

Influenza Surveillance Report

www.infectiousdisease.dhh.la.gov

Week 40: 9/30/18 - 10/6/18

Influenza activity remained low through the summer months and early October. Rhino/Enteroviruses are circulating at a very high level and are the most common non-influenza viruses being reported by laboratories around the state.

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.

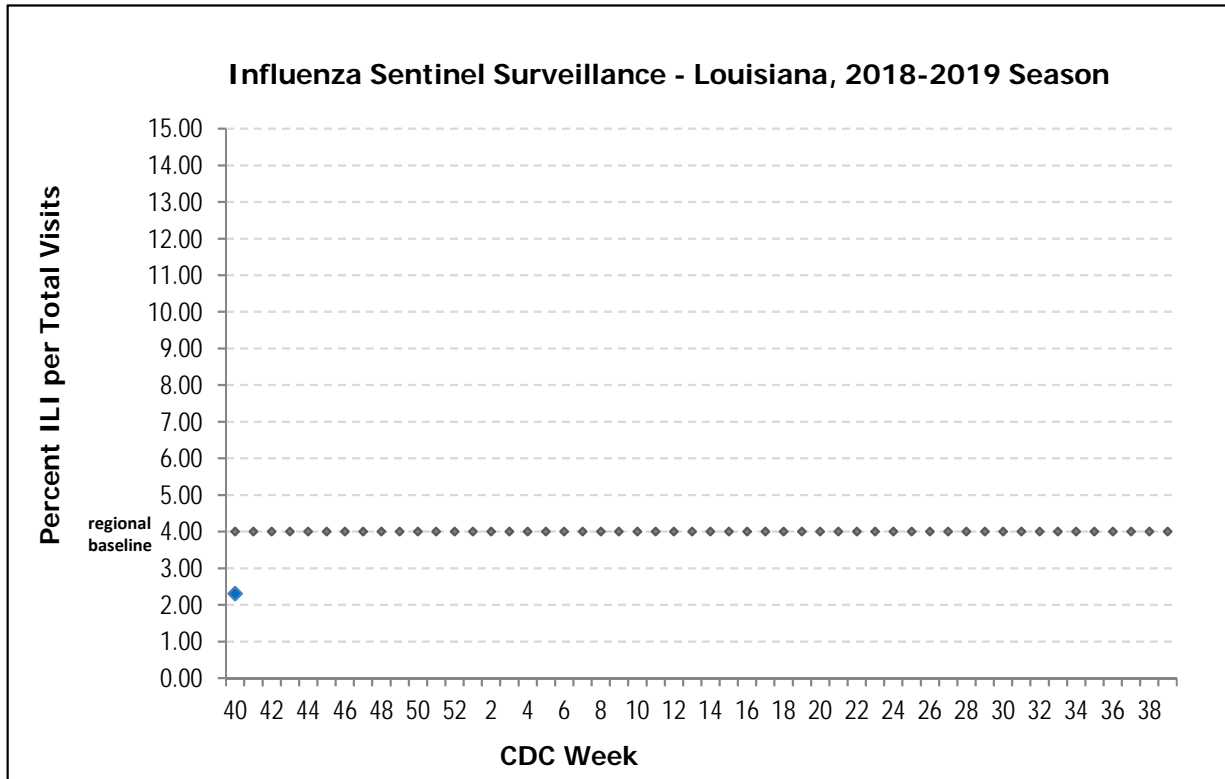


Laboratory testing: Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information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

