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Trends in Postpartum Depressive Symptoms — 27 States, 2004, 2008, and 2012

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Postpartum depression is common and associated with adverse infant and maternal outcomes (e.g., lower breastfeeding initiation and duration and poor maternal and infant bonding) (*1–3*). A developmental *Healthy People 2020* objective is to decrease the proportion of women delivering a live birth who experience postpartum depressive symptoms (PDS).* To provide a baseline for this objective, CDC sought to describe self-reported PDS overall, by reporting state, and by selected sociodemographic factors, using 2004, 2008, and 2012 data from the Pregnancy Risk Assessment Monitoring System (PRAMS). A decline in the prevalence of PDS was observed from 2004 (14.8%) to 2012 (9.8%) among 13 states with data for all three periods ($p<0.01$). Statistically significant ($p<0.05$) declines in PDS prevalence were observed for eight states, and no significant changes were observed for five states. In 2012, the overall PDS prevalence was 11.5% for 27 states and ranged from 8.0% (Georgia) to 20.1% (Arkansas). By selected characteristics, PDS prevalence was highest among new mothers who 1) were aged ≤19 years or 20–24 years, 2) were of American Indian/Alaska Native or Asian/Pacific Islander race/ethnicity, 3) had ≤12 years of education, 4) were unmarried, 5) were postpartum smokers, 6) had three or more stressful life events in the year before birth, 7) gave birth to term, low-birthweight infants, and 8) had infants requiring neonatal intensive care unit admission at birth. Although the study did not investigate reasons for the decline, better recognition of risk factors for depression and improved screening and treatment before and during pregnancy, including increased use of antidepressants, might have contributed to the decline. However, more efforts are needed to reduce PDS prevalence in certain states and subpopulations of women. Ongoing surveillance and activities to promote appropriate screening, referral, and treatment are needed to reduce PDS among U.S. women.

PRAMS is an ongoing, population-based surveillance system that collects state-specific data on maternal attitudes and experiences before, during, and soon after pregnancy among women who had a live birth during the preceding 2–9 months.† From year to year, PRAMS survey results are reported by varying numbers of states, New York City, and those areas of New York state outside of New York City (all of which, for simplicity, are referred to as "states" in this report).

For each reporting state, a monthly stratified PRAMS sample of 100–300 new mothers was selected systematically from birth certificates. States that met response rate thresholds for the three periods (≥70% for 2004, ≥65% for 2008, and ≥60% for 2012) were included in this analysis; the thresholds reflect PRAMS data quality goals and changing operational

* https://www.healthypeople.gov/2020/topics-objectives/topic/maternal-infant-and-child-health/objectives.

† https://www.cdc.gov/prams/methodology.htm.

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and general national survey response environments over time. The 2012 PRAMS sample represented 1,610,767 women from 27 reporting states and 41% of U.S. births.

Self-reported PDS was ascertained through five responses ("always," "often," "sometimes," "rarely," and "never") to the following two questions: 1) "Since your new baby was born, how often have you felt down, depressed, or hopeless?" and 2) "Since your new baby was born, how often have you had little interest or little pleasure in doing things?" Women responding "always" or "often" to either question were classified as experiencing PDS. In 2004 and 2008, these two questions were optional and included in 17 and 22 state surveys, respectively; in 2012, these questions were required for all 27 participating PRAMS states.

Annual PDS prevalence estimates and 95% confidence intervals were calculated for all states with available data, for the 13 states with data for all three periods (Alaska, Colorado, Georgia, Hawaii, Maine, Maryland, Minnesota, Nebraska, Oregon, Rhode Island, Utah, Vermont, and Washington) and for each individual reporting state. Combined and state-specific linear trends over time were assessed using logistic regression models that included birth year and state variables to account for baseline state-specific differences in prevalence. To estimate the average annual change in the prevalence of PDS during 2004–2012, the percentage-point change was calculated using the beta coefficient of the infant's birth year from the models. Associations between PDS and maternal characteristics (maternal age, race/ethnicity, education, marital status, number of previous live births, and postpartum smoking status), experiences (number of stressful life events experienced in the 12 months before birth), and infant outcomes (gestational age and birthweight and infant neonatal intensive care unit [NICU] admission) were assessed with chi-square tests using 2012 data. In addition, annual percentage-point changes in the prevalence of PDS during 2004–2012 were calculated by selected characteristics. Analyses were conducted using statistical software to account for the complex survey design. Differences with p-values of <0.05 were considered significant.

