# Influenza Surveillance Report

www.infectiousdisease.dhh.la.gov **Week 50: 12/10/17-12/16/17**

**Influenza activity continues to increase in Louisiana. The percent of positive influenza tests also continues to increase. The most commonly reported other respiratory viruses are RSV and Rhino/Enterovirus.**

**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.**

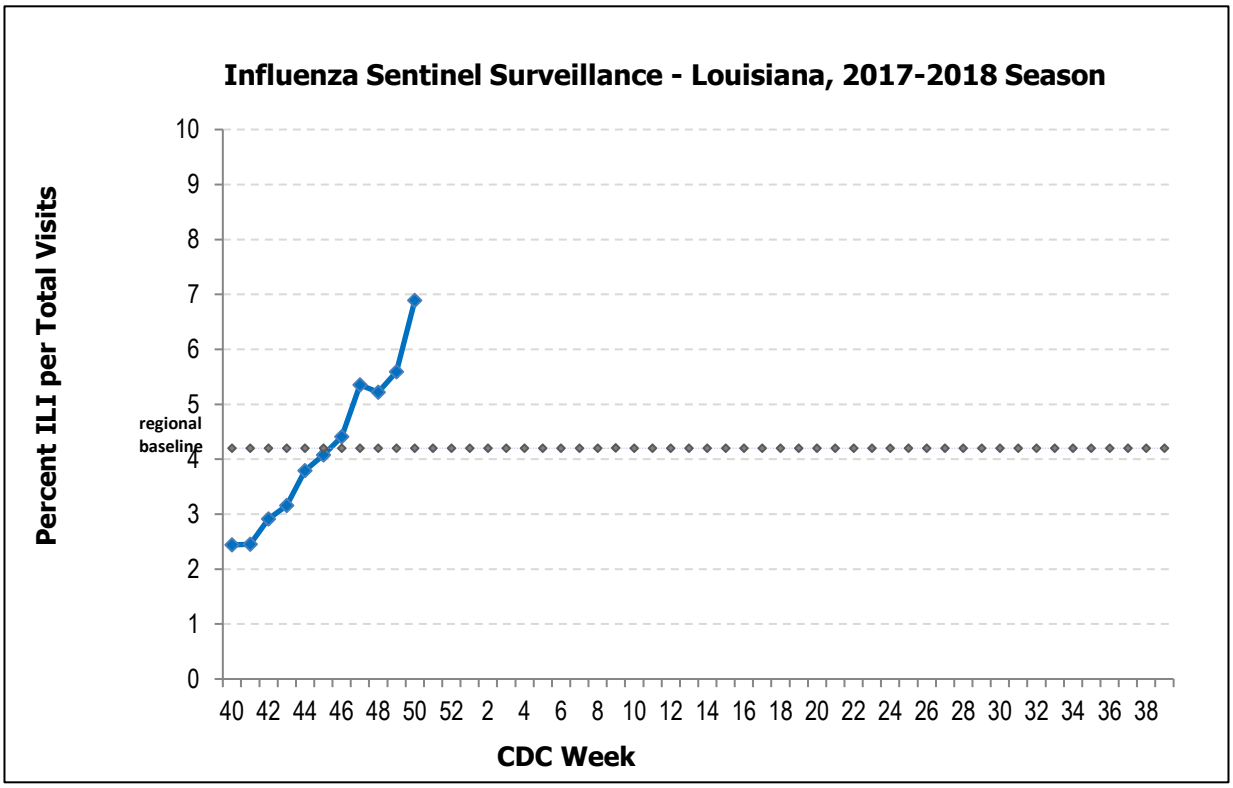
Taken together, ILI surveillance and laboratory surveillance provide a clear picture of the influenza activity occurring in Louisiana each week. If you have any questions about our surveillance system or would like more information, please contact Julie Hand at 504-568-8298 or julie.hand@la.gov.

