Influenza Surveillance Report

2018–2019 Season

December 2019

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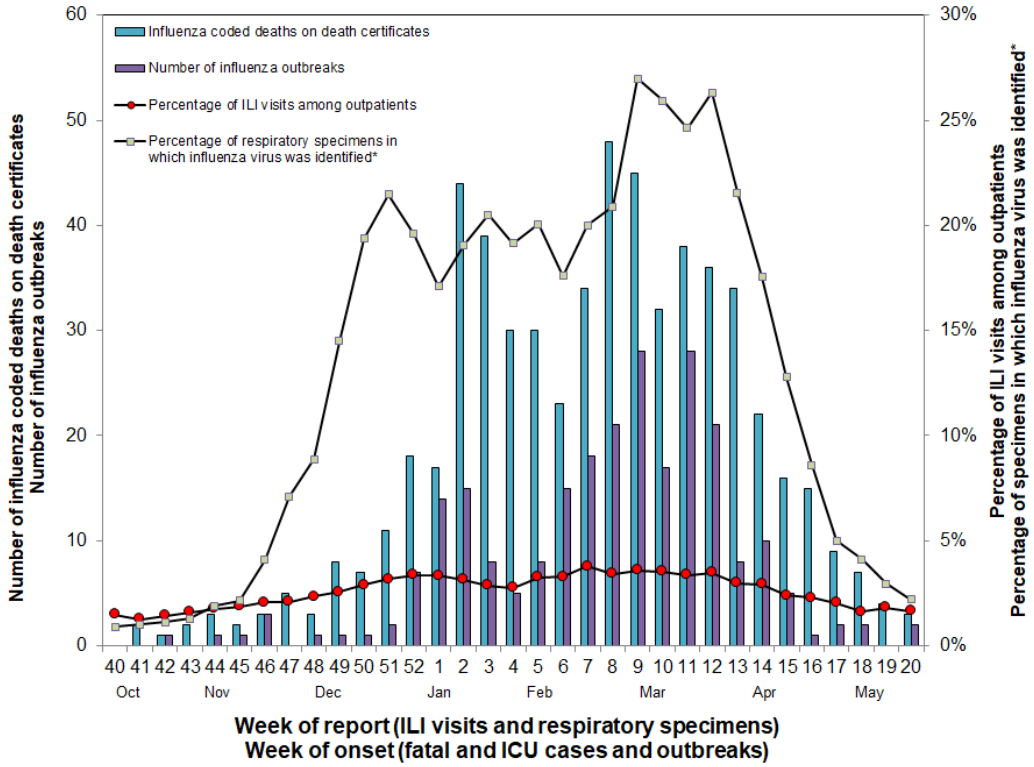
Table of Contents

Notes: This report will primarily focus on influenza surveillance in California; however, information on other respiratory viruses is provided where data are available. The majority of data in this report covers the influenza season (September 30, 2018–May 18, 2019 [calendar weeks 2018-40 – 2019-20]); however, some data sources cover the period September 30, 2018–September 28, 2019 (calendar weeks 2018-40 – 2019-39). Data presented in this report are as of October 5, 2019; any deviations from this are noted where applicable.

Synopsis

Nationally, the 2018–2019 influenza season (September 30, 2018–May 18, 2019) was a moderate severity season. Influenza-like illness (ILI) activity in the United States began increasing in November, peaked during mid-February, and returned to baseline in mid-April; the season lasted 21 weeks, making it the longest season in 10 years. Illness attributed to influenza A viruses predominated, with very little influenza B activity. Two waves of influenza A were notable during this prolonged season: influenza A(H1N1)pdm09 viruses from October 2018 to mid-February 2019 and influenza A(H3N2) viruses from February through May 2019.[1,2] In California, influenza activity was also moderate in severity, with moderate severity levels of hospitalizations for pneumonia and influenza at Northern Kaiser Permanente facilities and influenza-coded deaths on death certificates; however, outpatient visits for ILI remained within low severity levels. Influenza activity in California began increasing in mid-November, reached an initial peak in late December and early January, remained elevated until increasing to the season peak in mid- to late February, before returning to baseline levels in mid-April (Figure 1). The duration of this season was likely due to the initial predominance of influenza A (H1N1)pdm09 viruses through February, followed by a second wave, and subsequent predominance, of influenza A (H3N2) viruses during March through May. Very few influenza B viruses were identified.

Figure 1. Selected influenza surveillance parameters, California Department of Public Health, 2018–2019



*Specimens tested at clinical sentinel laboratories only

The percentage of ILI visits among outpatients had two periods of peak activity. The first, and smaller of the two peaks, occurred during the week ending December 29, 2018 (3.4%),

corresponding to the period in which influenza A (H1N1)pdm09 viruses were predominating. The second, and larger of the two peaks, occurred during the week ending February 16, 2019 (3.8%), corresponding to when influenza A (H3N2) virus activity was beginning to increase while influenza A (H1N1)pdm09 viruses were still circulating. The percentage of specimens testing positive for influenza at sentinel clinical laboratories began increasing in mid-November, reached a period of sustained elevated activity around 20% of specimens testing positive for influenza from the week ending December 15, 2018 through the week ending February 23, 2019 before increasing to the season peak (27.0%) during the week ending March 2, 2019. Activity remained near 25% of specimens testing positive through the week ending March 23, 2019 before beginning to decrease. The duration of this season was similar to that of the 2017–2018 influenza season; however, the severity of the 2017–2018 was much higher. A total of 301 confirmed respiratory outbreaks were reported during the 2018–2019 season; 246 were associated with influenza. Among the 246 influenza-associated outbreaks, influenza A was the most commonly identified influenza virus. The majority of influenza-associated outbreaks occurred in residential healthcare facilities; however, outbreaks occurring in residential care facilities are more likely to be identified and reported to CDPH than other respiratory outbreaks.

Fifteen laboratory-confirmed influenza-associated pediatric deaths were reported to the California Department of Public Health (CDPH) during September 30, 2018–September 28, 2019. This number is within the range (5 [reported during the 2007–2008 season] to 37 [reported during the 2008–2009 season]) of past influenza seasons since fatal pediatric influenza surveillance began in 2003. During the 2018–2019 season, 615 influenza coded deaths were identified on death certificates compared to 1,665 identified in 2017–2018.

Surveillance Data

A. CDPH Virologic Surveillance

The CDPH obtains data on laboratory-confirmed influenza and other respiratory viruses from a number of laboratories throughout the state. These laboratories include the CDPH Viral and Rickettsial Disease Laboratory (VRDL) and 24 local public health laboratories, collectively known as the Respiratory Laboratory Network (RLN), and 16 clinical, academic, and hospital laboratories, which are referred to as clinical sentinel laboratories.

During the 2018–2019 influenza season, influenza A viruses were the most commonly identified influenza viruses identified by RLN and clinical sentinel laboratories. Influenza A (H1N1)pdm09 viruses predominated overall and through February, but influenza A (H3N2) viruses predominated from March through May in California (Figure 2). Very few influenza B viruses were identified during the 2018–2019 influenza season. These virologic surveillance data are similar to national findings.[1,2]

The proportion of specimens testing positive at clinical sentinel laboratories for all types of influenza first exceeded 10% – an indication that higher than normal levels of influenza virus were circulating – during the week ending December 8, 2018 (Figure 3). The proportion of influenza-positive specimens peaked at 27.0% during the week ending March 2, 2019; however, a

sustained level of elevated activity occurred during the week ending December 22, 2018 (21.5% of specimens tested positive for influenza) through the week ending March 30, 2019 (21.6% of specimens tested positive for influenza). Activity did not decline to less than 10% until the week ending April 20, 2019. National influenza activity peaked for six consecutive weeks during February 9–March 16 (range = 25.1%–26.2%).[1,2]

1. Respiratory Laboratory Network (RLN) Surveillance

The RLN laboratories offer polymerase chain reaction (PCR) testing for influenza A and influenza B, including influenza A subtyping and influenza B lineage typing, and some offer testing for respiratory syncytial virus (RSV), a common respiratory virus. RLN laboratories often receive specimens that have already tested positive for influenza at a clinical laboratory; therefore, the percentage of specimens testing positive for influenza at RLN laboratories is not an accurate indicator of influenza activity.

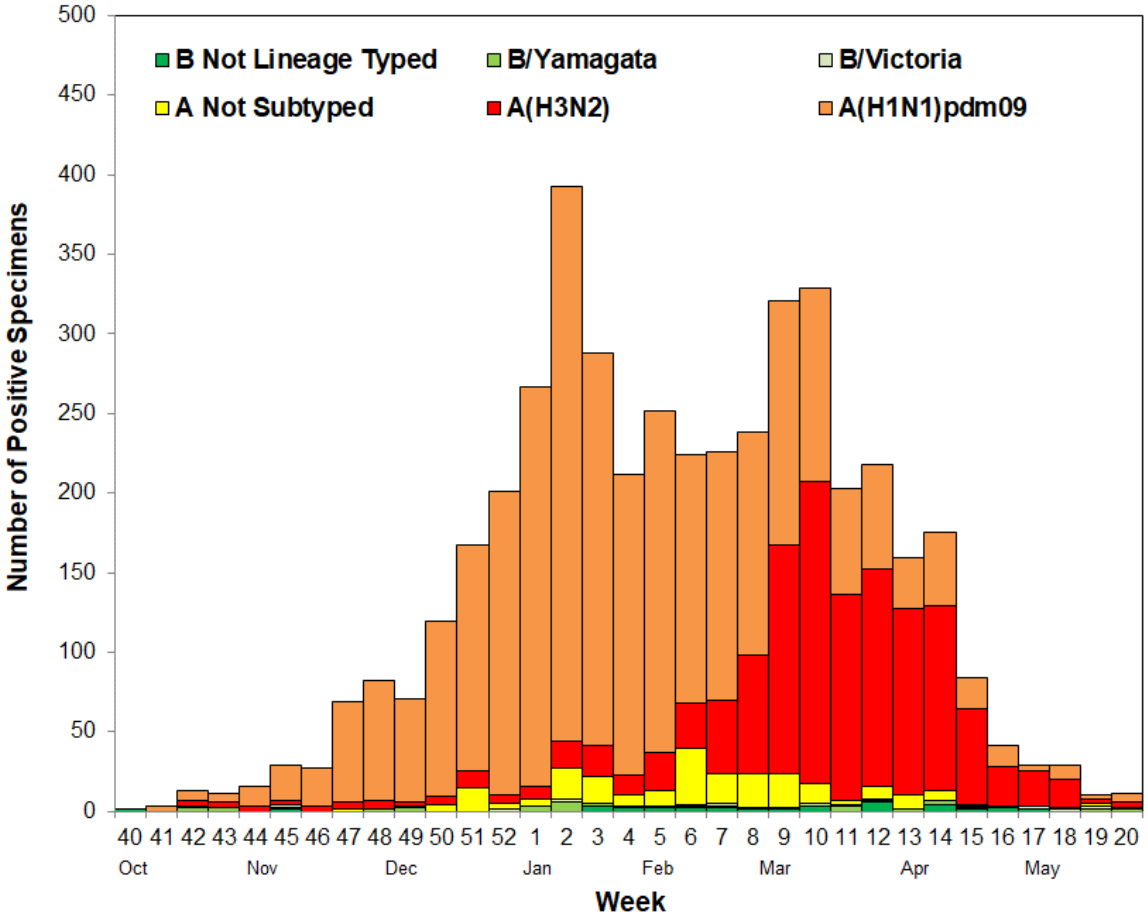
Of 7,815 specimens tested by RLN laboratories from September 30, 2018 through May 18, 2019, 4,514 (57.8%) were positive for influenza; of these, 4,426 (98.1%) were influenza A and 88 (1.9%) were influenza B (Table 1). Of the 4,514 positive influenza A specimens, 1,243 (28.1%) were A (H3N2), 2,962 (66.9%) were A (H1N1)pdm09, and 225 (5.1%) were not subtyped. Of the 88 positive influenza B specimens, 33 (37.5%) were B/Yamagata lineage, 23 (26.1%) were B/Victoria lineage, and 32 (36.4%) were not lineage typed. In addition to influenza testing, 1,384 specimens were tested for RSV by RLN laboratories; 167 (12.1%) were positive.