On average, the PRAMS surveys were completed 125 days after delivery (range = 60–270 days); timing of survey completion did not differ by PDS status. Among states with available data, the prevalence of self-reported PDS declined from 15.5% in 2004 to 13.6% in 2008 and to 11.5% in 2012 (linear trend p<0.01) (Figure) (Table 1). The overall decline was consistent with the changes among the 13 states with data for all three periods; PDS prevalence declined from 14.8% in 2004 to 12.6% in 2008 to 9.8% in 2012 (linear trend p<0.01). The estimated annual percentage-point change during 2004–2012 was -0.6% for all states and for the 13 states with data for all three periods (Table 1). Statistically significant declines in prevalence were observed in eight of 13 states (Alaska, Colorado, Georgia, Hawaii, Minnesota, Nebraska, Utah, and Washington). No statistically significant changes in prevalence were observed in five states (Maine, Maryland, Oregon, Rhode Island, and

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Vermont); for three states (Maryland, Oregon, and Vermont), prevalence estimates decreased at each period, but did not reach statistical significance.

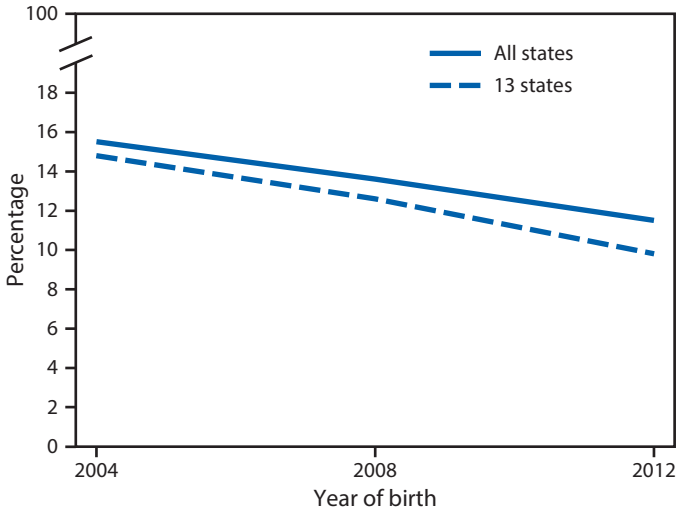
In 2012, the overall prevalence of PDS was 11.5%, representing 184,828 women with PDS in the 27 reporting states. In 2012, state-specific PDS ranged from 8.0% in Georgia to 20.1% in Arkansas (Table 1). In 2012, by selected characteristics, PDS prevalence was highest among the following: women who 1) were aged ≤19 years and 20–24 years (age group), 2) were American Indian/Alaska Natives or Asian/Pacific Islanders (race/ethnicity), 3) had ≤12 years of education (education level), 4) were unmarried (marital status), 5) were postpartum smokers (smoking status), 6) had three or more stressful life events in the year before birth (number of stressful life events), 7) gave birth to term, low-birthweight infants (gestational age and weight), and 8) had infants requiring NICU admission at birth (NICU status) ($p<0.05$ for all) (Table 2). Notably from 2004 to 2012, PDS prevalence did not significantly decline among American Indian/Alaska Native women and women with term, low-birthweight infants ($p>0.05$), with PDS prevalence remaining above 17% in 2012.

Discussion

In this population-based sample of postpartum women, a decline in the prevalence of self-reported PDS was observed from 2004 to 2012 overall and in eight of the 13 states with data for all three periods. Postpartum depression is associated with adverse maternal, infant, and child outcomes, including lower rates of breastfeeding initiation and shorter duration (*1*), poor maternal and infant bonding (*2*), and infant developmental disorders (*3*). The specific etiology of postpartum depression is unknown; however, risk factors include depression during pregnancy, low social support, stressful life events during pregnancy, preterm birth, and a traumatic birth experience (*4*). Contextual factors, such as the reduction in the birth rate of teens aged 15–19 years from 41.5 in 2007 to 24.2 per 1,000 females in 2014 and reduction in the preterm birth rate from 10.4% in 2007 to 9.5% in 2014 (*5*), reduction of women experiencing self-reported stressful life events in the year preceding birth by 0.54 percentage points per year from 2000 to 2010 (*6*), and an increase in antidepressant prescriptions to pregnant women from 0.7% in 2002–2006 to 2.1% in 2007–2010 (*7*) might have influenced the observed decline in PDS.