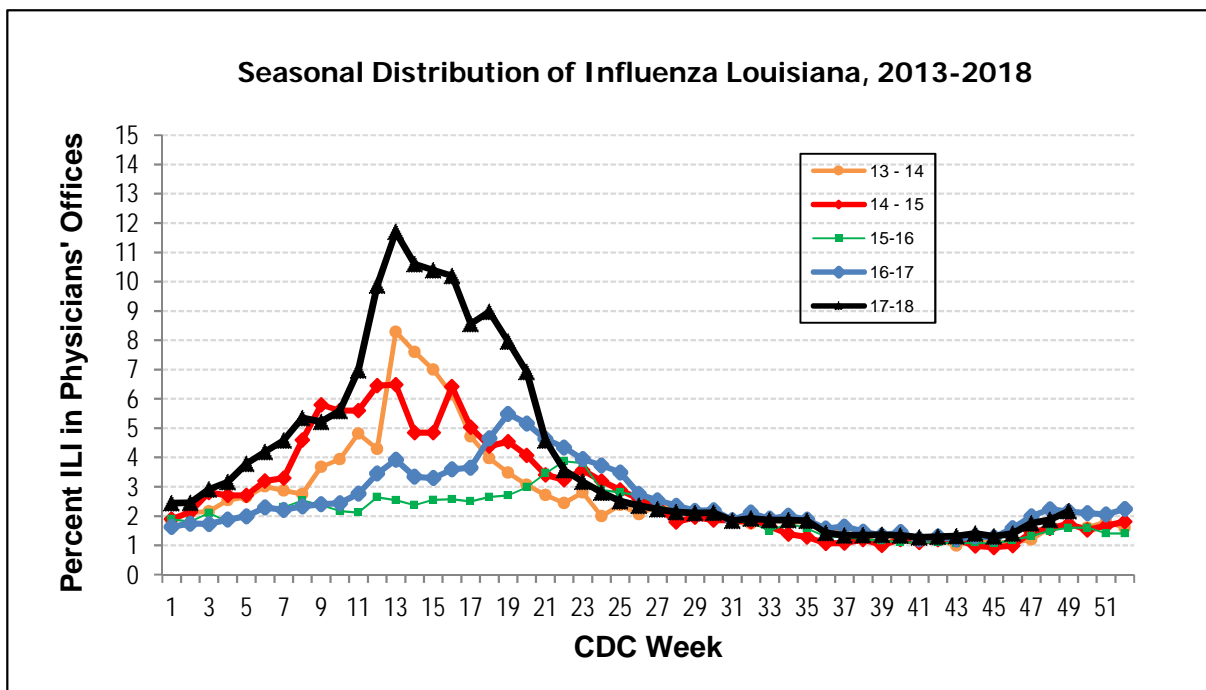
- Page 2 : ILI Activity
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- Page 4: Geographic Distribution
- Page 5 & 6: Regional & National Data

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.