Table 1. RLN influenza and respiratory syncytial virus (RSV) surveillance results, September 30, 2018–May 18, 2019

	Total*		Northern		Bay Area		Central		Upper Southern		Lower Southern	
	No.	**(%)**	**No.**	**(%)**	**No.**	**(%)**	**No.**	**(%)**	**No.**	**(%)**	**No.**	**(%)**
Specimens tested for influenza	**7,815**		**205**		**2,502**		**930**		**2,214**		**1,964**	
Positive for influenza	4,514	(57.8)†	90	(43.9)†	1,198	(47.9)†	670	(72.0)†	909	(41.1)†	1,647	(83.9)†
Influenza A	4,426	(98.1)‡	90	(100.0)‡	1,183	(98.7)‡	664	(99.1)‡	891	(98.0)‡	1,598	(97.0)‡
*A (H1N1)pdm09***	2,962	(66.9)§	60	(66.7)§	780	(65.9)§	398	(59.9)§	602	(67.6)§	1,122	(70.2)§
*A (H3N2)***	1,243	(28.1)§	29	(32.2)§	370	(31.3)§	246	(37.0)§	167	(18.7)§	431	(27.0)§
Subtyping not performed	225	(5.1)§	1	(1.1)§	34	(2.9)§	22	(3.3)§	122	(13.7)§	46	(2.9)§
Influenza B	88	(1.9)‡	0	(0.0)‡	15	(1.3)‡	6	(0.9)‡	18	(2.0)‡	49	(3.0)‡
Yamagata	33	(37.5)¥	0	(0.0)¥	6	(40.0)¥	0	(0.0)¥	6	(33.3)¥	21	(42.9)¥
Victoria	23	(26.1)¥	0	(0.0)¥	4	(26.7)¥	0	(0.0)¥	3	(16.7)¥	16	(32.7)¥
Lineage typing not performed	32	(36.4)¥	0	(0.0)¥	5	(33.3)¥	6	(100.0)¥	9	(50.0)¥	12	(24.5)¥
Specimens tested for RSV	**1,384**		**72**		**775**		**392**		**41**		**104**	
Positive for RSV	167	(12.1)	12	(16.7)	119	(15.4)	29	(7.4)	7	(17.1)	0	(0.0)

* Participating laboratories:
Statewide: CDPH Viral and Rickettsial Disease Laboratory
Northern: Humboldt, Sacramento, and Shasta county public health laboratories
Bay Area: Alameda, Contra Costa, San Francisco, San Mateo, Santa Clara, Solano, and Sonoma county public health laboratories
Central: Monterey, San Joaquin, Stanislaus, and Tulare county public health laboratories
Upper Southern: Long Beach, Los Angeles, San Luis Obispo, Santa Barbara, and Ventura county public health laboratories
Lower Southern: Imperial, Orange, Riverside, San Bernardino, and San Diego county public health laboratories
† Percent is of the total specimens tested for influenza by PCR
‡ Percent is of the specimens positive for influenza
§ Percent is of the influenza A positive specimens
¥ Percent is of the influenza B positive specimens
** Four co-infections with influenza A (H1N1)pdm09 and influenza A (H3N2) are included. These occurred in the Bay Area (1), Central (2), and Lower Southern (1) regions.

Figure 2. Influenza positive specimens by type and subtype, Respiratory Laboratory Network Laboratories, 2018–2019



2. Clinical Sentinel Laboratory Surveillance

The clinical sentinel laboratories use various methods to test for influenza, including rapid test, direct fluorescent assay, viral culture, and PCR. Because clinical sentinel laboratory specimens submitted for influenza testing are collected from patients in healthcare settings, they are more likely to reflect influenza activity than specimens tested at RLN laboratories; however, many clinical laboratories do not perform influenza A subtyping or influenza B lineage typing.

From September 30, 2018 through May 18, 2019, clinical sentinel laboratories tested 117,334 specimens for influenza, of which 19,590 (16.7%) were positive for influenza. Of the 19,590 specimens that tested positive, 19,197 (98.0%) were positive for influenza A and 393 (2.0%) were positive for influenza B (Table 2). In addition, clinical sentinel laboratories tested 104,992 specimens for RSV, of which 9,521 (9.1%) were positive.

During the 2018–2019 season, influenza activity reported by clinical laboratories exceeded 10% of specimens testing positive for 19 weeks, including a sustained period of elevated activity for 15 weeks between the first week (week ending December 22, 2018) and last week (week ending March 30, 2019) during which more than 20% of specimens tested positive for influenza (Figure 3). The prolonged period of elevated activity was likely due to regional differences in the percentage of specimens testing positive for influenza (Figure 4). Early peaks in activity were

experienced in the Lower Southern (week ending December 15, 2018) and Central (week ending December 22, 2018) regions of California when influenza A (H1N1)pdm09 viruses were predominating, and later peaks in activity were experienced in the Bay Area (week ending March 2, 2019), Upper Southern (week ending March 9, 2019), and Northern (week ending March 23, 2019) regions when influenza A (H3N2) viruses were predominating. The Central region also had a secondary peak during the week ending March 23, 2019.

RSV activity had a more defined peak in activity than influenza activity, peaking during the week ending February 9, 2019 and was higher than activity during the 2017–2018 season (Figure 5). Rhinoviruses and enteroviruses were the most frequently detected viruses among other tested respiratory viruses (Figure 6).

Table 2. Influenza and respiratory syncytial virus (RSV) detections in clinical sentinel laboratories*, September 30, 2018–May 18, 2019

	Total*		Northern		Bay Area		Central		Upper Southern		Lower Southern	
	No.	(%)	No.	(%)	No.	(%)	No.	(%)	No.	(%)	No.	(%)
Influenza												
Specimens tested	**117,334**		**9,235**		**31,890**		**13,286**		**22,368**		**12,154**	
Positive for influenza	19,590	(16.7)†	2,247	(24.3)†	7,702	(24.2)†	3,792	(28.5)†	2,161	(9.7)†	1,579	(13.0)†
Influenza A	19,197	(98.0)‡	2,207	(98.2)‡	7,562	(98.2)‡	3,755	(99.0)‡	2,113	(97.8)‡	1,500	(95.0)‡
Influenza B	393	(2.0)‡	40	(1.8)‡	140	(1.8)‡	37	(1.0)‡	48	(2.2)‡	79	(5.0)‡
RSV												
Specimens tested	**104,992**		**7,490**		**32,414**		**9,063**		**21,114**		**6,510**	
Positive for RSV	9,521	(9.1)	841	(11.2)	2,824	(8.7)	1,474	(16.3)	1,715	(8.1)	808	(12.4)

* Number of participating laboratories by region and county:

Northern: Butte(1). In addition, Northern California Kaiser Permanente has facilities in multiple counties within the Northern California region.

Bay Area: Alameda(1), Marin(1), and San Francisco(1). In addition, Northern California Kaiser Permanente has facilities in multiple counties within the Northern California region.

Central: Madera(1). In addition, Northern California Kaiser Permanente has facilities in multiple counties within the Central California region.

Upper Southern: Long Beach(1) and Los Angeles(3).

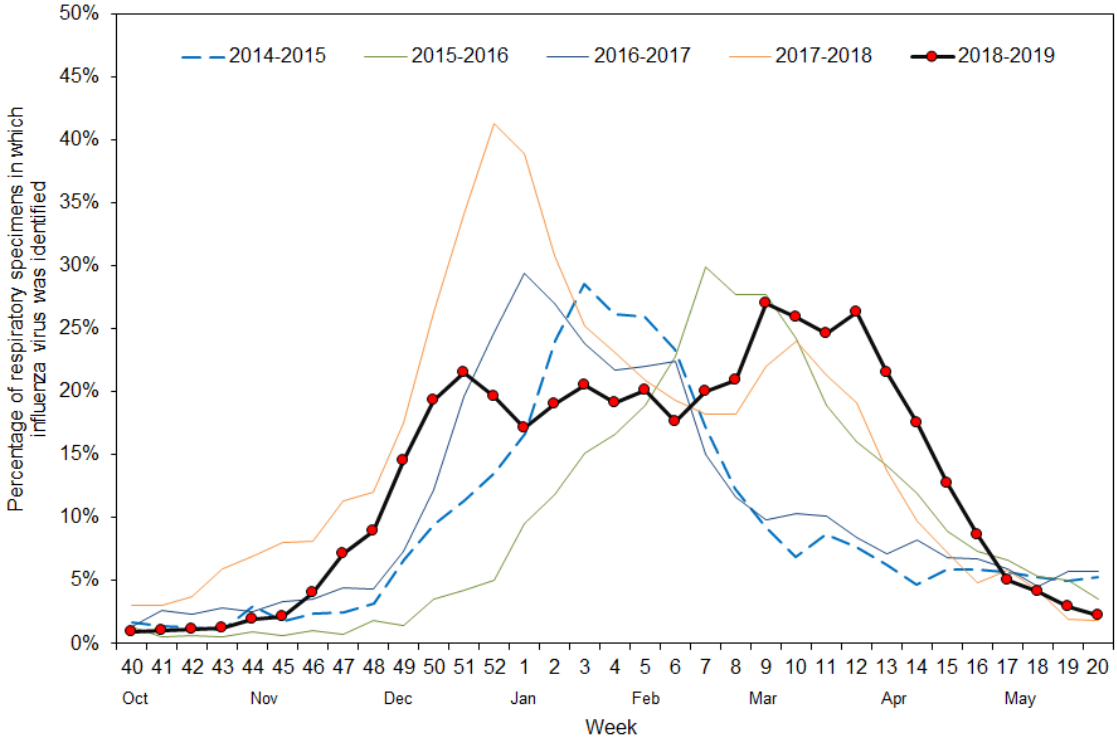
Lower Southern: Imperial(3) and San Diego(2).

In addition, Southern California Kaiser Permanente provides aggregated data for all their facilities, which are located in multiple counties within the Upper Southern and Lower Southern regions; therefore, Southern California Kaiser Permanente data are included in the total but not in the Upper Southern and Lower Southern region columns.

† Percent is of the total specimens tested for influenza

‡ Percent is of the specimens positive for influenza

Figure 3. Percentage of specimens from which influenza was detected in clinical sentinel laboratories, 2014–2019



Note: The 2014–15 season contains a week 53. Data have been shifted so that week 1 aligns across years.

