Influenza Surveillance Update

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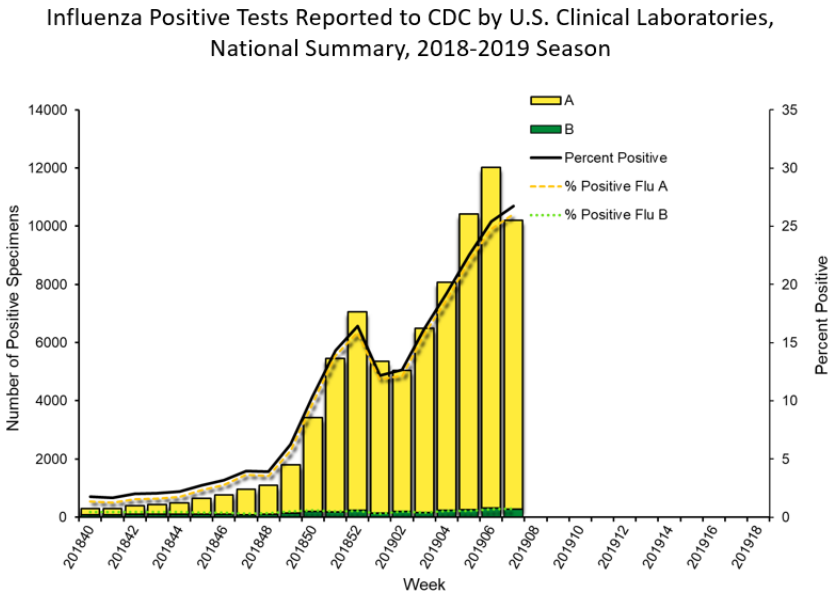
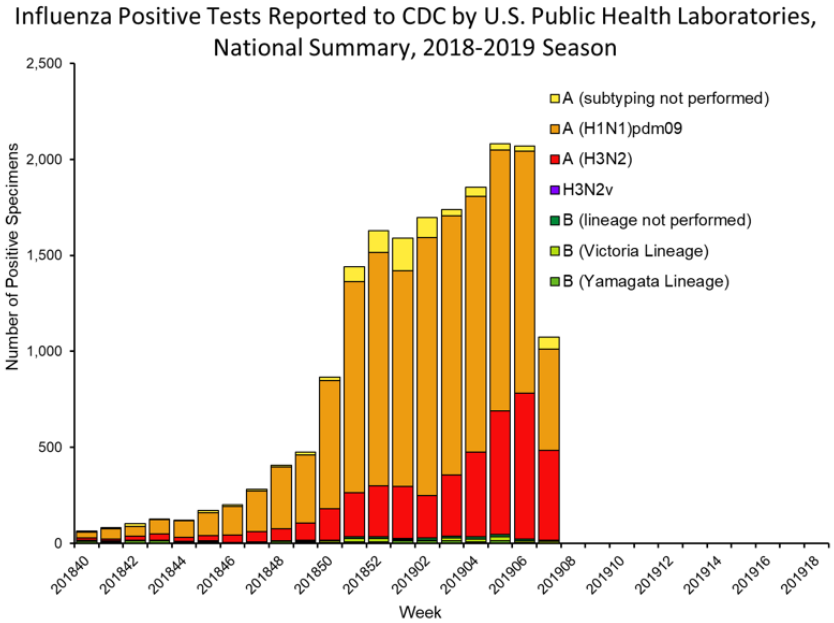
Advisory Committee on Immunization Practices
February 27, 2019

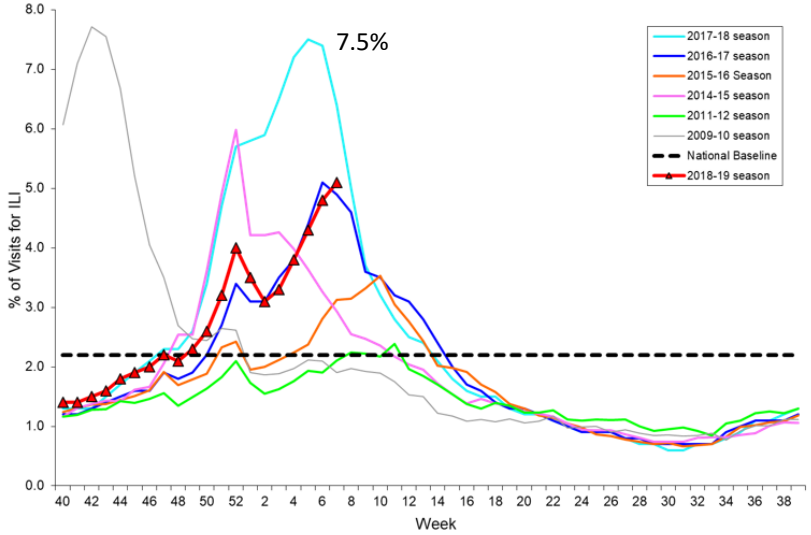
Influenza Virologic Surveillance, 2018-2019 Season



