

Influenza Surveillance Report

www.infectiousdisease.dhh.la.gov

Week 48: 11/25/18 - 12/1/18

Influenza activity remains above baseline in Louisiana. Percent positivity of influenza tests remains below 3%. Rhino/Enteroviruses and RSV represent the majority (70%) 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.

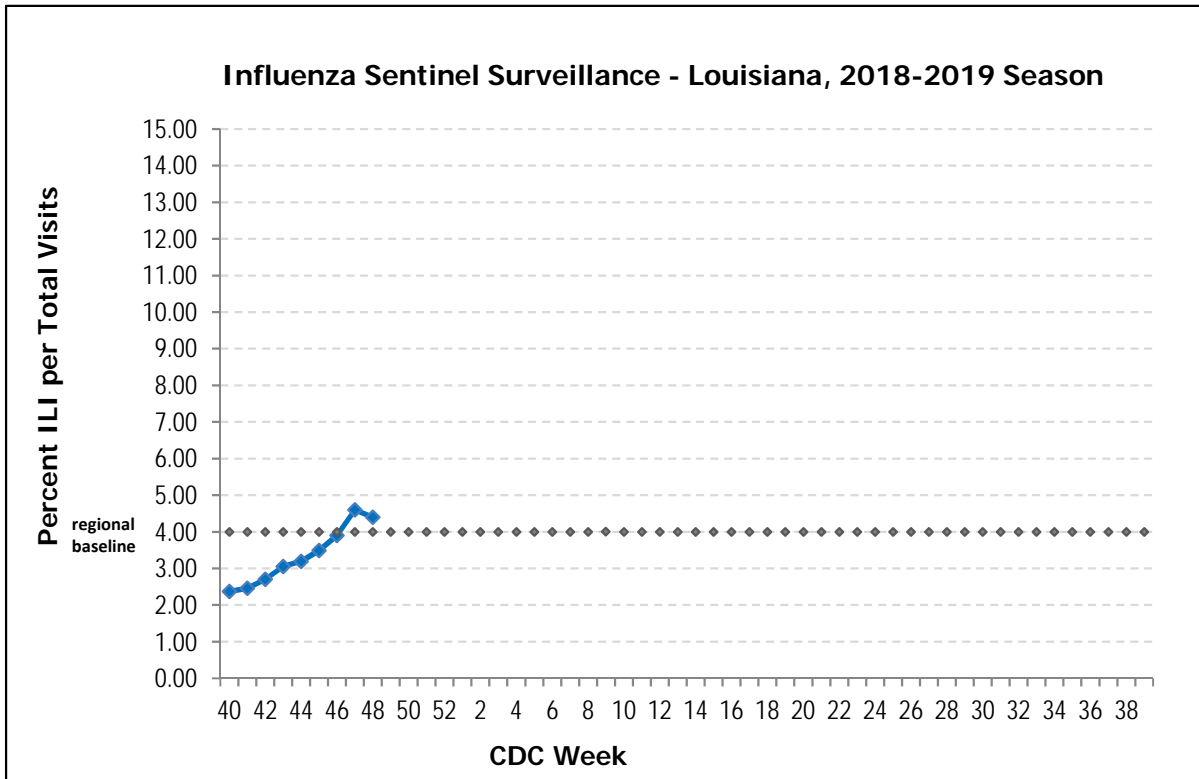


Laboratory testing: Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information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