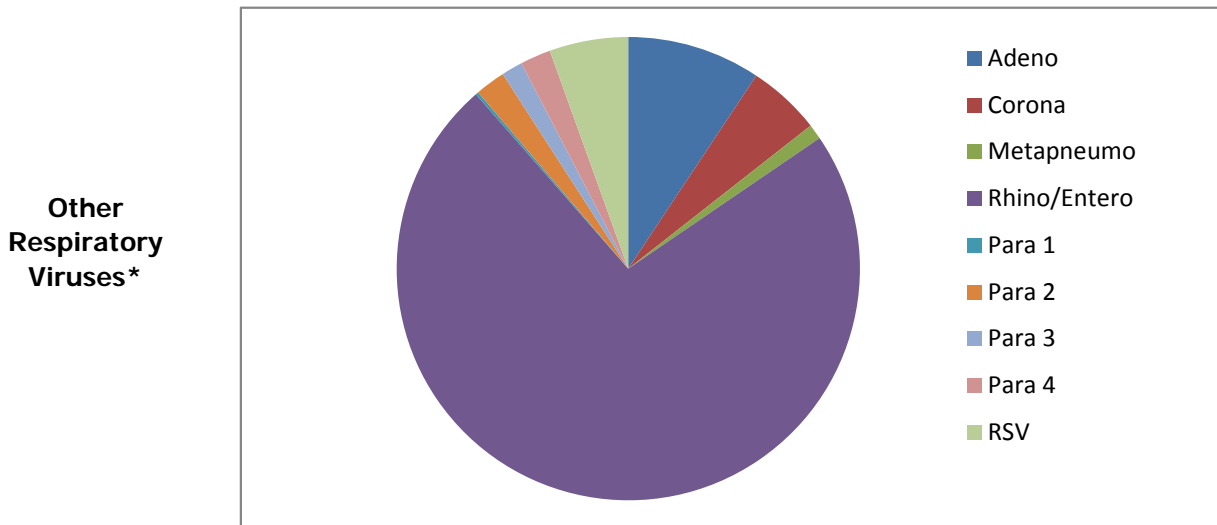
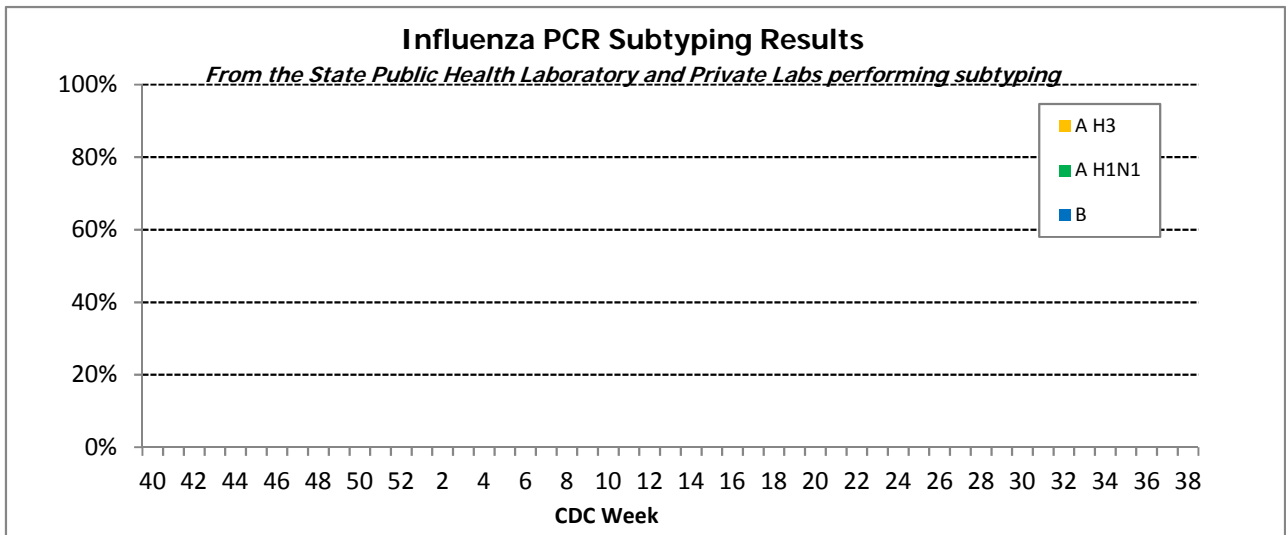
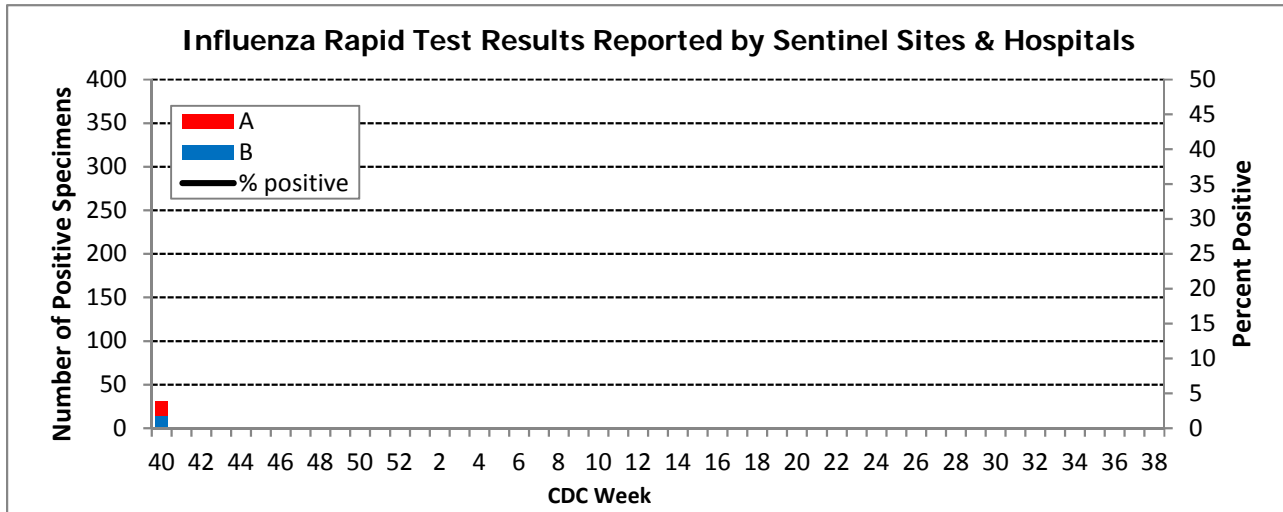


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.