Figure 4. Percentage of specimens from which influenza was detected in clinical sentinel laboratories by California region, 2018–2019

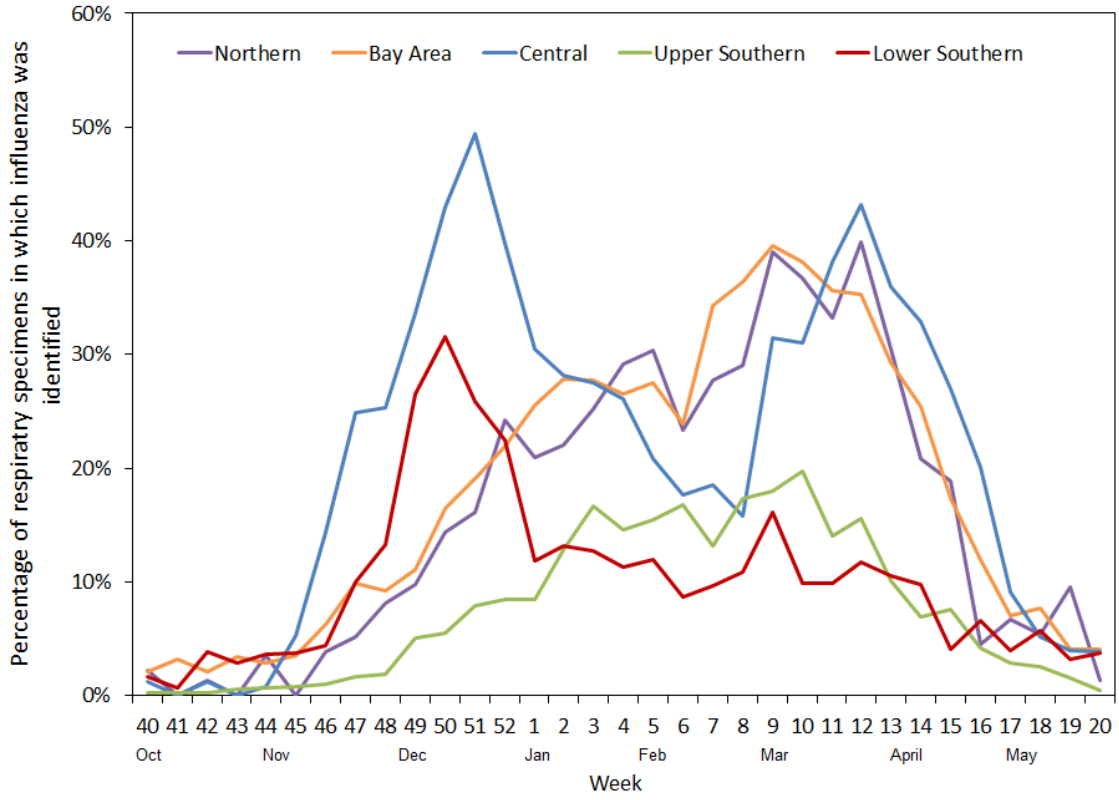
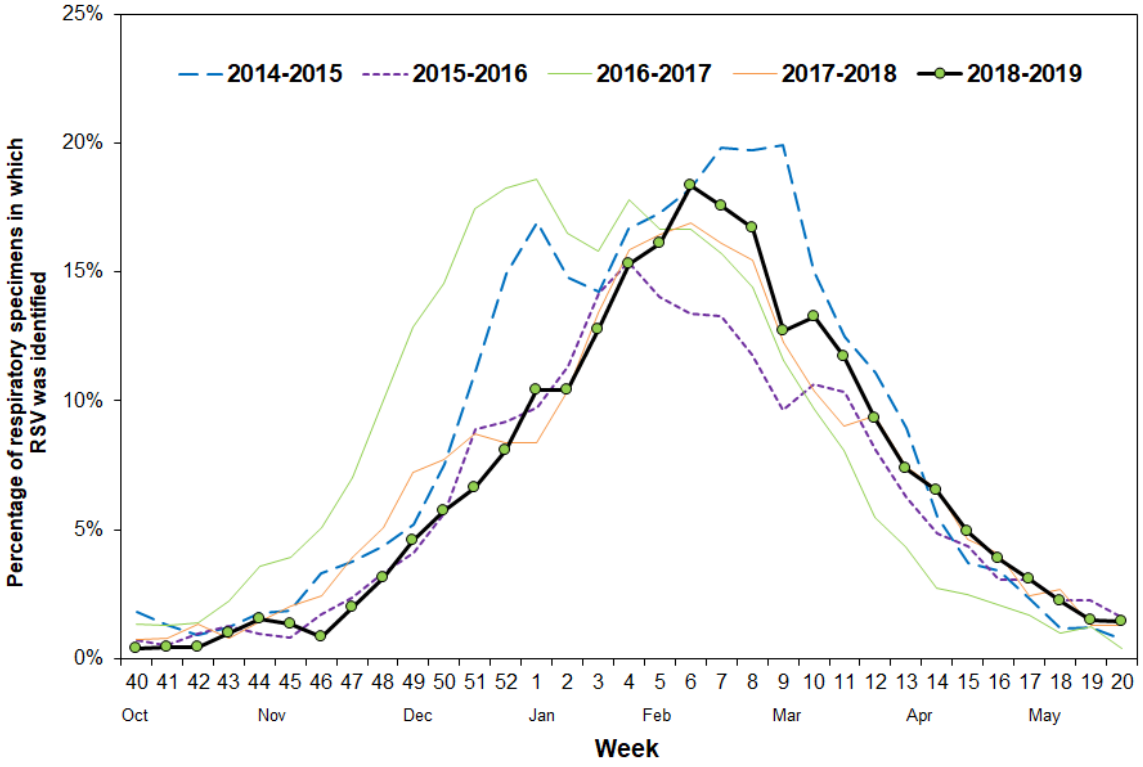
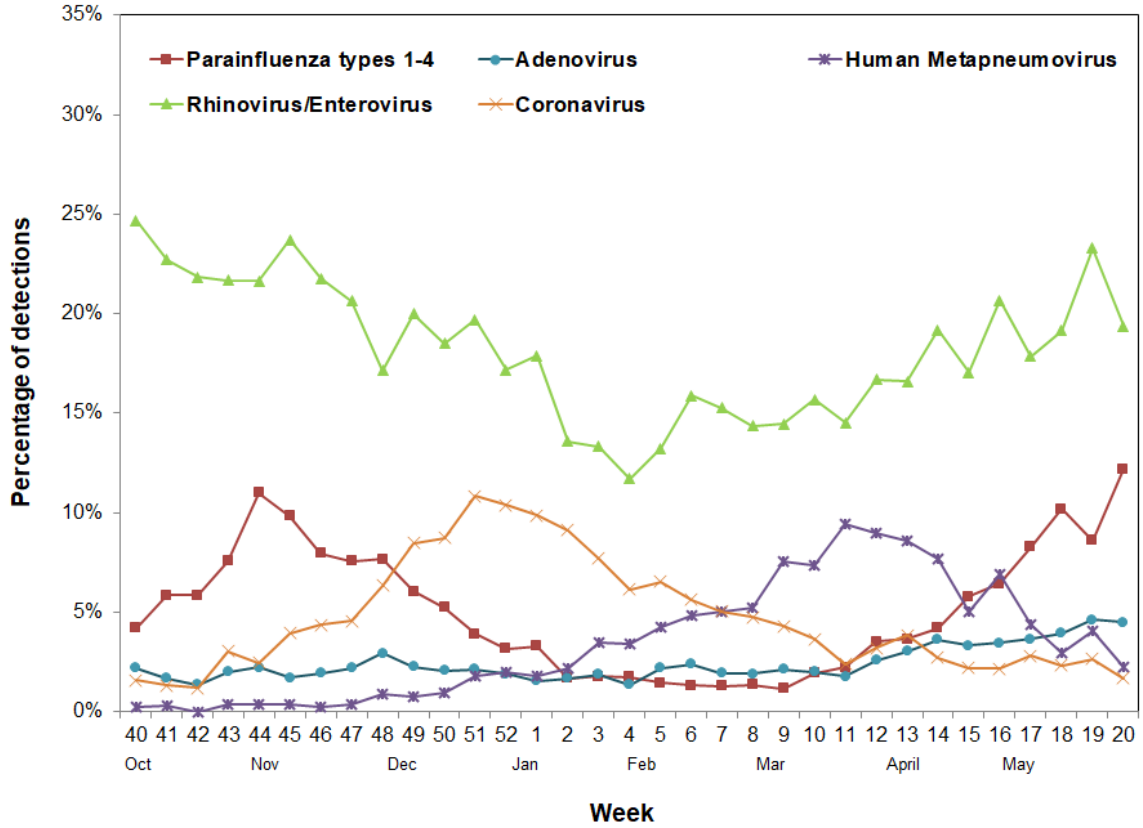


Figure 5. Percentage of specimens from which RSV was detected in clinical sentinel laboratories, 2014–2019



Note: The 2014–15 season contains a week 53. Data have been shifted so that week 1 aligns across years.

Figure 6. Percentage of specimens from which other respiratory viruses were detected in clinical sentinel laboratories, 2018–2019



3. Influenza Virus Characterization

Close monitoring of influenza viruses is required to better assess the potential impact on public health. CDC characterizes influenza viruses through one or more tests including genomic sequencing, hemagglutination inhibition (HI) and/or neutralization based Focus Reduction assays (FRA). These data are used to compare how similar, or well-inhibited, currently circulating influenza viruses are to the reference viruses used for developing new influenza vaccines and to monitor evolutionary changes that continually occur in influenza viruses circulating in humans. Antigenic and genetic characterization of circulating influenza viruses gives an indication of the influenza vaccine's ability to induce an immune response against the wide array of influenza viruses that are co-circulating every season. However, annual vaccine effectiveness estimates are needed to determine how much protection was provided to the population by vaccination.

For nearly all influenza-positive surveillance samples received at CDC, genomic sequencing is performed to determine the genetic identity of circulating influenza viruses and to monitor the evolutionary trajectory of viruses circulating in our population. Virus gene segments are classified into genetic clades/subclades based on phylogenetic analysis. However, genetic changes that classify the clades/subclades do not always result in antigenic changes. Antigenic drift is a term used to describe gradual antigenic variation that occurs as viruses evolve changes to escape host immune pressure. Antigenic drift is evaluated by comparing antigenic properties of cell-propagated reference viruses representing currently recommended vaccine components with those of cell-propagated circulating viruses.

Influenza virus reference strains included in the 2018–2019 northern hemisphere influenza vaccine were:

- A/Singapore/INFIMH-16-0019/2016-like (H3N2), which is a member of the 3c.2a1 clade
- A/Michigan/45/2015-like (H1N1), which is a member of the 6B.1 clade
- B/Colorado/06/2017-like (Victoria), which is a member of the V1A1.1 clade
- B/Phuket/3073/2013-like (Yamagata), which is a member of the Y3 clade (only included in quadrivalent influenza vaccines)

The Centers for Disease Control and Prevention (CDC) performed genomic sequencing on a total of 247 influenza viruses isolated from influenza positive samples collected throughout California during the 2018–2019 influenza season, of which 97 were antigenically characterized.