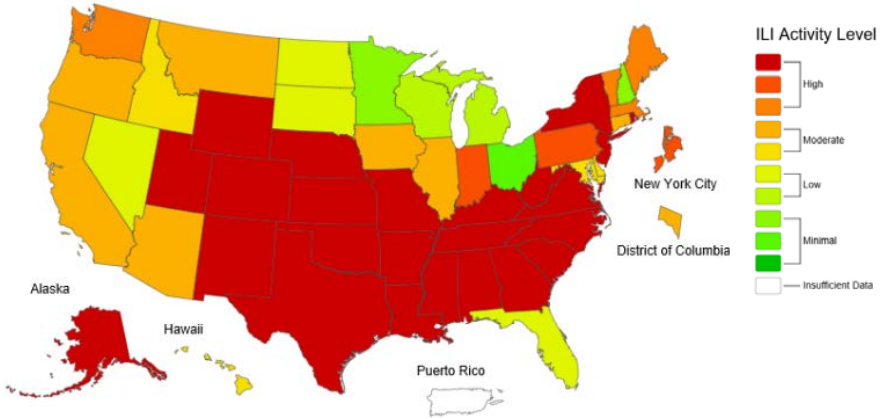


Outpatient Visits for Influenza–like Illness

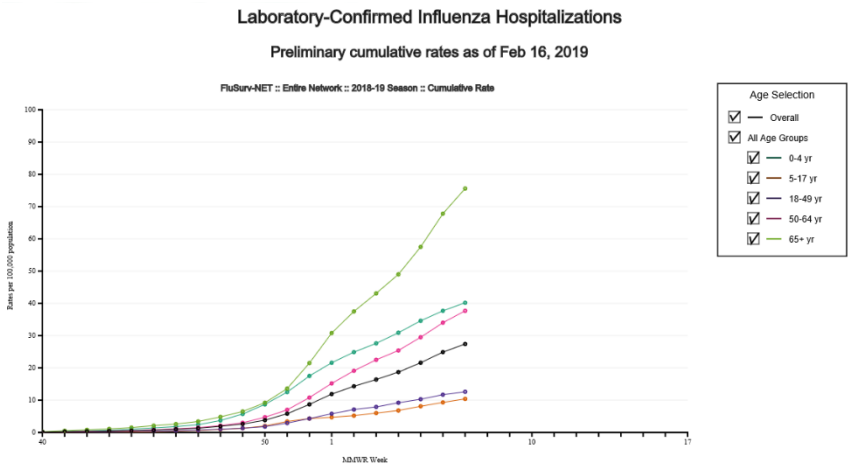
Percentage of Visits for Influenza-like Illness (ILI) Reported by the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet), Weekly National Summary, 2018-2019 and Selected Previous Seasons