**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.

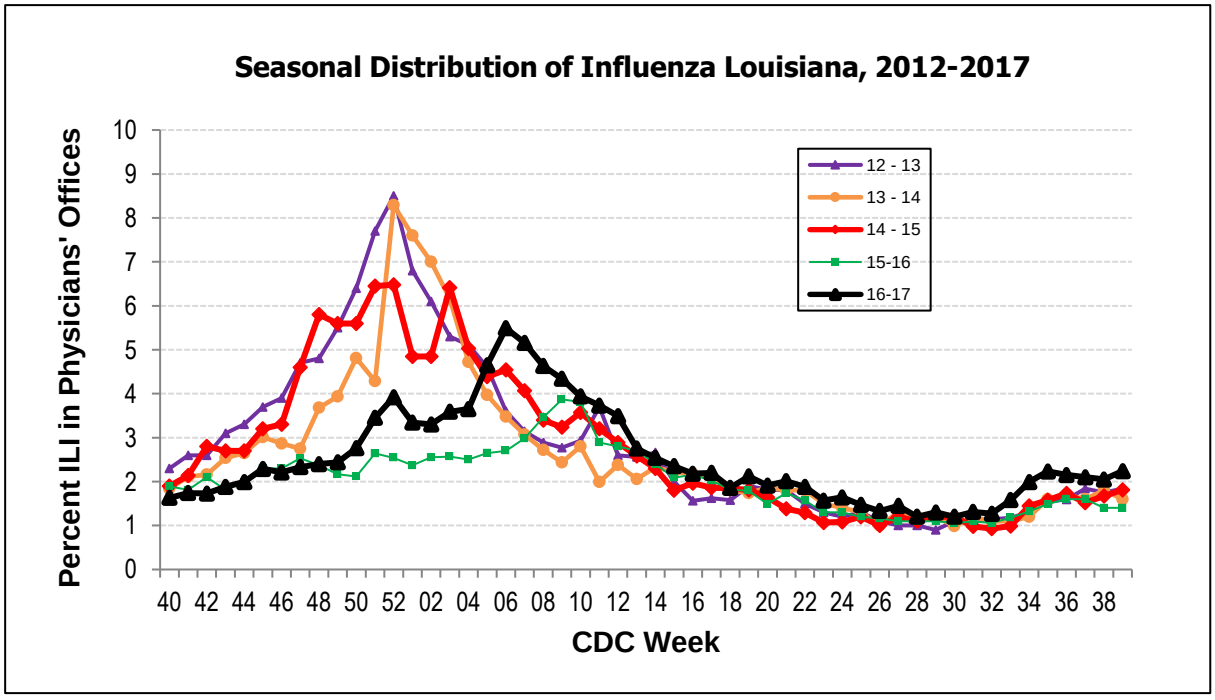

**Laboratory testing:** Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information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

## 2017-2018 Season

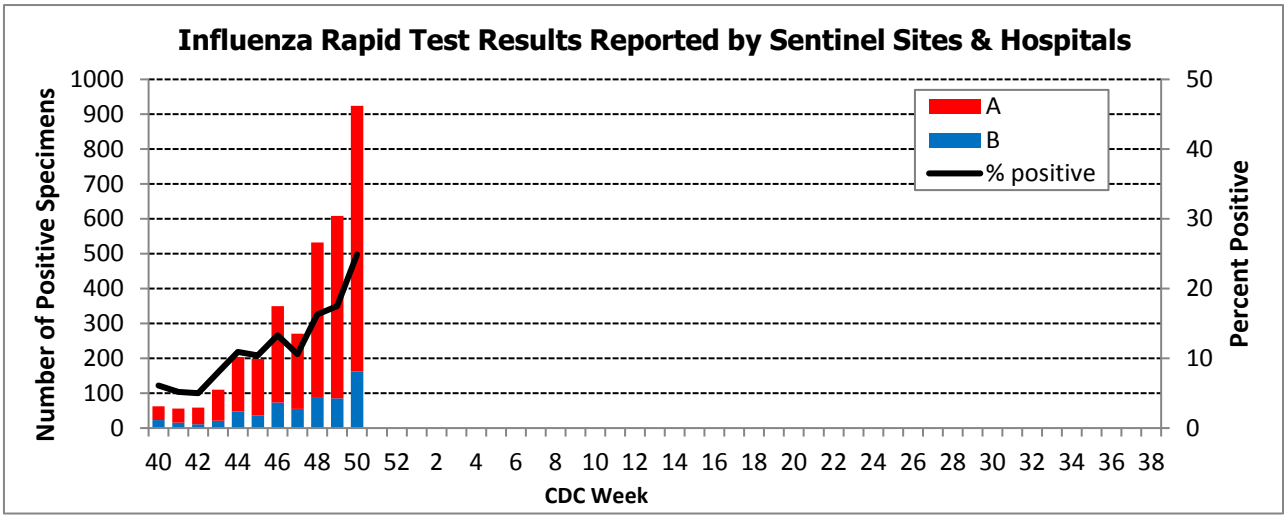
This graph shows the percentage of visits for ILI over the total number of visits for sentinel surveillance sites. This is the best approach to estimate the magnitude of influenza transmission. ILI counts do include some viral infections other than influenza, but experience over the last 50 years has 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.