Seventy-seven influenza A (H3N2) viruses from California were genomically sequenced during the 2018–2019 influenza season, of which 41 were antigenically characterized. The 77 influenza A (H3N2) viruses were members of three clades/subclades, 3c.2a (5; 6.4%), 3c.2a1 (18; 23.4%), and 3c.3a (54; 70.1%). Of the 41 influenza A (H3N2) viruses antigenically characterized, 26 (63.4%) were well-inhibited by A/Singapore/INFIMH-16-0019/2016-like (H3N2) antisera and 15 (36.6%) were poorly inhibited by A/Singapore/INFIMH-16-0019/2016-like (H3N2) antisera. All 15 of the poorly inhibited viruses were members of the 3c.3a clade (Table 3a).

One hundred forty-two influenza A (H1N1)pdm09 viruses from California were genomically sequenced during the 2018–2019 influenza season, of which 35 were antigenically characterized.

The 142 influenza A (H1N1)pdm09 viruses were members of two clades/subclades, 6B.1 (1; 0.7%) and 6B.1A (141; 99.3%). Of the 35 influenza A (H1N1)pdm09 viruses antigenically characterized, 33 (94.3%) were well-inhibited by A/Michigan/45/2015-like (H1N1) antisera and 2 (5.7%) were poorly inhibited by A/Michigan/45/2015-like (H1N1) antisera. Both of the poorly inhibited viruses were members of the 6B.1A clade (Table 3b). However, to underscore that a change in clade designation does not necessarily confer antigenic changes, 32/34 (94%) of the clade 6B.1A influenza A (H1N1)pdm09 viruses were well inhibited by serum antibodies raised against the A/Michigan/45/2015 H1N1 component of the influenza vaccine.

Eleven influenza B (Victoria) viruses from California were genomically sequenced during the 2018–2019 influenza season, of which 7 were antigenically characterized. The 11 influenza B (Victoria) viruses were members of three clades/subclades, V1A (1; 9.1%), V1A.1 (3; 27.3%), and V1A-3DEL (7; 63.6%). Of the 7 influenza B (Victoria) viruses antigenically characterized, four (57.1%) were well-inhibited by B/Colorado/06/2017-like (Victoria) antisera and 3 (42.9%) were poorly inhibited by B/Colorado/06/2017-like (Victoria) antisera. All 3 of the poorly inhibited viruses were members of the V1A-3DEL clade (Table 3c).

Seventeen influenza B (Yamagata) viruses from California were genomically sequenced during the 2018–2019 influenza season, of which 14 were antigenically characterized. The 17 influenza B (Yamagata) viruses were members of a single clade, Y3 (17; 100%). Of the 14 influenza B (Yamagata) viruses antigenically characterized, all (100%) were well-inhibited by B/Phuket/3073/2013-like (Yamagata) (Table 3d).

Table 3 a–d. Influenza virus antigenic characterization and genomic sequencing by influenza A subtype and influenza B lineage type — California, 2018–2019 influenza season

a. Influenza A (H3N2) viruses

	Virus Clade			
Antigenic Characterization	**3C.2a**	**3C.2a1***	**3C.3a**	**Total**
Well inhibited by A/Singapore/INFIMH-16-0019/2016*	4	15	7	26
Poorly inhibited by A/Singapore/INFIMH-16-0019/2016*	0	0	15	15
Not antigenically characterized	1	3	32	36
Total A (H3N2)	5	18	54	77

* A/Singapore/INFIMH-16-0019/2016 is the influenza A (H3N2) component included in the 2018–2019 quadrivalent and trivalent influenza vaccines and is a member of the 3c.2a1 clade

b. Influenza A (H1N1)pdm09 viruses

	Virus Clade		
Antigenic Characterization	**6B.1***	**6B.1A**	**Total**
Well inhibited by A/Michigan/45/2015*	1	32	33
Poorly inhibited by A/Michigan/45/2015*	0	2	2
Not antigenically characterized	0	107	107
Total A (H1N1)pdm09	1	141	142

* A/Michigan/45/2015 is the influenza A (H1N1)pdm09 component included in the 2018–2019 quadrivalent and trivalent influenza vaccines and is a member of the 6B.1 clade

c. Influenza B (Victoria) viruses

	Virus Clade			
Antigenic Characterization	**V1A**	**V1A.1***	**V1A-3DEL**	**Total**
Well inhibited by B/Colorado/06/2017*	0	3	1	4
Poorly inhibited by B/Colorado/06/2017*	0	0	3	3
Not antigenically characterized	1	0	3	4
Total B (Victoria)	1	3	7	11

* B/Colorado/06/2017-like is the influenza B (Victoria) lineage component included in the 2018–2019 quadrivalent and trivalent influenza vaccines and is a member of the V1A.1 clade

d. Influenza B (Yamagata) viruses

	Virus Clade	
Antigenic Characterization	**Y3***	**Total**
Well inhibited by B/Phuket/3073/2013*	14	14
Poorly inhibited by B/Phuket/3073/2013*	0	0
Not antigenically characterized	3	3
Total B (Yamagata)	17	17

* B/Phuket/3073/2013 is the influenza B (Yamagata) component included in the 2018–2019 quadrivalent influenza vaccine and is a member of the Y3 clade

4. Antiviral Resistance Testing

The CDPH-VRDL monitors antiviral resistance (AVR) for a select subset of influenza A and B viruses using a high throughput pyrosequencing assay to detect mutations known to confer NAI resistance. Of the 327 influenza specimens tested by the CDPH-VRDL during the 2018–2019 influenza season, one influenza A (H1N1)pdm09 virus was found to be resistant to NAIs (Table 4).

Table 4. Number of specimens tested for antiviral resistance, California, 2018–2019 season

	Neuraminidase Inhibitor Resistance*
Influenza A (H1N1)pdm09	1/168
Influenza A (H3N2)	0/128
Influenza B	0/31

* California data are for viruses isolated from specimens collected during September 30, 2018–September 28, 2019 and characterized through October 5, 2019

CDC also performs antiviral resistance testing as part of its routine national surveillance. CDC tested 2,602 influenza viruses during September 30, 2018 through May 18, 2019 from throughout the United States, including California, for resistance to the influenza neuraminidase inhibitor antiviral medications recommended for use against seasonal influenza (oseltamivir, peramivir, zanamivir, and baloxavir). All 1,198 influenza A (H3N2) viruses tested for oseltamivir, peramivir, and zanamivir susceptibility were susceptible to all three medications. No baloxivir-resistant viruses were detected among 964 A (H3N2) viruses tested. Among 1,198 influenza A (H1N1)pdm09 viruses tested for oseltamivir, peramivir, and zanamivir susceptibility, eight (0.7%) showed reduced or highly reduced susceptibility to oseltamivir and six (0.5%) showed reduced or highly reduced susceptibility to peramivir, and none showed reduced susceptibility to zanamivir. Among 1,162 influenza A (H1N1)pdm09 viruses also tested for baloxavir susceptibility,

no resistant viruses were detected. Among 232 influenza B (Victoria) viruses tested for oseltamivir, peramivir, and zanamivir susceptibility, 0 (0%) showed reduced susceptibility to oseltamivir, one (0.4%) showed reduced or highly reduced susceptibility to peramivir, and 0 (0%) showed reduced susceptibility to zanamivir. Among 229 influenza B (Victoria) viruses also tested for baloxavir susceptibility, no resistant viruses were detected. Among 187 influenza B (Yamagata) viruses tested for oseltamivir, peramivir, and zanamivir susceptibility, 0 (0%) showed reduced susceptibility to oseltamivir, one (0.5%) showed reduced or highly reduced susceptibility to peramivir, and 0 (0%) showed reduced susceptibility to zanamivir. Among 187 influenza B (Yamagata) viruses also tested for baloxavir susceptibility, no resistant viruses were detected.[1]

5. Novel Influenza A Viruses

No novel influenza viruses were detected in California by the CDPH-VRDL or RLN laboratories by real-time reverse transcription polymerase chain reaction (rRT-PCR) during the 2018–2019 season.

B. Case-Based Surveillance

1. Influenza-associated Pediatric Deaths

Laboratory-confirmed influenza-associated pediatric deaths (<18 years of age) are nationally notifiable and are also reportable in California [Title 17, California Code of Regulations (CCR) §2500].

During the 2018–2019 influenza season, CDPH received 15 reports of influenza-associated pediatric deaths. Eight (53%) had onset during the weeks ending December 22, 2018–March 30, 2019, which corresponded to the extended period of peak influenza activity seen during the 2018–2019 influenza season based on data from clinical sentinel laboratories, and seven (47%) had onset outside of this peak period, including two (13%) with onset during the summer months (May 19, 2019 through September 28, 2019). Of the 15 influenza-associated pediatric deaths, 10 (67%) had at least one underlying medical condition, including those conditions defined by the Advisory Committee for Immunization Practices (ACIP) as being associated with severe influenza,[3] and five (33%) were previously healthy. Ten (67%) of the 15 influenza-associated pediatric deaths, died at home, in the emergency department, or on their first day of hospital admission. Twelve (80%) were not vaccinated against influenza during the 2018–2019 influenza season, one (7%) was vaccinated, and two (13%) had unknown vaccination status. All 15 influenza-associated deaths were due to influenza A; eight (53%) were influenza A (H3N2), four (27%) were influenza A (H1N1)pdm09, and three (20%) were influenza A with unknown subtype.

2. California Emerging Infections Program Data: Influenza-associated Hospitalizations

The California Emerging Infections Program (CEIP), Influenza Surveillance Network (FluSurv-NET) conducts population-based surveillance for laboratory-confirmed influenza-associated hospitalizations among persons of all ages in Alameda, Contra Costa and San Francisco counties. FluSurv-NET is a national network which covers over 70 counties in the 10 Emerging Infections

Program (EIP) states (CA, CO, CT, GA, MD, MN, NM, NY, OR, and TN) and three additional states (MI, OH, and UT).

During the 2018–2019 season, the incidence of influenza-associated hospitalizations per 100,000 population began increasing in mid-December and peaked during the week ending March 2, 2019 with an incidence of 5.6 influenza hospitalizations per 100,000 population (Figure 7). This rate was substantially lower than the peak rate during the 2016–2017 and 2017–2018 influenza seasons (12.2 and 20.4 influenza hospitalizations per 100,000, respectively). Of the 2,037 patients hospitalized in the three counties monitored by CEIP for influenza 1,936 (95.0%) had influenza A infections, 93 (4.6%) had influenza B infections, and 5 (0.2%) had influenza A and B co-infections. Three patients had an influenza infection, but the influenza type was not known. The highest cumulative rate of hospitalization was among adults aged >64 years, followed by the 50–64 year and 0–4 year age groups (Figure 8). Patients >64 years of age accounted for 52.9% of the total reported hospitalized cases.