Influenza-like Illness Activity Level
2018-19 Season, Week 7 ending Feb 16, 2019

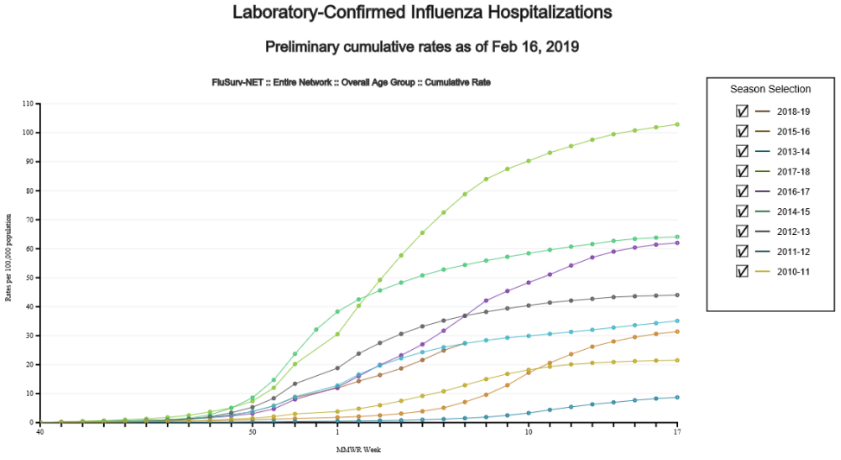


Laboratory Confirmed Influenza-Associated Hospitalizations, FluSurvNet, 2018-19

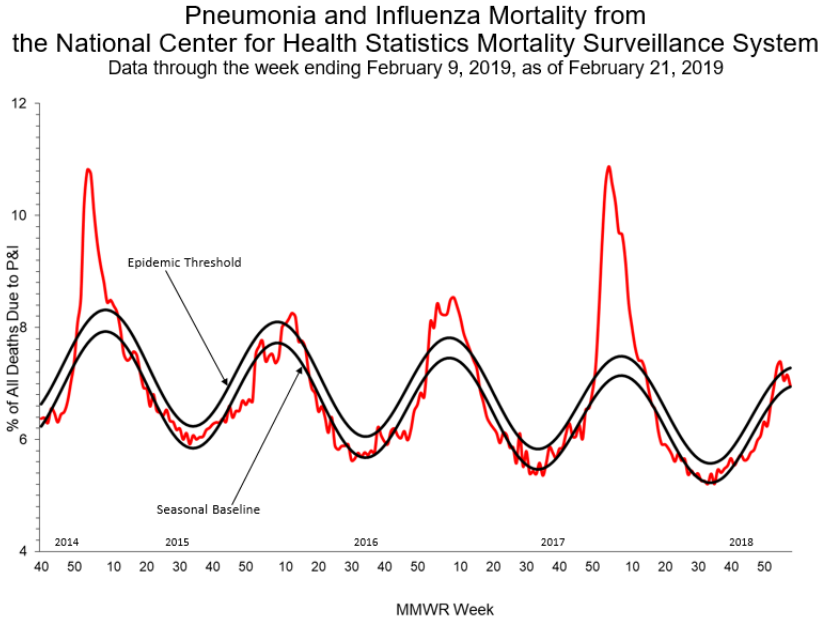


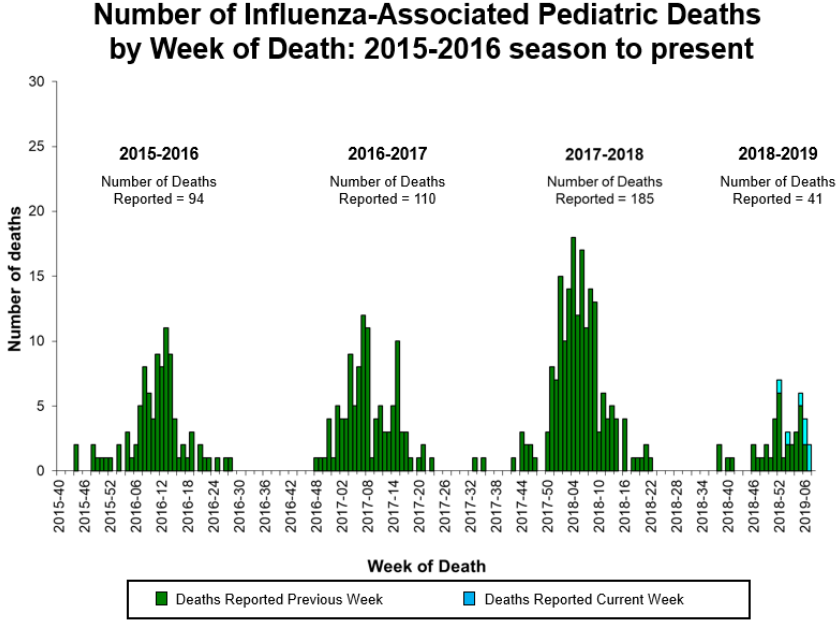
Overall: 27.4

≥65: 75.6 50-64: 37.7 18-49: 12.6 5-17 10.4 0-4: 40.2



Influenza-Associated Mortality





2018-19 Flu Season: Preliminary Burden Estimates

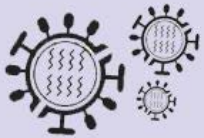
CDC estimates that, from **October 1, 2018,** through **February 16, 2019**, there have been:

17.7 million – 20.4 million
flu **illnesses**

8.2 million – 9.6 million
flu **medical visits**

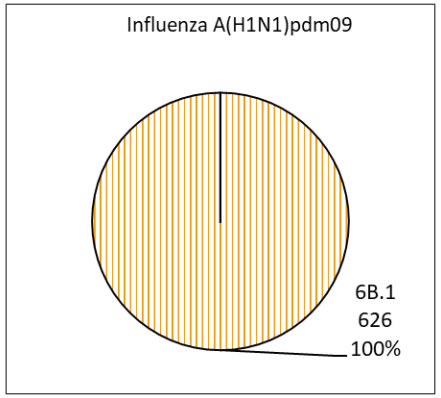
214,000 – 256,000
flu **hospitalizations**