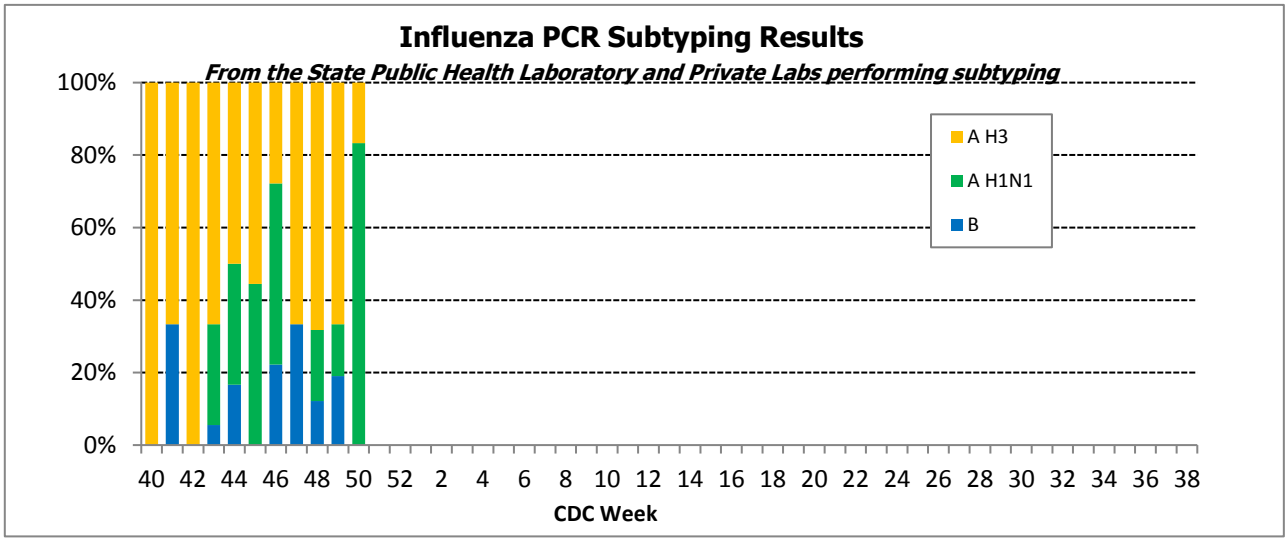



This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.