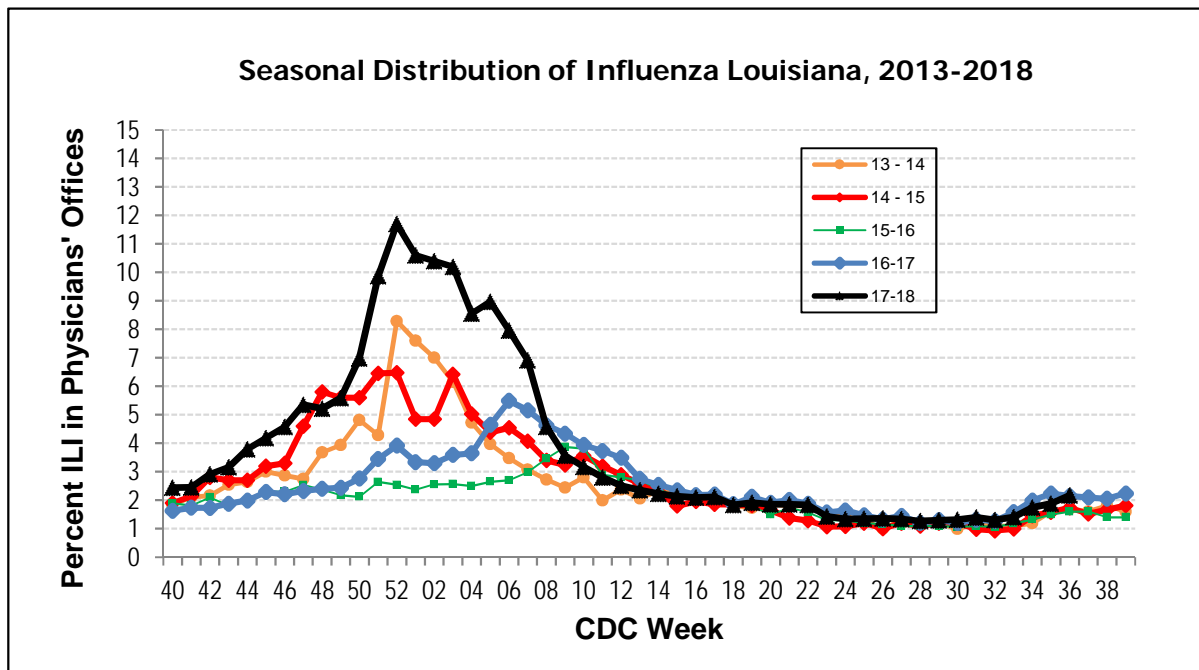
Page 2 : ILI Activity
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Page 5 & 6: Regional & National Data

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.