13,600 – 22,300
flu **deaths**



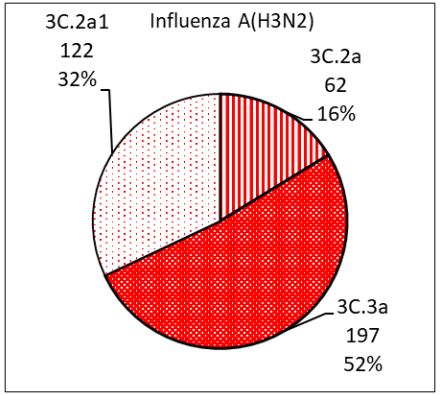
www.cdc.gov/flu/

Characterization of U.S. Influenza A (H1N1)pdm09 Viruses Collected September 30, 2018 to Present



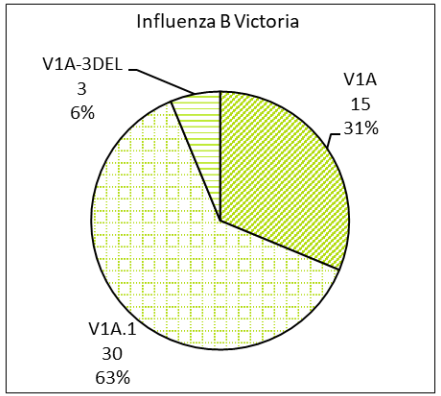
- All 626 influenza A (H1N1)pdm09 viruses tested belong to genetic group 6B.1
- Considerable genetic diversity within clade 6B.1 has emerged
- 259 of 263 (98.5%) A(H1N1)pdm09 viruses antigenically characterized using a hemagglutination inhibition (HI) assay with ferret antisera were similar to the egg and cell culture-propagated A/Michigan/45/2015 reference virus
- Testing with human sera showed reduced titers against some recent influenza A (H1N1)pdm09 viruses compared to titers against A/Michigan/45/2015

Characterization of U.S. Influenza A (H3N2) Viruses Collected September 30, 2018 to Present



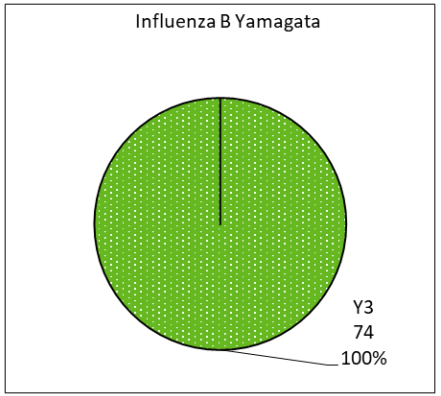
- Phylogenetic analysis of the HA genes of recent H3N2 viruses show extensive genetic diversity with multiples clades/subclades co-circulating
- The proportion and geographic spread of viruses belonging to clade 3C.3a has increased in recent weeks
- 128 of 194 (66%) A(H3N2) viruses antigenically characterized by FRA were well-inhibited 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.
- 65 of 66 (98.5%) viruses that reacted poorly against the A/Singapore reference virus (≥ 8-fold reduced) belonged to clade 3C.3a

Characterization of U.S. Influenza B Victoria Lineage Viruses Collected September 30, 2018 to Present



- Three genetic groups of B/Victoria lineage viruses are co-circulating
- 33 of 40 (82.5%) B/Victoria lineage viruses antigenically characterized were similar to the cell-propagated B/Colorado/06/2017-like V1A.1 reference virus.
- All 7 viruses that reacted poorly belonged to clade V1A

Characterization of U.S. Influenza B Yamagata Lineage Viruses Collected September 30, 2018 to Present



- All B/Yamagata lineage viruses tested belong to a single genetic group, Y3
- All influenza B/Yamagata-lineage viruses antigenically characterized are 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.

Vaccine Virus Selection for 2019-20

- WHO Consultation on the Composition of Influenza Virus Vaccines for Use in the 2019-2020 Northern Hemisphere Influenza Season - February 18 – 21
  - A/Brisbane/02/2018 (H1N1)pdm09-like virus
  - A(H3N2) virus to be announced on 21 March 2019
  - B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage)
  - B/Phuket/3073/2013-like virus (B/Yamagata/16/88 lineage) – quadrivalent only
- March 6, 2019: Vaccines and Related Biological Products Committee Meeting

Summary

- Influenza activity remains elevated
- Influenza A(H1N1)pdm09 viruses have predominated overall but H3N2 viruses were detected more commonly than H1N1 viruses in the Southeast and have increased in other regions in recent weeks
- An increasing proportion of the H3N2 viruses belong to the 3C.3a genetic group which is antigenically distinct from the 3C.2a genetic group
- WHO's recommendation for the H3N2 component for the 2019-20 Northern Hemisphere vaccine has been delayed until March 21 to allow for the collection of more data and to allow for completion of testing of potential candidate vaccine viruses

For more information, contact CDC
1-800-CDC-INFO (232-4636)
TTY: 1-888-232-6348 www.cdc.gov

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.