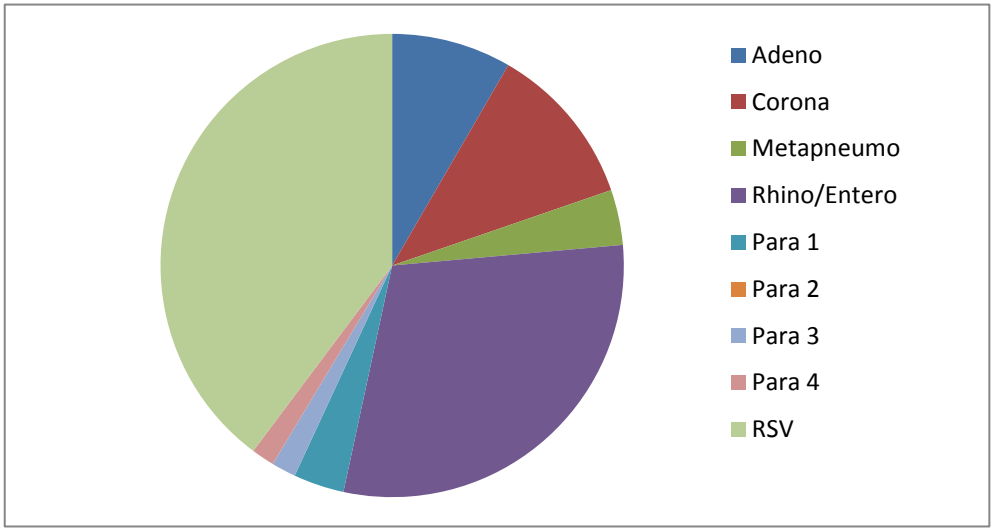


## Virologic Surveillance



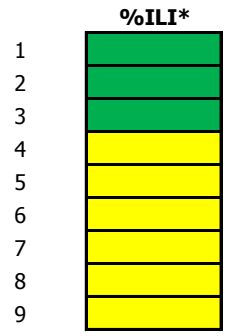



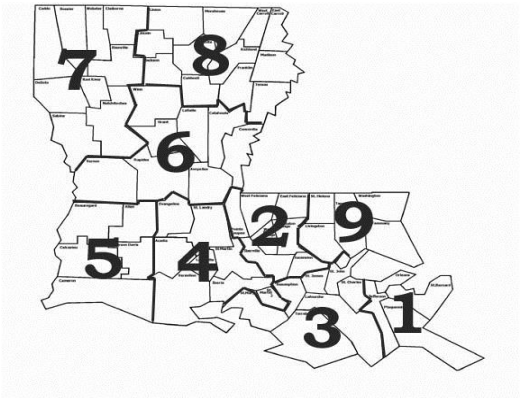

**Other Respiratory Viruses***




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

## Geographical Distribution of ILI

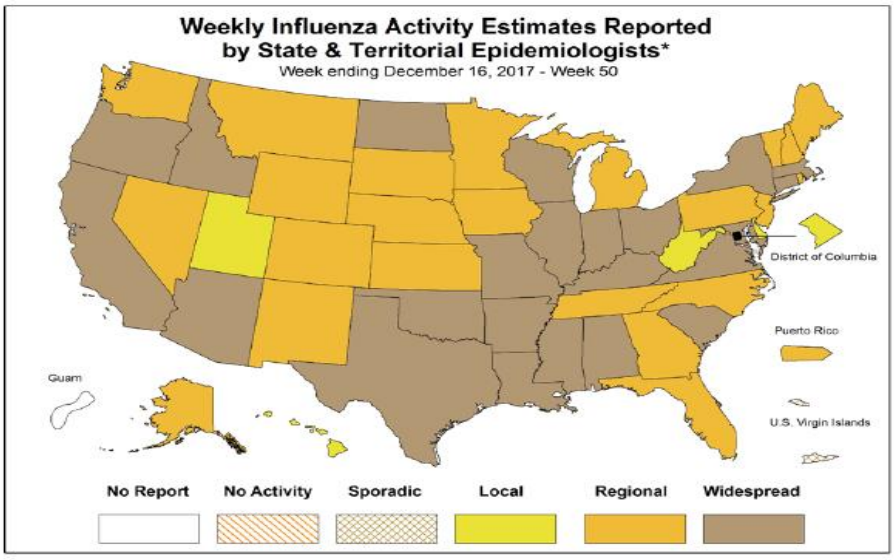



| | |
|---|---|
| Low <2% | |
| MedLow 2-5% | |
| MedHigh 5-10% | |
| Very High >10% | |

