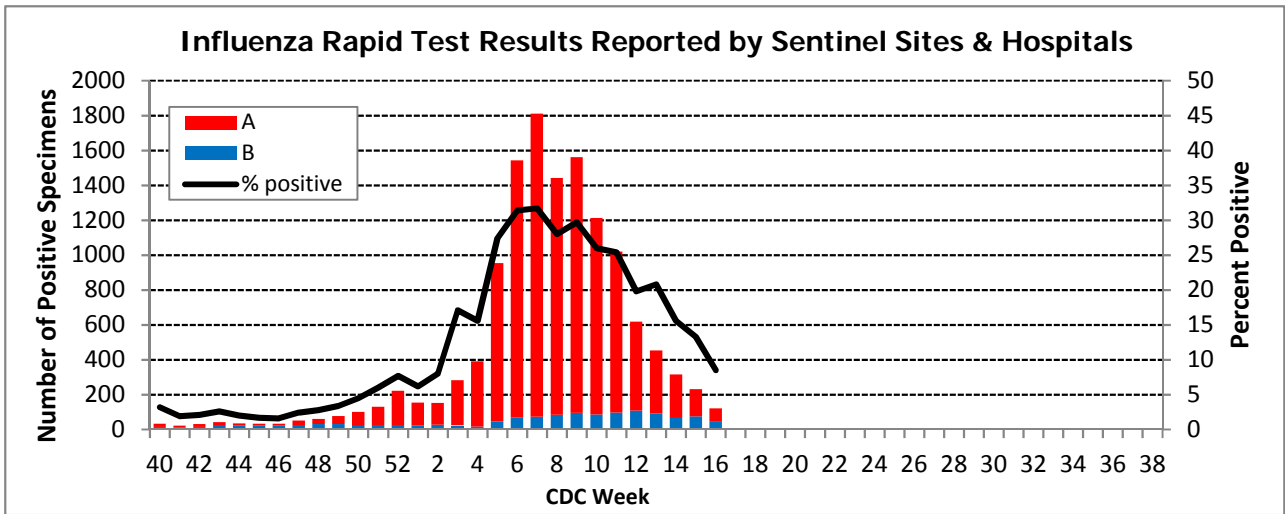


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.



# 2018-2019 Season

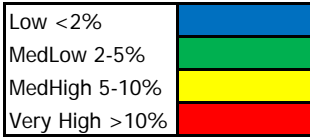
## Virologic Surveillance



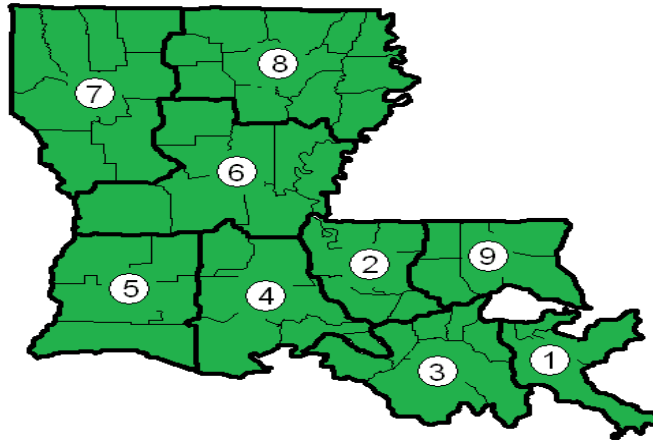
\*Based on results from the State Public Health Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 2 weeks.