Figure 7. Incidence of influenza-associated hospitalizations in CEIP counties, 2016–2019

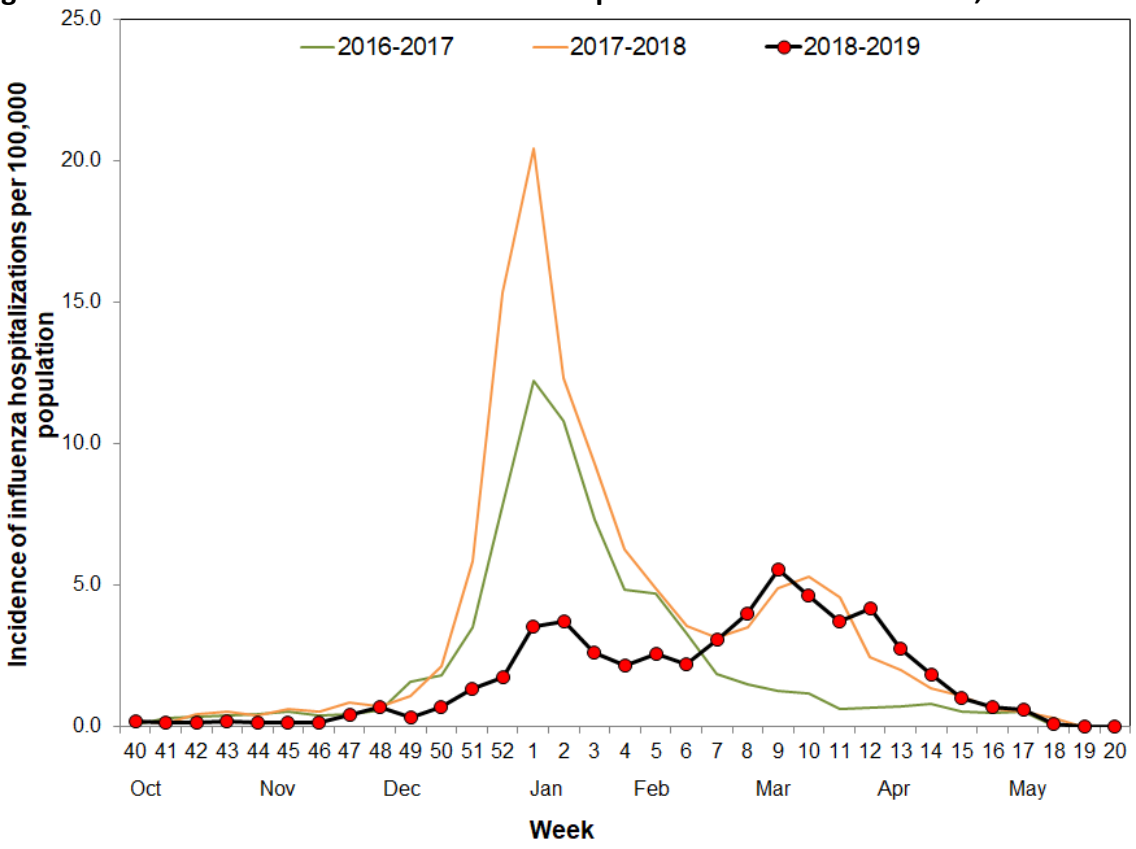
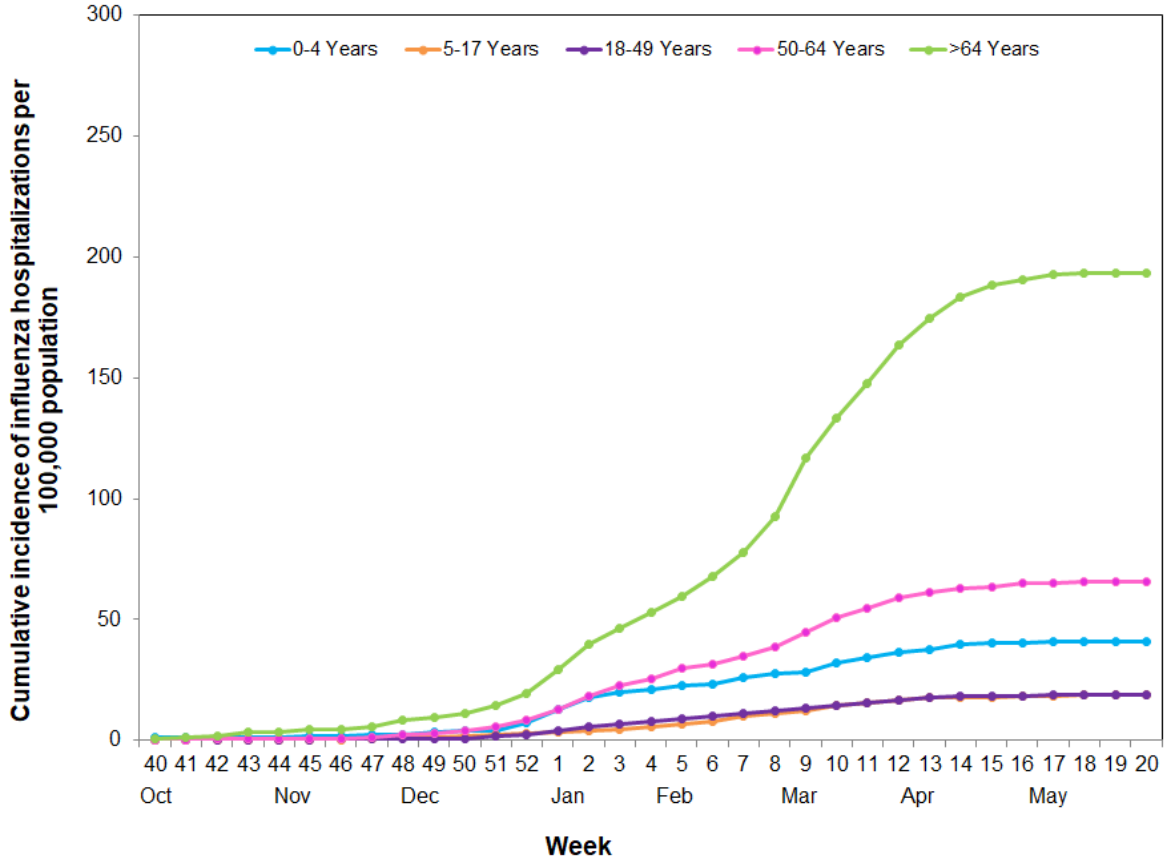


Figure 8. Cumulative incidence of influenza hospitalizations in CEIP counties by age group, 2018–2019



C. Syndromic Surveillance

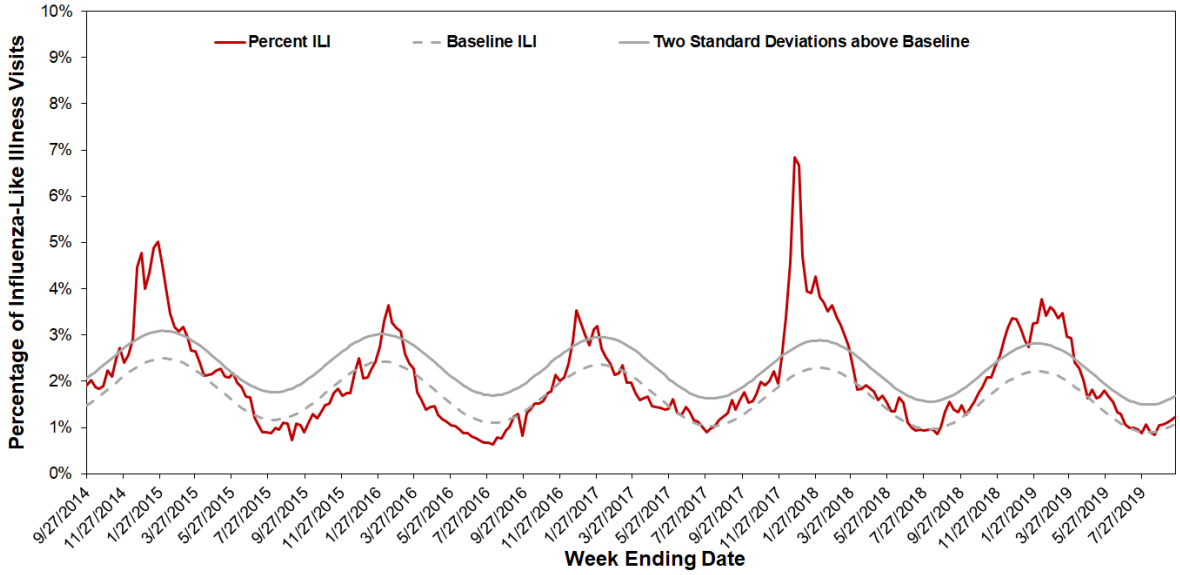
1. Influenza-like Illness Outpatient Surveillance (Sentinel Providers)

In collaboration with CDC, the CDPH works with volunteer sentinel providers throughout the state to conduct year-round surveillance for ILI in outpatients. Sentinel providers may be individual practitioners or represent whole healthcare systems in a variety of outpatient settings including, but not limited to, hospital outpatient clinics, emergency departments, and student health services. Sentinel providers report on a weekly basis the number of patients with ILI and the total number of patients seen for any reason. ILI is defined as any illness with (1) fever (≥100°F or 37.8°C) and (2) cough and/or sore throat, in the absence of a known cause other than influenza.

In California, 115 sentinel providers reported ILI activity on a regular basis (i.e., at least 17 of the 33 weeks from September 30, 2018 to May 18, 2019). There was minimal ILI activity until early December, when sentinel providers began reporting increases in patients with ILI (Figure 9). The percentage of ILI visits among outpatients had two periods of peak activity. The first, and smaller of the two peaks, occurred during the week ending December 29, 2018 (3.4%), corresponding to the peak in influenza A (H1N1)pdm09 virus activity. The second, and larger of the two peaks, occurred during the week ending February 16, 2019 (3.8%), corresponding to the peak in influenza A (H3N2) virus activity. ILI activity remained elevated through early April, returning to

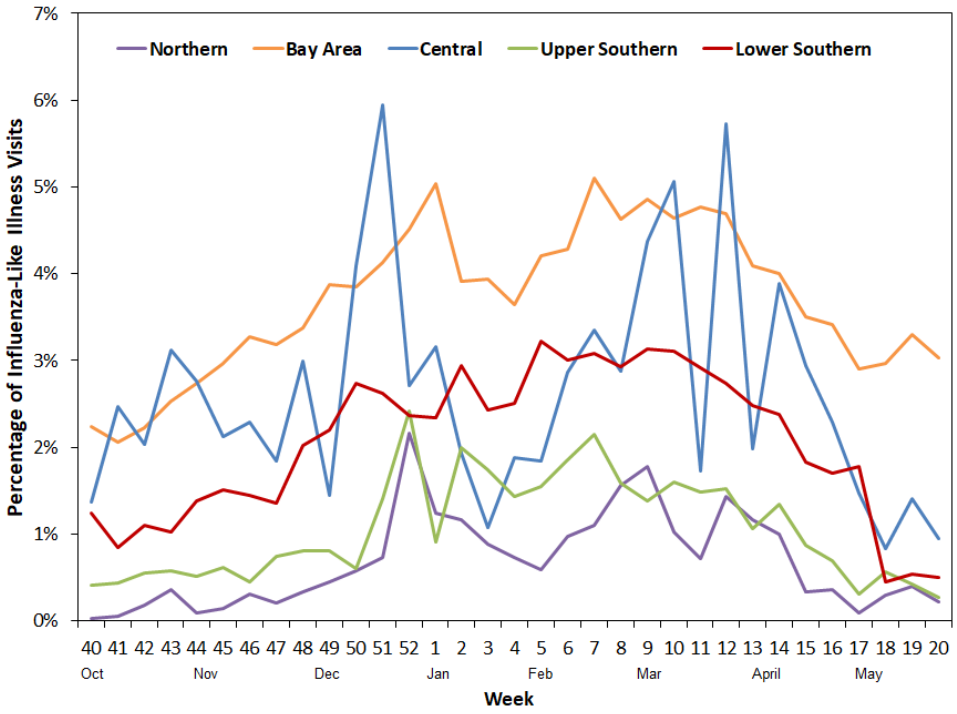
seasonal baseline levels in mid-April. The percentage of visits for ILI exceeded two standard deviations above baseline levels between the weeks ending December 8, 2018 and April 6, 2019, with the exception of the week ending January 26, 2019. Most California regions also showed more than one period of peak in outpatient ILI activity as well (Figure 10).