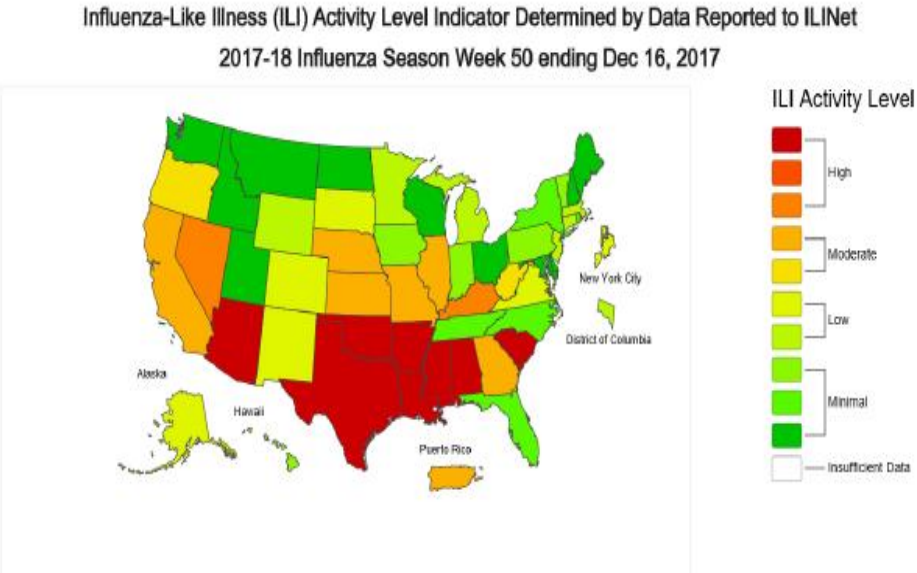
** %ILI over the last 4 weeks based on sentinel surveillance data*

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




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

**ILINet Activity Indicator Map**



## National Surveillance

During week 50, influenza activity sharply increased in the United States.

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 3.5%, which is above the national baseline of 2.2%.

## Clinical Laboratory Data

| | Week 50 | Data Cumulative since October 1, 2017 (Week 40) |
|---|---|---|
| **No. of specimens tested** | 23,607 | 225,889 |
| **No. of positive specimens (%)** | 3,308 (14.0%) | 13,475 (6.0%) |
| ***Positive specimens by type*** | | |
| **Influenza A** | 2,812 (85.0%) | 10,567 (78.4%) |
| **Influenza B** | 496 (15.0%) | 2,908 (21.6%) |

## Public Health Laboratory Data

| | Week 50 | Data Cumulative since October 1, 2017 (Week 40) |
|---|---|---|
| **No. of specimens tested** | 1,623 | 15,994 |
| **No. of positive specimens*** | 795 | 5,046 |
| ***Positive specimens by type/subtype*** | | |
| **Influenza A** | 689 (86.7%) | 4,387 (86.9%) |
| **(H1N1)pdm09** | 58 (8.4%) | 366 (8.3%) |
| **H3N2** | 611 (88.7%) | 3,965 (90.4%) |
| **Subtyping not performed** | 20 (2.9%) | 56 (1.3%) |
| **Influenza B** | 106 (13.3%) | 659 (13.1%) |
| **Yamagata lineage** | 75 (70.8%) | 438 (66.5%) |
| **Victoria lineage** | 10 (9.4%) | 39 (5.9%) |
| **Lineage not performed** | 21 (19.8%) | 182 (27.6%) |

## 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: 4.2%) Data as of Friday, December 22, 2017*

| 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 |
|---|---|---|---|---|---|---|---|---|---|---|
| 201747 | 275 | 1335 | 1099 | 853 | 353 | 257 | 3897 | 94065 | 4.1 | 4.2 |
| 201748 | 281 | 1358 | 1486 | 1326 | 527 | 394 | 5091 | 118575 | 4.3 | 4.7 |
| 201749 | 270 | 1258 | 1616 | 1139 | 490 | 323 | 4826 | 106206 | 4.5 | 5.2 |
| 201750 | 262 | 1656 | 2758 | 1874 | 782 | 490 | 7560 | 112603 | 6.7 | 8.3 |