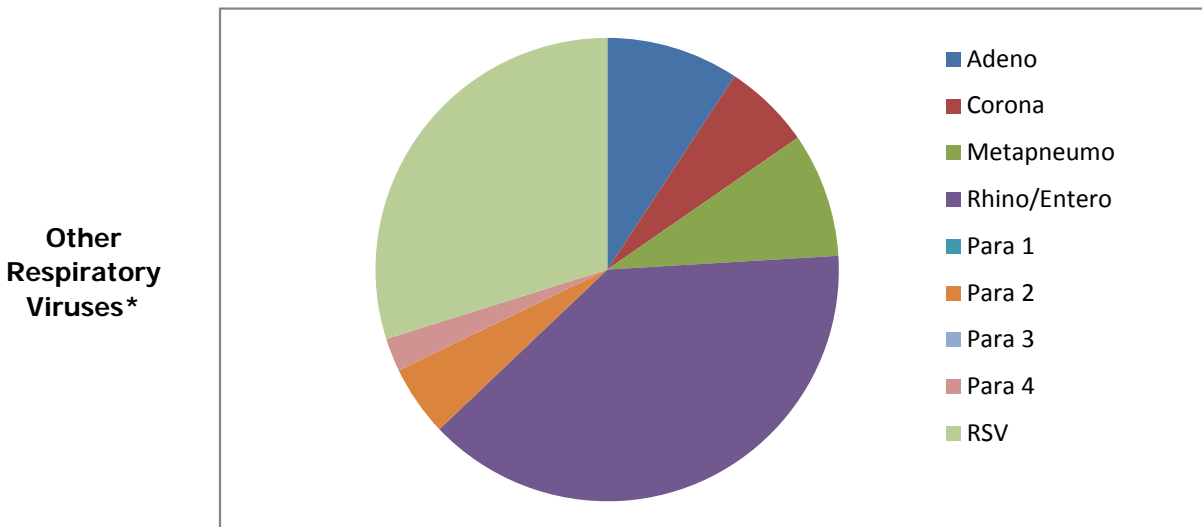
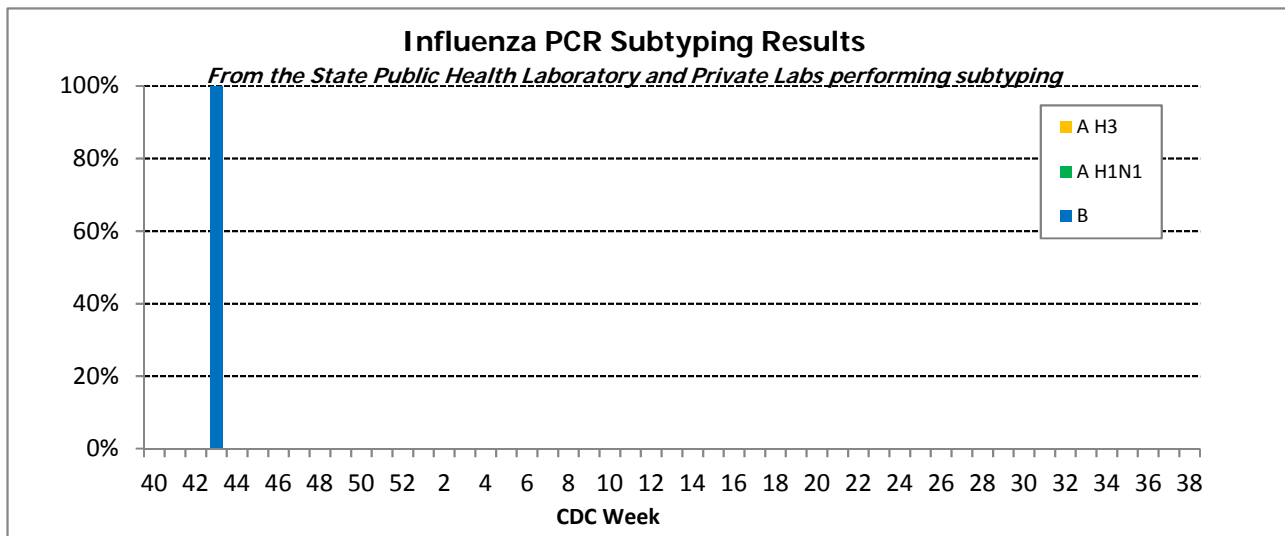
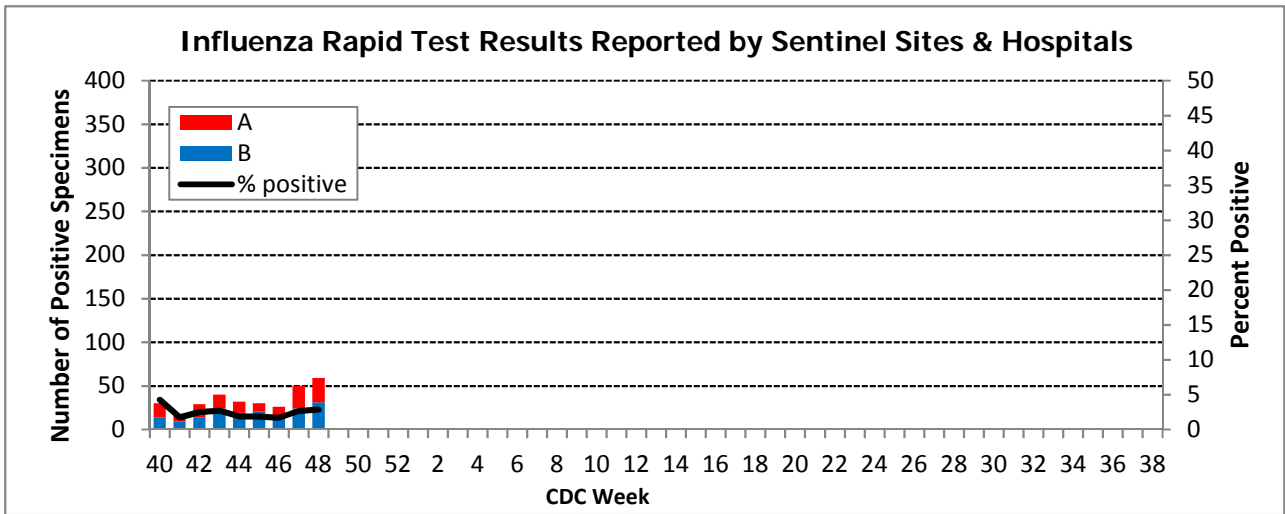