Postpartum depression is treatable with pharmacologic therapy and/or behavioral health interventions. However, depression is often underdiagnosed and untreated; nearly 60% of women with depressive symptoms do not receive a clinical diagnosis, and 50% of women with a diagnosis do not receive any treatment (*8*). Despite the observed decline, PDS remain

FIGURE. Percentage of new mothers with postpartum depressive symptoms — Pregnancy Risk Assessment Monitoring System (PRAMS) reporting states,* 2004, 2008, 2012†,§



* From year to year, PRAMS survey results are reported by varying numbers of states, New York City, and those areas of New York state outside of New York City (all of which, for simplicity, are referred to as "states" in this report).
† The overall trend includes states with data for any period. Thirteen states had data for all three periods: Alaska, Colorado, Georgia, Hawaii, Maine, Maryland, Minnesota, Nebraska, Oregon, Rhode Island, Utah, Vermont, and Washington.
§ Significant linear trend assessed using logistic regression model, which included birth year and state variables to account for baseline state-specific differences in prevalence.

Summary

What is already known about this topic?

Postpartum depressive symptoms (PDS) are common and are associated with adverse maternal and infant outcomes (e.g., lower breastfeeding initiation and duration and poor maternal and infant bonding). Postpartum depression is treatable.

What is added by this report?

This report provides recent state-specific trends in self-reported PDS. Among the 13 states with data for all three periods (2004, 2008, and 2012), self-reported prevalence of PDS declined from 14.8% in 2004 to 9.8% in 2012. During 2004–2012, statistically significant declines were observed in eight of 13 states (Alaska, Colorado, Georgia, Hawaii, Minnesota, Nebraska, Utah, and Washington), and no statistically significant changes in prevalence were observed in five states (Maine, Maryland, Oregon, Rhode Island, and Vermont). In 2012, the overall PDS prevalence was 11.5% for 27 states.

What are the implications for public health practice?

Despite the observed decline, PDS remain common. A developmental *Healthy People 2020* objective is to decrease the proportion of women delivering a live birth who experience PDS. This report highlights the disparities in the prevalence of self-reported PDS by reporting state and subgroups of women. Ongoing surveillance and activities to promote universal screening followed by appropriate referral and treatment are needed to reduce PDS among U.S. women.

TABLE 1. Percentage of new mothers with postpartum depressive symptoms, by reporting state — Pregnancy Risk Assessment Monitoring System (PRAMS), United States, 2004, 2008, and 2012