Figure 9. Percentage of influenza-like illness visits among patients seen by California Sentinel Providers, 2014–2019*



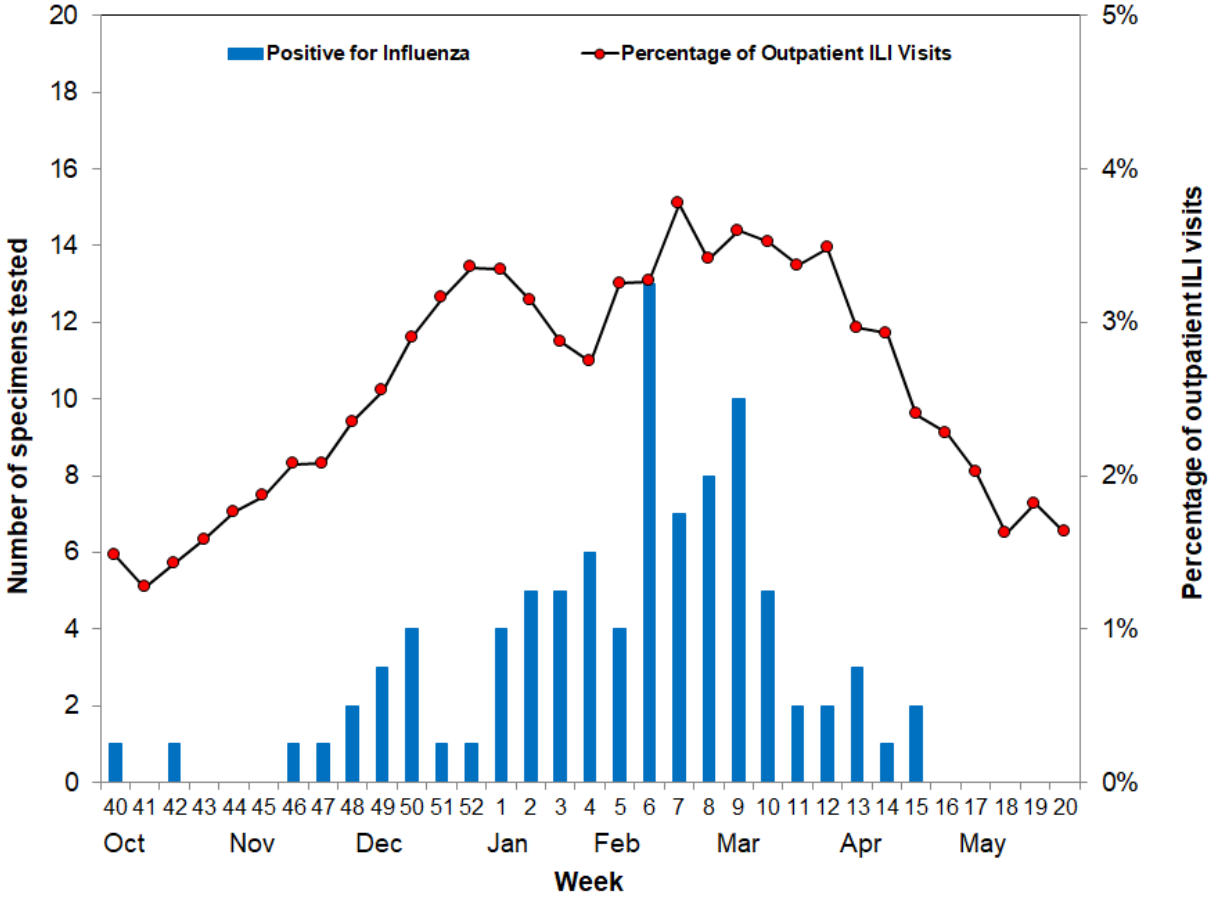
* The seasonal baseline was calculated using a regression model applied to data from the previous five years. Two standard deviations above the seasonal baseline is the point at which the observed percentage of ILI is significantly higher than would be expected at that time of the year.

Figure 10. Percentage of influenza-like illness visits among patients seen by California Sentinel Providers by California region, 2018–2019



Sentinel providers voluntarily submit specimens from patients with ILI to the CDPH-VRDL for influenza testing. Many of these specimens are sent to CDC for further characterization, providing important information about what influenza virus strains are circulating in the community. From September 30, 2018 through May 18, 2019, sentinel providers submitted 182 respiratory specimens; 93 (51.1%) were positive for influenza. Of these, 89 (95.7%) were influenza A and 4 (4.3%) were influenza B. Of the 89 positive influenza A specimens, 55 (61.8%) were A (H3N2) and 34 (38.2%) were A (H1N1)pdm09. Of the 4 positive influenza B specimens, 1 (25.0%) was B Yamagata, 2 (50.0%) were B Victoria, and one (25.0%) was not lineage-typed. The number of specimens submitted by sentinel providers that tested positive for influenza peaked during the week ending February 9, 2019, which was one week prior to the larger peak in ILI activity (Figure 11). The smaller peak in ILI activity during the week ending December 29, 2018 coincided with a drop in submitted specimens, which was likely due to the Christmas and New Year's holidays.

Figure 11. Sentinel Provider specimens tested by week of collection and influenza result, and percentage of influenza-like illness visits by week of visit, September 30, 2018–May 18, 2019



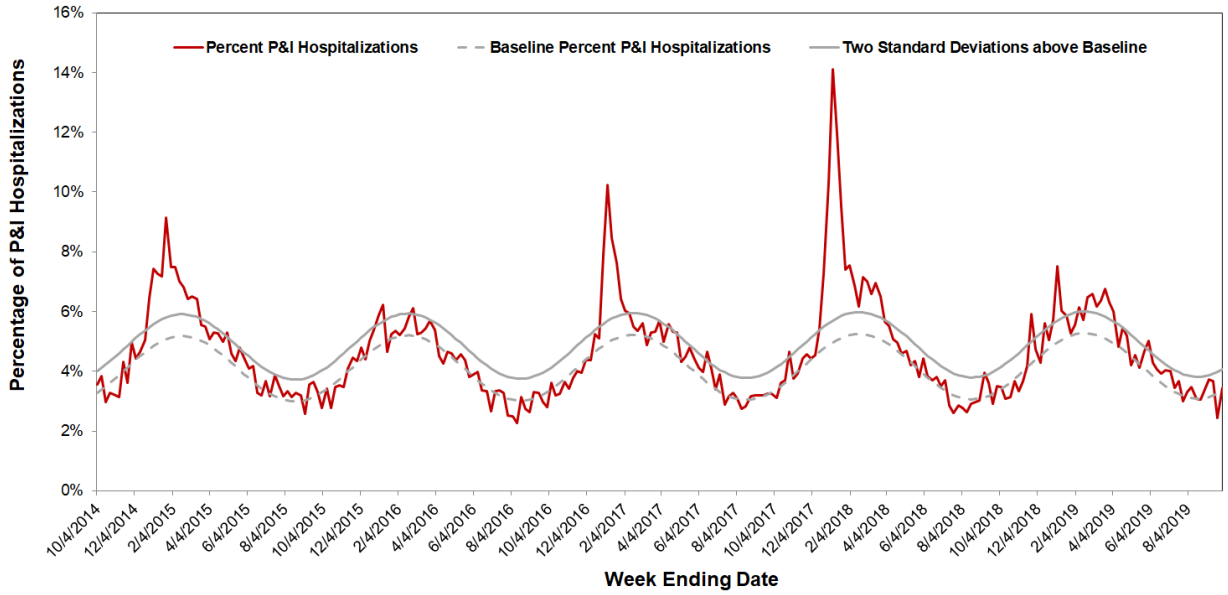
2. Kaiser Permanente Northern California Pneumonia and Influenza Admission Data

The CDPH collaborates with Northern California Kaiser Permanente to monitor trends in pneumonia and influenza-associated hospitalizations. Patients with admission diagnoses of "flu," "pneumonia," or "influenza" are defined as pneumonia and influenza (P&I) admissions. The number of P&I admissions is divided by the total number of hospital admissions occurring in the

same time period to estimate the percentage of P&I admissions. Admissions for pregnancy, labor and delivery, birth, and outpatient procedures are excluded from the denominator.

During the 2018–2019 influenza season, the percentage of P&I admissions in Northern California Kaiser Permanente hospitals began increasing in mid-November, peaking at 7.5% during the week ending January 5, 2019. The percentage of P&I admissions decreased to baseline levels in late January prior to increasing to a second period of elevated activity during the weeks ending February 23, 2019 through April 6, 2019 (Figure 12).

Figure 12. Percentage of pneumonia and influenza admissions in Northern California Kaiser Permanente hospitals, 2014–2019*

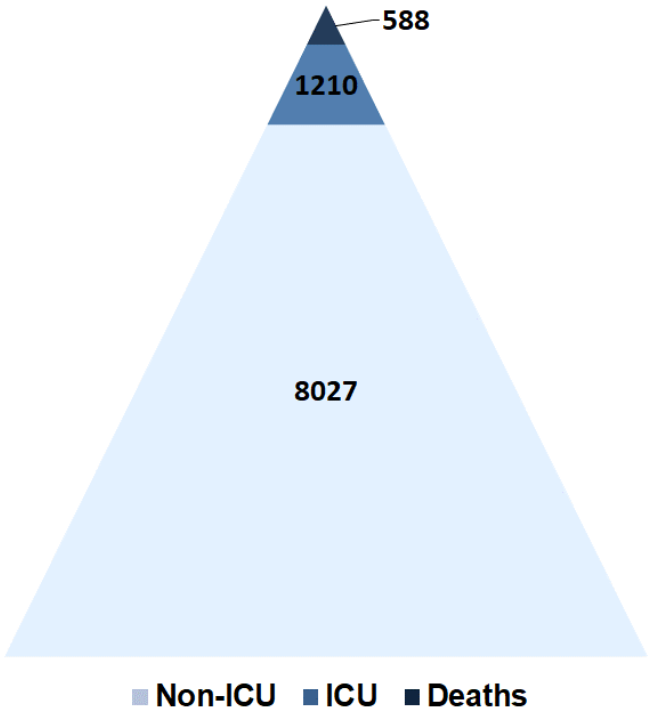


* The seasonal baseline was calculated using a regression model applied to data from the previous five years. Two standard deviations above the seasonal baseline is the point at which the observed percentage of pneumonia and influenza hospitalizations in Kaiser Permanente hospitals in Northern California is significantly higher than would be expected at that time of the year.