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.



2018-2019 Season

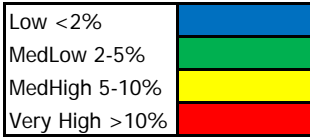
Virologic Surveillance



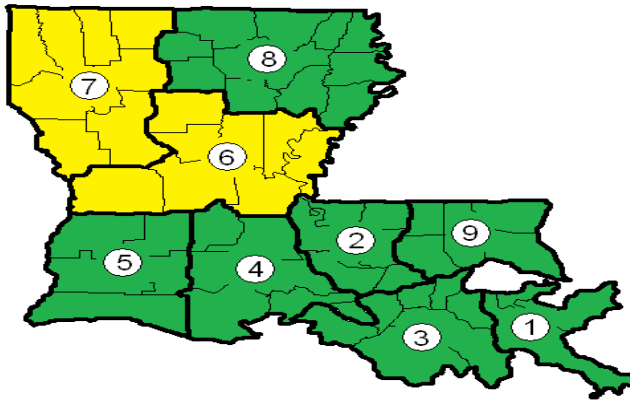
*Based on results from the State Public Health Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 2 weeks.

2018-2019 Season

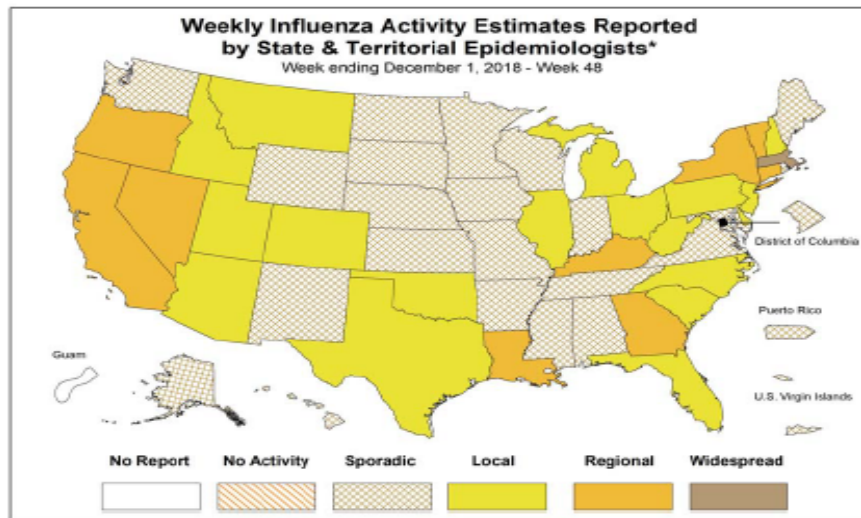
Geographical Distribution of ILI*



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



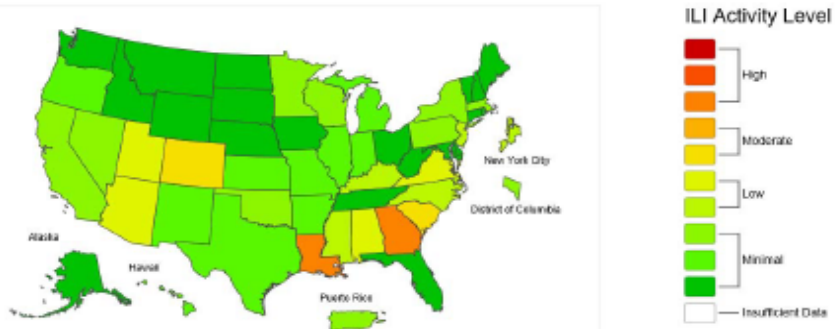
Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists



* 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 48 ending Dec: 01, 2018

ILINet Activity Indicator Map



2018-2019 Season

National Surveillance

Influenza activity in the United States increased slightly.

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.

No influenza-associated pediatric deaths were reported to CDC for week 48.

Clinical Laboratory Data

	Week 48	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	21,851	186,197
No. of positive specimens (%)	925 (4.2%)	5,059 (2.7%)
<i>Positive specimens by type</i>		
Influenza A	846 (91.5%)	4,303 (85.1%)
Influenza B	79 (8.5%)	756 (14.9%)

Public Health Laboratory Data

	Week 48	Data Cumulative since September 30, 2018 (week 40)
No. of specimens tested	670	7,809
No. of positive specimens*	180	1,111
<i>Positive specimens by type/subtype</i>		
Influenza A	170 (94.4%)	1,008 (90.7%)
(H1N1)pdm09	125 (82.2%)	740 (80.8%)
H3N2	27 (17.8%)	176 (19.2%)
Subtyping not performed	18	92
Influenza B	10 (5.6%)	103 (9.3%)
Yamagata lineage	7 (100%)	60 (74.1%)
Victoria lineage	0 (0%)	21 (25.9%)
Lineage not performed	3	22