Reporting states	2004 (17 states) % (95% CI)	2008 (22 states) % (95% CI)	2012 (27 states) % (95% CI)	Linear trend* p-value	Average annual percentage-point change from 2004 to 2012†
All 27 states	**15.5 (14.8–16.3)**	**13.6 (12.9–14.3)**	**11.5 (11.0–12.0)**	**<0.01**	**-0.6**
13 states§	**14.8 (13.9–15.6)**	**12.6 (11.7–13.5)**	**9.8 (9.1–10.6)**	**<0.01**	**-0.6**
Alaska	16.6 (14.2–19.3)	13.1 (10.9–15.6)	12.2 (9.9–14.9)	0.02	-0.5
Arkansas	—¶	—¶	20.1 (16.1–24.9)	—**	—††
Colorado	15.0 (12.8–17.4)	13.4 (11.5–15.5)	8.9 (7.0–11.3)	<0.01	-0.7
Delaware	—§§	14.3 (12.4–16.4)	13.6 (11.6–15.9)	—**	—††
Georgia	17.2 (14.8–20.0)	12.7 (9.8–16.3)	8.0 (6.1–10.3)	<0.01	-1.1
Hawaii	16.8 (15.3–18.5)	14.5 (12.9–16.3)	10.6 (8.8–12.7)	<0.01	-0.8
Illinois	—¶	—¶	8.1 (6.5–10.1)	—**	—††
Maine	11.1 (9.2–13.4)	12.6 (10.5–15.1)	10.5 (8.1–13.6)	0.76	—††
Maryland	15.2 (12.7–18.2)	13.4 (11.1–16.2)	12.1 (9.8–14.9)	0.11	—††
Massachusetts	—§§	12.7 (10.8–15.0)	11.9 (10.0–14.2)	—**	—††
Minnesota	12.7 (10.7–15.0)	9.8 (8.2–11.6)	9.3 (7.4–11.5)	0.03	-0.4
Missouri	—§§	—§§	14.9 (12.3–17.8)	—**	—††
Nebraska	14.3 (12.5–16.2)	10.8 (9.1–12.7)	11.1 (9.1–13.4)	0.03	-0.4
New Jersey	—¶	—¶	9.7 (8.0–11.7)	—**	—††
New Mexico	19.5 (17.4–21.7)	—§§	14.0 (11.8–16.6)	—**	—††
New York¶¶	14.5 (12.0–17.5)	12.6 (10.3–15.2)	—§§	—**	—††
New York City	—¶	—§§	11.8 (9.9–14.0)	—**	—††
North Carolina	17.7 (15.4–20.2)	14.0 (12.1–16.2)	—§§	—**	—††
Ohio	—§§	16.3 (13.9–19.0)	13.2 (11.2–15.3)	—**	—††
Oklahoma	—¶	—¶	14.9 (12.3–18.0)	—**	—††
Oregon	13.2 (11.0–15.74)	12.3 (10.0–14.9)	9.5 (6.9–12.8)	0.06	—††
Pennsylvania	—§§	11.9 (9.9–14.2)	12.3 (9.9–15.1)	—**	—††
Rhode Island	13.4 (11.5–15.6)	13.6 (11.5–16.0)	13.9 (11.9–16.1)	0.75	—††
South Carolina	19.6 (16.4–23.2)	—§§	—§§	—**	—††
Tennessee	—§§	21.1 (17.5–25.2)	17.0 (14.1–20.5)	—**	—††
Utah	14.8 (13.1–16.6)	12.4 (10.8–14.2)	11.3 (9.1–13.3)	0.01	-0.4
Vermont	12.2 (10.3–14.4)	11.6 (9.8–13.8)	10.1 (8.4–12.1)	0.13	—††
Washington	13.5 (11.4–16.0)	13.4 (11.3–15.9)	10.1 (7.9–12.5)	0.03	-0.4
Wisconsin	—§§	13.5 (11.4–16.1)	11.1 (8.9–13.8)	—**	—††
Wyoming	—§§	11.6 (9.4–14.3)	13.8 (10.7–17.6)	—**	—††

Abbreviation: CI = confidence interval.

* State-specific linear trends were assessed using logistic regression models among states with all three periods using year of birth as the predictor. Overall linear trends for all states and for combined 13 states with data for all three periods also were adjusted for state in regression models.

† Average annual percentage-point change during 2004–2012 was calculated using the beta coefficient of the infant's birth year from the linear model and the average percentage over 2004–2012.

§ Included 13 states that had data for all three periods: Alaska, Colorado, Georgia, Hawaii, Maine, Maryland, Minnesota, Nebraska, Oregon, Rhode Island, Utah, Vermont, and Washington.

¶ PRAMS state did not ask the postpartum depressive symptoms questions on the survey that year.

** Insufficient data (<3 years) to assess linear trend.

†† Annual percentage point-change was not computed because of either nonsignificant linear trend or insufficient data to calculate linear trend.

§§ States did not participate in PRAMS or participated in PRAMS but did not meet response rate threshold for that year for data to be included.

¶¶ Areas of New York state outside of New York City.

common, affecting 11.5% of new mothers in 2012, with prevalence varying by reporting state and subgroups of women. These findings underscore the need for universal screening and appropriate treatment for pregnant and postpartum women, as recommended by the American College of Obstetricians and Gynecologists (ACOG) (*4*), the American Academy of Pediatrics (AAP) (*9*), and the U.S. Preventive Services Task Force.§ ACOG recommends that providers screen for depressive symptoms at least once during pregnancy or postpartum, using a validated screening tool (*4*). In addition, AAP recognizes that depression screening is part of family-centered well-child care, given pediatricians' early access to the mother-infant duo (*9*). Collaboration between obstetric and pediatric providers is recommended for symptomatic women identified during newborn care (*4*,*9*). Recent efforts to address maternal depression include extending postpartum Medicaid coverage for women, integration of behavioral health services within primary care, and provider reimbursement for postpartum depression screening at well-baby visits.