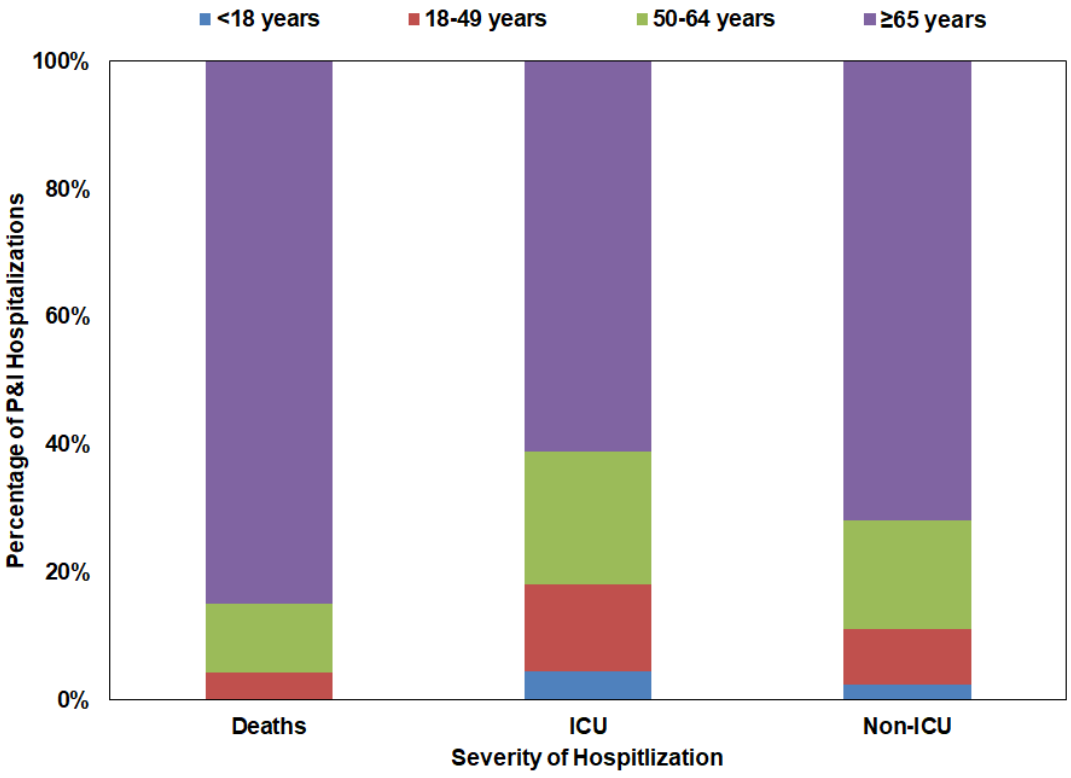
During September 30, 2018–September 28, 2019, the majority of hospitalizations due to pneumonia and influenza did not result in intensive care unit (ICU) admission or death; however, 1,210 ICU admissions and 588 deaths occurred among persons with P&I admission diagnoses (Figure 13a). The majority of P&I admissions occurred among person ≥65 years of age across all severity categories, especially among deaths (Figure 13b). Please note that pneumonia and influenza admissions serve as a proxy for influenza activity but do not necessarily represent laboratory-confirmed influenza infections.

Figure 13. Number (a) and age group distribution (b) of non-ICU admissions, ICU admissions, and Deaths associated with P&I Admissions in Kaiser Permanente Northern California Hospitals, September 30, 2018–September 28, 2019

(a)



(b)



3. Influenza Mortality Surveillance from Death Certificates

Deaths occurring in California among residents who had influenza noted in any cause of death field on the death certificate (influenza specified in a text cause of death field or an influenza ICD-10 code in a coded cause of death field) are defined as influenza-coded deaths. The percentage of influenza-coded deaths is calculated by dividing the number of influenza-coded deaths by the total number of all cause deaths during the same period. Influenza-coded deaths are not necessarily laboratory-confirmed and are an underestimate of all influenza-associated deaths.

During September 30, 2018–September 28, 2019, 615 influenza-coded deaths were identified (Figure 14). The percentage of influenza-coded deaths began increasing in mid-December, had an early peak of 0.8% during the week ending January 12, 2019, and was followed by a period of decline before increasing again to a second peak of 0.8% during the week ending February 23, 2019 (Figure 15). The percentage of influenza-coded deaths remained elevated through late April. The number of influenza-coded deaths during the 2018–2019 influenza season was substantially lower than what was seen during the 2017–2018 influenza season (Table 5).

Figure 14. Number of Influenza-Coded Deaths Identified from Death Certificates by Week of Death, September 30, 2018–September 28, 2019

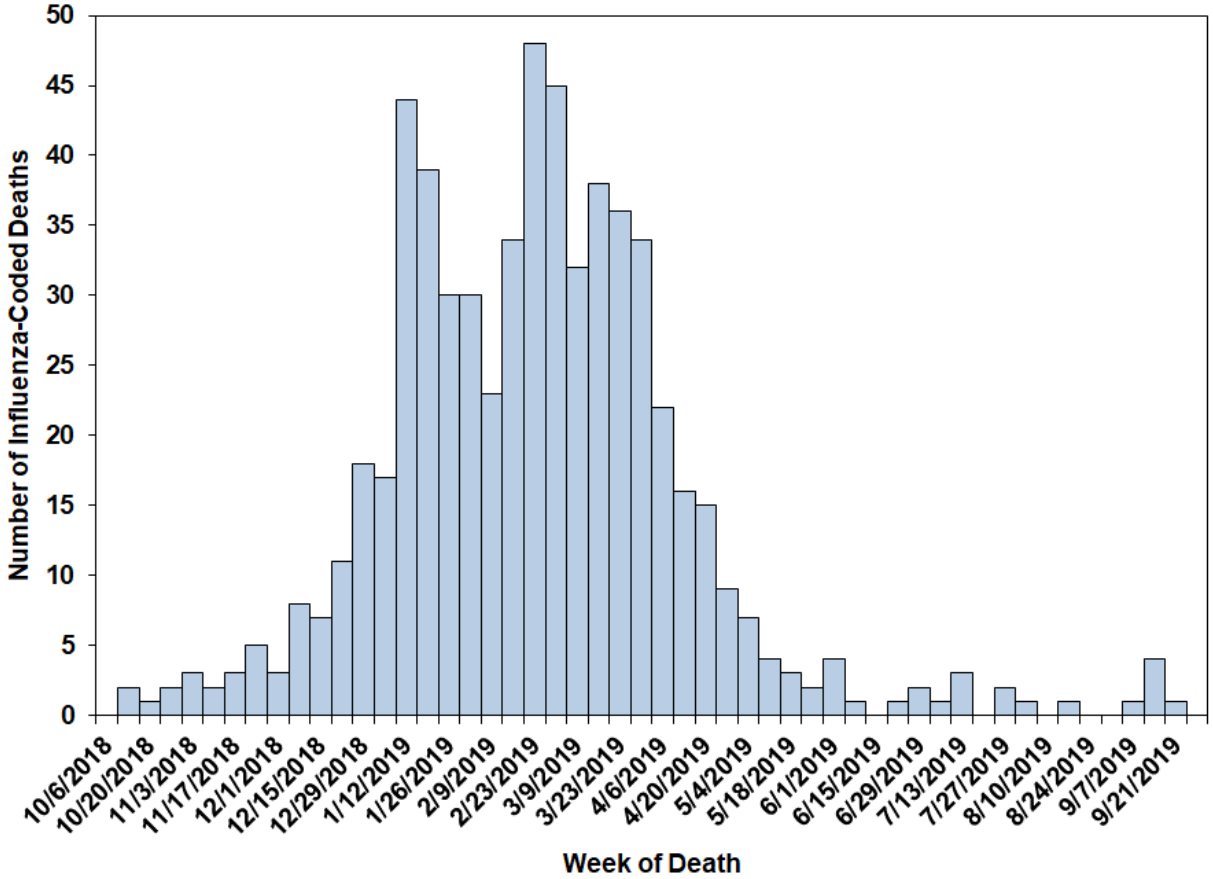
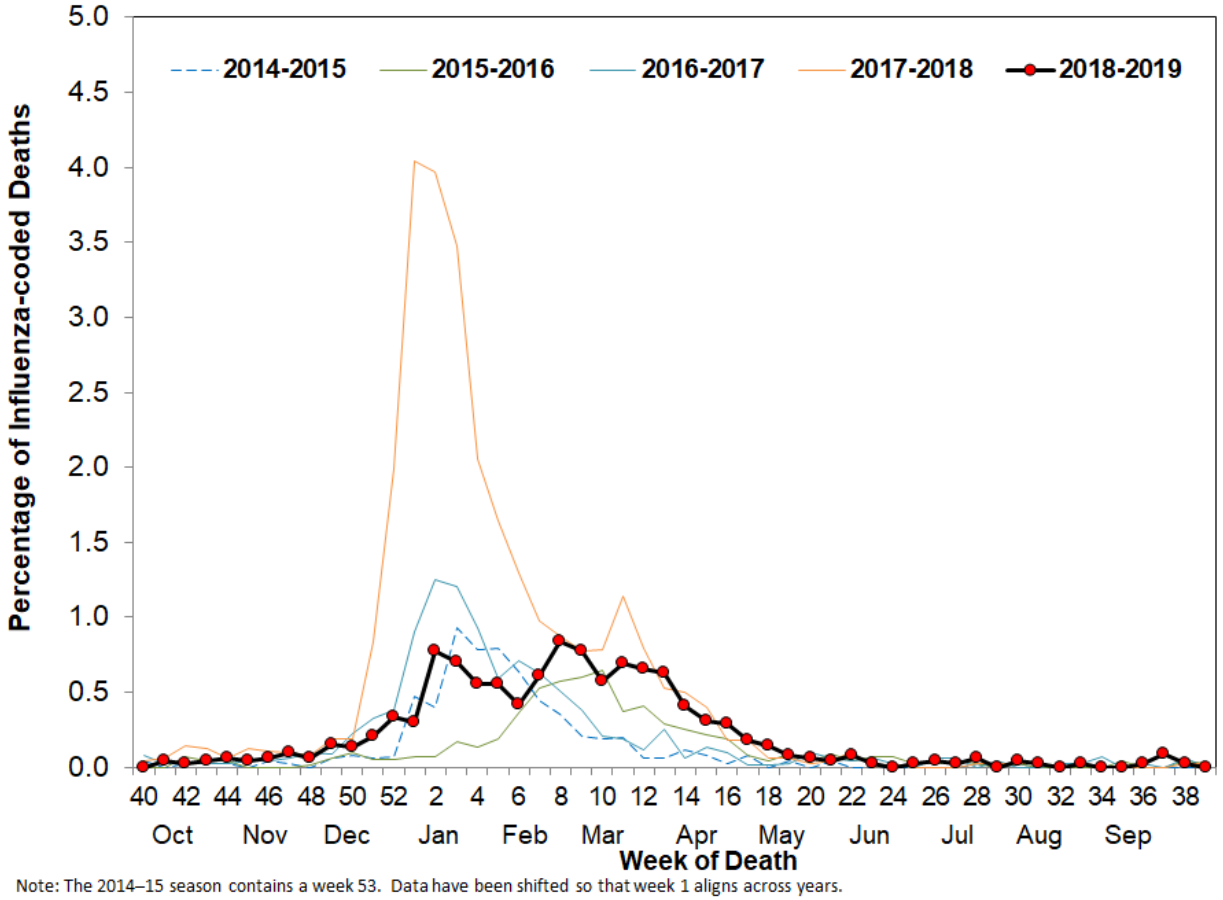


Figure 15. Percentage of Influenza-coded Deaths Occurring in California among California Residents, 2014–2019



Note: The 2014–15 season contains a week 53. Data have been shifted so that week 1 aligns across years.