2018-2019 Season

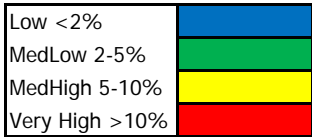
Virologic Surveillance



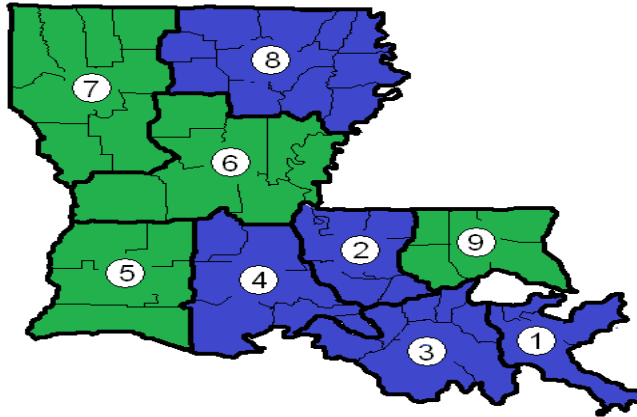
*Based on results from the State Public Health Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 4 weeks.

2018-2019 Season

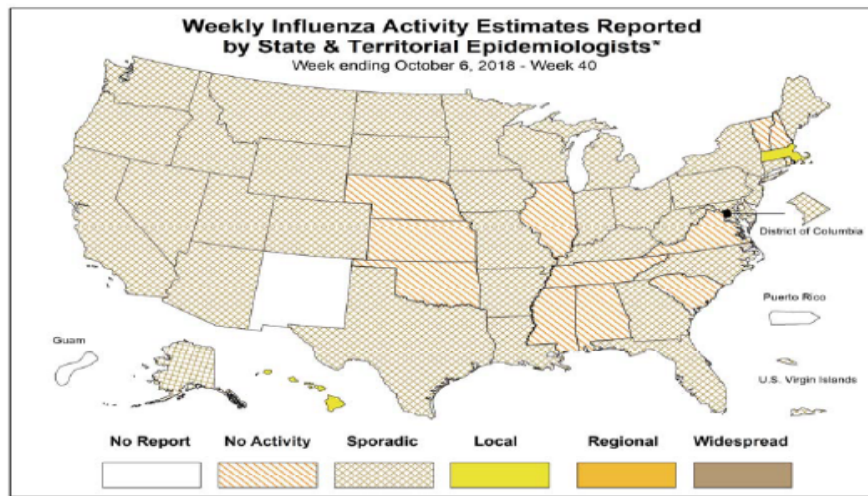
Geographical Distribution of ILI*



* %ILI over the last 4 weeks based on sentinel surveillance data



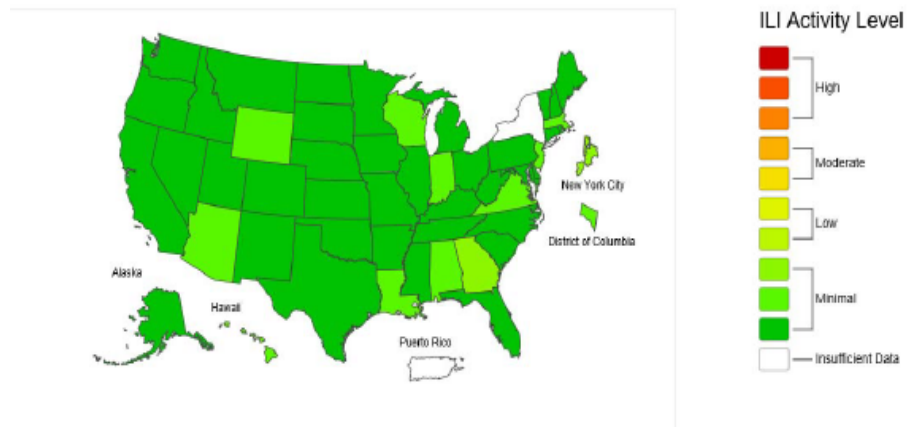
Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists



* 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 40 ending Oct 06, 2018

ILINet Activity Indicator Map



2018-2019 Season

National Surveillance

Influenza activity in the United States remained low throughout the summer months and early October.

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.

The proportion of outpatient visits for influenza-like illness (ILI) was 1.2%, which is below the national baseline of 2.2%.