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, December 7, 2018

CDC Week	# Sites Reporting	ILI 0-4 years	ILI 5-24 years	ILI 25-49 years	ILI 50-64 years	ILI 65 and older	Total ILI	Total Patient Visits	% Unweighted ILI	% Weighted ILI
201845	288	1046	1093	682	218	162	3201	113737	2.8	2.9
201846	286	1245	1079	731	260	182	3497	109473	3.2	3.2
201847	277	1295	896	781	319	199	3490	96826	3.6	3.5
201848	272	1289	1052	903	404	241	3889	116903	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
201845	8	127	0	12	2	0	0	1	0	24	3014	45	1.49	30	15
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	22	3187	104	3.26	91	13
201848	7	38	0	6	6	0	0	0	1	19	2546	64	2.51	59	5

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	158	0 (0%)	0 (0%)	158	0 (0%)	0 (0%)	158	0 (0%)	0 (0%)
A(H1N1)pdm09	93	0 (0%)	0 (0%)	93	0 (0%)	0 (0%)	93	0 (0%)	0 (0%)
A(H3N2)	43	0 (0%)	0 (0%)	43	0 (0%)	0 (0%)	43	0 (0%)	0 (0%)
B/Victoria	7	0 (0%)	0 (0%)	7	0 (0%)	0 (0%)	7	0 (0%)	0 (0%)
B/Yamagata	15	0 (0%)	0 (0%)	15	0 (0%)	0 (0%)	15	0 (0%)	0 (0%)

Antigenic & Genetic Characterization:

CDC has antigenically or genetically characterized 163 influenza viruses collected September 30, 2018 – December 1, 2018, and submitted by U.S. laboratories, including 94 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 94 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Sixty-seven A(H1N1)pdm09 viruses were antigenically characterized, and all 67 (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. 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). 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 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 8 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.