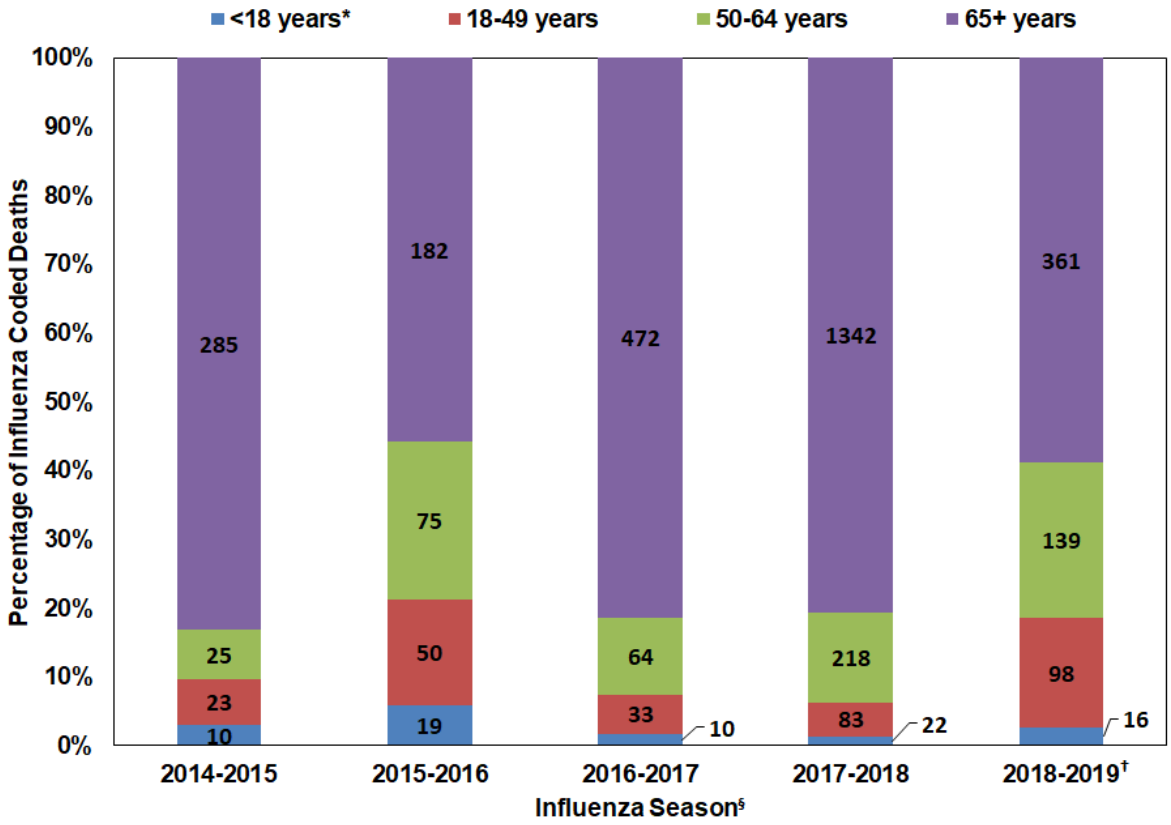
Table 5. Number and Percentage of Influenza-coded Deaths Occurring in California among California Residents, 2014–2015 through 2018–2019 Influenza Seasons

Influenza Season*	Total Number of Influenza-coded Deaths	Peak Percentage of Influenza-coded Deaths
2014–2015	343	0.9%
2015–2016	326	0.7%
2016–2017	579	1.2%
2017–2018	1,665	4.0%
2018–2019	615	0.8%

* 2014–2015 influenza season: September 28, 2014–October 3, 2015; influenza A (H3N2) predominant season
2015–2016 influenza season: October 4, 2015–October 1, 2016; mixed influenza A and influenza B season
2016–2017 influenza season: October 2, 2016–September 30, 2017; influenza A (H3N2) predominant season
2017–2018 influenza season: October 1, 2017–September 29, 2018; influenza A (H3N2) predominant season
2018–2019 influenza season: September 30, 2018–September 28, 2019; mixed influenza A (H1N1)pdm09 and influenza A (H3N2) season

During the 2018–2019 influenza season, fewer deaths occurred among persons <65 years of age (41.1%) than among persons ≥65 years of age; however, the percentage of deaths occurring among persons <65 years of age is consistent with other seasons during which influenza A (H1N1)pdm09 has circulated in greater numbers, such as the 2015–2016 season (Figure 16).

Figure 16. Age Distribution of Influenza-coded Deaths Occurring in California among California Residents, 2014–2015 Season through 2018–2019 Season



* Methods used to identify pediatric influenza-coded deaths on death certificates differ from those used to the identify influenza-associated pediatric deaths presented on page 11. Please see pages 11 and 18 for additional details.

† One death during the 2018–2019 influenza season has unknown age and is not included in the figure.

§ 2014–2015 influenza season: September 28, 2014–October 3, 2015; influenza A (H3N2) predominant season
2015–2016 influenza season: October 4, 2015–October 1, 2016; mixed influenza A and influenza B season
2016–2017 influenza season: October 2, 2016–September 30, 2017; influenza A (H3N2) predominant season
2017–2018 influenza season: October 1, 2017–September 29, 2018; influenza A (H3N2) predominant season
2018–2019 influenza season: September 30, 2018–September 28, 2019; mixed influenza A (H1N1)pdm09 and influenza A (H3N2) season

D. Outbreaks of Respiratory Illness, Including Influenza

Outbreaks are required to be reported to the local health authority under Title 17, CCR 2500; however, outbreaks occurring in residential care facilities are more likely to be identified and reported to CDPH than other respiratory outbreaks. In general, respiratory, non-tuberculosis outbreaks are defined as a sudden increase of acute respiratory illnesses over the normal background rate.

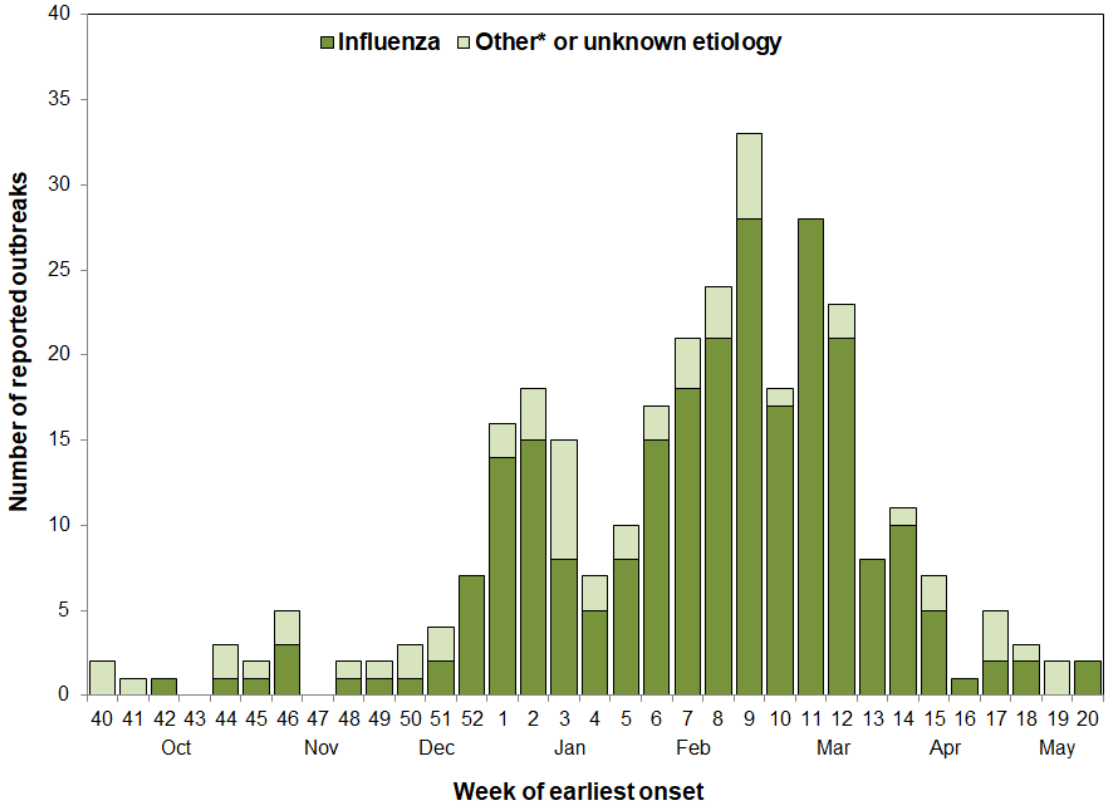
From September 30, 2018 to May 18, 2019 local health departments reported a total of 301 confirmed non-tuberculosis respiratory outbreaks to the CDPH. The outbreaks were reported from 34 local health jurisdictions throughout the state. Of the 301 confirmed respiratory outbreaks, influenza was the most commonly identified pathogen (246; 81.7%). Twenty-five (8.3%) confirmed respiratory outbreaks had no identified etiology. The remaining 30 (10.0%) outbreaks identified RSV (5), rhinovirus (3), pertussis (14), human metapneumovirus (3), parainfluenza virus (3), and Group A streptococcal infection (2).

The first influenza-associated outbreak identified during the 2018–2019 influenza season occurred in late October 2018 (Figure 17). Influenza outbreaks continued to occur through May, with peak activity occurring in during the first half of March. Ten confirmed influenza outbreaks were reported to the CDPH with initial case onset during the weeks ending May 19, 2019 through September 28, 2019.

Of the 246 influenza-associated outbreaks, 215 (87.4%) were associated with influenza A and 7 (2.8%) were associated with influenza B. An additional 3 (1.2%) outbreaks were associated with both influenza A and influenza B, and 21 (8.5%) were associated with influenza, but the influenza type was not known. Of the 215 outbreaks where influenza A viruses were identified, 41 had subtyping information available; 18 (43.9%) were A (H3N2), and 23 (56.1%) were A (H1N1)pdm09. Of the 7 outbreaks where influenza B viruses were identified, 1 had lineage typing performed; one (100%) was B/Yamagata lineage. Most influenza A (174; 80.9%) and influenza B (6; 85.7%) specimens were not subtyped or lineage typed.

Of the 246 influenza-associated outbreaks, 129 (52.4%) occurred in residential healthcare facilities, such as skilled nursing facilities, and 44 (17.9%) occurred in assisted or independent living facilities (congregate residential facilities not providing routine healthcare). Local health departments also reported influenza outbreaks in schools (38; 15.4%), correctional facilities (13; 5.3%), acute care facilities (4; 1.6%), and other medical facilities (9; 3.7%). Nine (3.7%) occurred in other congregate settings.

Figure 17. Reported respiratory outbreaks by week of earliest onset, September 30, 2018–May 18, 2019



* Other etiologies identified by laboratory confirmation included RSV (5), rhinovirus (3), pertussis (14), human metapneumovirus (3), parainfluenza virus (3), and streptococcal infection (2).

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