Clinical Laboratory Data

	Week 40
No. of specimens tested	12,336
No. of positive specimens (%)	107 (0.9%)
Positive specimens by type	
Influenza A	75 (70.1%)
Influenza B	32 (29.9%)

Public Health Laboratory Data

	Week 40
No. of specimens tested	340
No. of positive specimens*	24
Positive specimens by type/subtype	
Influenza A	19 (79.2%)
(H1N1)pdm09	9 (75.0%)
H3N2	3 (25.0%)
Subtyping not performed	7
Influenza B	5 (20.8%)
Yamagata lineage	4 (80.0%)
Victoria lineage	1 (20.0%)
Lineage not performed	0

HHS Surveillance Region Data:

*U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet)
2017-2018 Influenza Season
HHS Region 6 (AR, LA, NM, OK, and TX) (Baseline: 4.0%)
Data as of Friday, October 12, 2018*

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
201840	266	673	736	434	192	133	2168	108414	2	2.2

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
201840	8	45	0	2	0	0	0	0	0	18	1574	21	1.33	10	11
Total	0	45	0	2	0	0	0	0	0	.	1574	21	1.33	10	11

2018-2019 Season

Antiviral Resistance:

Antiviral Resistance: During May 20-October 6, 2018, 156 specimens (61 influenza A(H1N1)pdm09, 51 influenza A(H3N2), and 44 influenza B viruses) collected in the United States were tested for susceptibility to the neuraminidase inhibitors (oseltamivir, zanamivir, and peramivir). All tested viruses were sensitive to all three recommended antiviral medications.

While all of the recently circulating influenza viruses are susceptible to the neuraminidase inhibitor antiviral medications oseltamivir, zanamivir, and peramivir, rare sporadic instances of oseltamivir-resistant and peramivir-resistant influenza A(H1N1)pdm09 viruses and oseltamivir-resistant influenza A(H3N2) viruses have been detected worldwide. Antiviral treatment as early as possible is recommended for patients with confirmed or suspected influenza who have severe, complicated, or progressive illness; who require hospitalization; or who are at [high risk](#) for serious influenza-related complications. Additional information on recommendations for treatment and chemoprophylaxis of influenza virus infection with antiviral agents is available at <http://www.cdc.gov/flu/antivirals/index.htm>.

Antigenic & Genetic Characterization:

CDC has antigenically or genetically characterized 170 influenza viruses collected May 20 – October 6, 2018, and submitted by U.S. laboratories, including 63 influenza A(H1N1)pdm09 viruses, 64 influenza A(H3N2) viruses, and 43 influenza B viruses.

Influenza A Viruses

- **A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 63 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Fifty-seven A(H1N1)pdm09 viruses were antigenically characterized, and 57 (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 2018-2019 Northern Hemisphere influenza vaccines.
- **A (H3N2):** Phylogenetic analysis of the HA genes from 64 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=24), subclade 3C.2a1 (n=35) or clade 3C.3a (n=5). Thirty influenza A(H3N2) viruses were antigenically characterized by FRA with ferret antisera, and 28 (93.3%) A(H3N2) viruses tested were well-inhibited (reacting at titers that were within fourfold 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 2018-2019 Northern Hemisphere influenza vaccines.

Influenza B Viruses

- **B/Victoria:** Phylogenetic analysis of 10 B/Victoria-lineage viruses indicate that all HA genes belonged to genetic clade V1A, however genetic subclades which are antigenically distinct have emerged. The majority of recent B/Victoria-lineage viruses belonged to a subclade of viruses with a 6-nucleotide deletion (encoding amino acids 162 and 163) in the HA (V1A.1, previously abbreviated as V1A-2Del). In addition, a small number of B/Victoria-lineage viruses have a three amino acid deletion (162-164) in the HA protein (abbreviated as V1A-3Del). Nine (90%) B/Victoria lineage viruses were well-inhibited by ferret antisera raised against cell-propagated B/Colorado/06/2017-like (V1A.1) reference virus, representing the B/Victoria lineage component of 2018-2019 Northern Hemisphere influenza vaccines. One (10%) B/Victoria lineage virus 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 reference virus, and belonged to clade V1A.
- **B/Yamagata:** Phylogenetic analysis of 33 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 32 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 2018-2019 Northern Hemisphere quadrivalent vaccines.