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 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 201747 | 8 | 70 | 0 | 12 | 19 | 0 | 1 | 0 | 3 | 25 | 3967 | 356 | 8.97 | 286 | 70 |
| 201748 | 8 | 200 | 0 | 14 | 67 | 0 | 6 | 0 | 4 | 24 | 4250 | 440 | 10.35 | 356 | 84 |
| 201749 | 8 | 125 | 4 | 11 | 30 | 0 | 6 | 0 | 2 | 23 | 4024 | 566 | 14.07 | 466 | 100 |
| 201750 | 7 | 71 | 0 | 14 | 15 | 0 | 1 | 0 | 5 | 19 | 3818 | 828 | 21.69 | 755 | 73 |

## Antiviral Resistance:

Neuraminidase Inhibitor Resistance Testing Results on Samples Collected Since October 1, 2017

| | Oseltamivir | | Zanamivir | | Peramivir | |
|---|---|---|---|---|---|---|
| | Virus Samples tested (n) | Resistant Viruses, Number (%) | Virus Samples tested (n) | Resistant Viruses, Number (%) | Virus Samples tested (n) | Resistant Viruses, Number (%) |
| Influenza A (H1N1)pdm09 | 79 | 0 (0.0) | 67 | 0 (0.0) | 79 | 0 (0.0) |
| Influenza A (H3N2) | 391 | 0 (0.0) | 391 | 0 (0.0) | 304 | 0 (0.0) |
| Influenza B | 85 | 0 (0.0) | 85 | 0 (0.0) | 85 | 0 (0.0) |

## Antigenic & Genetic Charactization:

CDC has antigenically or genetically characterized 526 influenza viruses collected during October 1 – December 16, 2017, and submitted by U.S. laboratories, including 63 influenza A(H1N1)pdm09 viruses, 336 influenza A(H3N2) viruses, and 127 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. 41 A(H1N1)pdm09 viruses were antigenically characterized, and all were antigenically similar (analyzed using HI with ferret antisera) to the reference 6B.1 virus A/Michigan/45/2015, representing the recommended influenza A(H1N1)pdm09 reference virus for the 2017–18 Northern Hemisphere influenza vaccines.

- **A(H3N2):** Phylogenetic analysis of the HA genes from 336 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=265), subclade 3C.2a1 (n=68) or clade 3C.3a (n=3). 88 influenza A(H3N2) viruses were antigenically characterized, and 87 (98.9%) 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/Michigan/15/2014 (3C.2a), a cell propagated A/Hong Kong/4801/2014-like reference virus representing the A(H3N2) component of 2017–18 Northern Hemisphere influenza vaccines.

### Influenza B Viruses

- **B/Victoria:** Phylogenetic analysis of 12 B/Victoria-lineage viruses indicate that all HA genes belonged to genetic clade V1A, the same genetic clade as the vaccine reference virus, B/Brisbane/60/2008. However, a small number of viruses identified in 2017 had a 6-nucleotide deletion (encoding amino acids 162 and 163) in the HA (abbreviated as V1A-2Del). One (50%) of two B/Victoria lineage viruses were well-inhibited by ferret antisera raised against cell -propagated B/Brisbane/60/2008 reference virus, representing a recommended B virus component of 2017–18 Northern Hemisphere influenza vaccines. One 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/Brisbane/60/2008, and this virus had the two amino acid deletion in the HA of the V1A-2Del viruses.

- **B/Yamagata:** Phylogenetic analysis of 115 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 70 influenza B/Yamagata-lineage viruses were antigenically characterized, and all were antigenically similar to cell propagated B/Phuket/3073/2013, the reference vaccine virus representing the influenza B/Yamagata-lineage component of the 2017–18 Northern Hemisphere quadrivalent vaccines.