## 2018-2019 Season

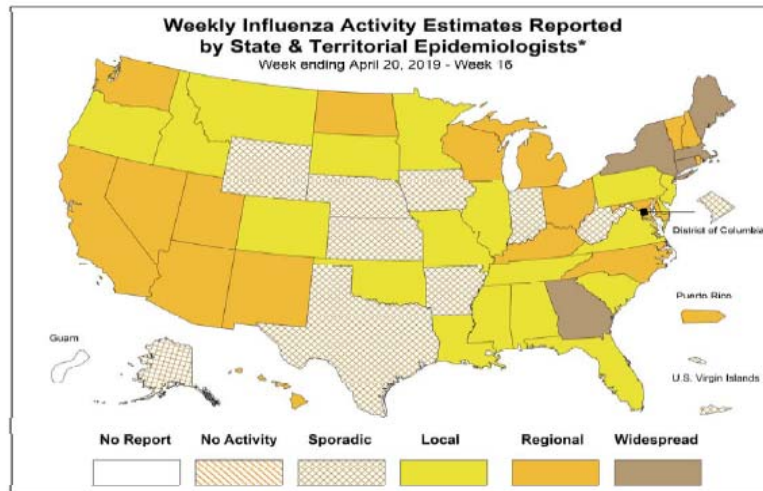
### Geographical Distribution of ILI\*



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

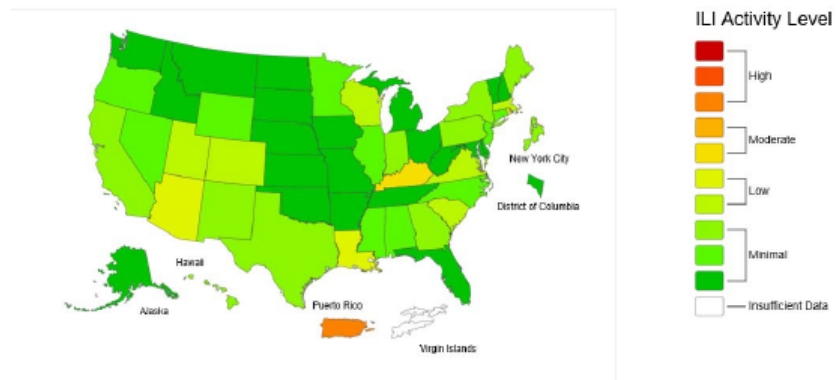


### Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists



Influenza-Like Illness (ILI) Activity Level Indicator Determined by Data Reported to ILINet  
2018-19 Influenza Season Week 16 ending Apr 20, 2019

### ILINet Activity Indicator Map



## 2018-2019 Season

### National Surveillance

Influenza activity continues to decrease in the United States.

The proportion of outpatient visits for influenza-like illness (ILI) decreased to 2.1%, which is below the national baseline of 2.2%.

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

Five influenza-associated pediatric deaths were reported to CDC during week 16.

### Clinical Laboratory Data

	Week 16	Data Cumulative since September 30, 2018 (week 40)
<b>No. of specimens tested</b>	18,777	1,051,664
<b>No. of positive specimens (%)</b>	1,516 (8.1%)	171,607 (16.3%)
<b>Positive specimens by type</b>		
<b>Influenza A</b>	1,155 (76.2%)	163,602 (95.3%)
<b>Influenza B</b>	361 (23.8%)	8,005 (4.7%)

### Public Health Laboratory Data

	Week 16	Data Cumulative since September 30, 2018 (week 40)
<b>No. of specimens tested</b>	584	73,182
<b>No. of positive specimens*</b>	177	39,096
<b>Positive specimens by type/subtype</b>		
<b>Influenza A</b>	149 (84.2%)	37,802 (96.7%)
(H1N1)pdm09	34 (23.3%)	21,130 (58.0%)
H3N2	112 (76.7%)	15,270 (42.0%)
Subtyping not performed	3	1,402
<b>Influenza B</b>	28 (15.8%)	1,294 (3.3%)
Yamagata lineage	3 (14.3%)	333 (39.6%)
Victoria lineage	18 (85.7%)	508 (60.4%)
Lineage not performed	7	453

### 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, April 26, 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
201913	289	1237	1674	1178	423	300	4812	109268	4.4	4.6
201914	287	944	1412	980	378	228	3942	103989	3.8	4.0
201915	283	892	1345	813	274	194	3518	106083	3.3	3.5
201916	275	832	1068	628	240	160	2928	100444	2.9	3.0

#### 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
201913	8	137	0	12	23	0	8	2	0	24	4332	554	12.79	435	119
201914	7	99	0	1	17	0	3	3	0	21	3179	301	9.47	227	74
201915	9	107	0	8	17	0	3	1	2	21	2848	254	9.60	160	94
201916	7	40	0	3	4	0	3	1	0	17	1207	79	6.55	35	44

## 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	2,077	2 (0.1%)	3 (0.1%)	2,077	0 (0%)	3 (0.1%)	2,077	0 (0%)	0 (0%)
A(H1N1)pdm09	1,006	2 (0.2%)	3 (0.3%)	1,006	0 (0%)	3 (0.3%)	1,006	0 (0%)	0 (0%)
A(H3N2)	789	0 (0%)	0 (0%)	789	0 (0%)	0 (0%)	789	0 (0%)	0 (0%)
B/Victoria	145	0 (0%)	0 (0%)	145	0 (0%)	0 (0%)	145	0 (0%)	0 (0%)
B/Yamagata	137	0 (0%)	0 (0%)	137	0 (0%)	0 (0%)	137	0 (0%)	0 (0%)

### Antigenic & Genetic Characterization:

CDC has antigenically or genetically characterized 2,015 influenza viruses collected September 30, 2018 – April 20, 2019, and submitted by U.S. laboratories, including 995 influenza A(H1N1)pdm09 viruses, 749 influenza A(H3N2) viruses, and 271 influenza B viruses.

#### Influenza A Viruses

- A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 995 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Three hundred and four A(H1N1)pdm09 viruses were antigenically characterized, and 295 (97%) 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 749 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=66), subclade 3C.2a1 (n=157) or clade 3C.3a (n=526). Three hundred seventy A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and 167 (45.1%) 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. Two hundred and three (54.9%) 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, 202 (99.5%) belonged to clade 3C.3a.

#### Influenza B Viruses

- B/Victoria:** Phylogenetic analysis of 140 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). One hundred and eight B/Victoria lineage viruses were antigenically characterized and 82 (75.9%) were antigenically similar with ferret antisera raised against cell-propagated B/Colorado/06/2017-like V1A.1 reference virus. Twenty-six (24.1%) viruses 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 131 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 107 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.