The findings in this report are subject to at least three limitations. First, PDS are self-reported and might not represent a clinical diagnosis of depression. The PRAMS PDS two-item screener is based on the Patient Health Questionnaire-2.

§ https://www.uspreventiveservicestaskforce.org/Page/Document/UpdateSummaryFinal/depression-in-adults-screening.

TABLE 2. Percentage of new mothers with postpartum depressive symptoms, by selected characteristics — Pregnancy Risk Assessment Monitoring System (PRAMS), 13 reporting states,* 2004, 2008, and 2012

Characteristic	2004 % (95% CI)	2008 % (95% CI)	2012 % (95% CI)	Linear trend† p-value	Average annual percentage-point change from 2004 to 2012§
Maternal age group (yrs)					
≤19	24.6 (21.3–28.3)	21.4 (17.2–26.3)	18.3 (14.9–22.2)	0.016	-0.8
20–24	18.5 (16.7–20.5)	16.8 (14.6–19.2)	11.5 (9.8–13.4)	<0.001	-0.9
25–34	12.4 (11.4–13.6)	10.2 (9.1–11.3)	8.6 (7.7–9.7)	<0.001	-0.5
≥35	11.0 (9.3–13.0)	8.8 (7.5–10.4)	8.9 (7.2–10.8)	0.102	—¶
Maternal race/Ethnicity**					
White, Non-Hispanic	11.9 (10.9–12.9)	10.4 (9.4–11.4)	8.6 (7.6–9.6)	<0.001	-0.4
Black, Non-Hispanic	21.5 (19.0–24.2)	18.9 (14.8–23.9)	10.8 (8.5–13.7)	<0.001	-1.3
Hispanic	18.2 (15.9–20.9)	13.4 (11.5–15.6)	10.5 (8.7–12.5)	<0.001	-0.9
American Indian/Alaska Native	22.8 (18.7–27.5)	19.0 (16.2–22.1)	17.5 (14.1–21.6)	0.071	—¶
Asian/Pacific Islander	18.5 (16.1–21.2)	14.9 (12.5–17.6)	14.0 (11.7–16.7)	0.018	-0.5
Other	29.8 (19.6–42.6)	17.6 (11.4–26.3)	10.7 (7.5–15.0)	<0.001	-2.0
Education level (yrs)					
<12	23.6 (21.0–26.3)	20.2 (17.1–23.6)	13.4 (11.2–16.0)	<0.001	-1.2
12	17.4 (15.9–19.1)	14.9 (13.1–17.0)	12.3 (10.6–14.2)	<0.001	-0.6
>12	10.4 (9.5–11.4)	9.1 (8.2–10.2)	8.0 (7.2–8.9)	<0.001	-0.3
Marital status					
Unmarried	22.0 (20.3–23.9)	18.5 (16.4–20.7)	12.7 (11.3–14.2)	<0.001	-0.1
Married	11.5 (10.7–12.5)	9.4 (8.6–10.3)	8.4 (7.5–9.3)	<0.001	-0.2
No. of previous live births					
First birth	13.5 (12.3–14.8)	12.0 (10.6–13.6)	9.4 (8.3–10.6)	<0.001	-0.5
Second or later birth	15.7 (14.6–16.8)	13.0 (11.8–14.3)	10.0 (9.0–11.0)	<0.001	-0.7
Postpartum smoking status					
Nonsmoker	12.4 (11.6–13.3)	11.1 (10.1–12.1)	8.7 (8.0–9.5)	<0.001	-0.5
Smoker	26.3 (23.7–29.2)	21.8 (18.8–25.1)	17.7 (14.9–20.8)	<0.001	-1.1
No. of stressful life events in 12 months before birth					
None	7.3 (6.3–8.5)	5.6 (4.7–6.6)	6.4 (5.2–7.7)	0.268	—¶
1–2	12.2 (11.0–13.4)	11.4 (10.1–13.0)	8.0 (7.0–9.2)	<0.001	-0.5
3–5	24.0 (21.9–26.3)	20.2 (17.8–22.8)	14.4 (12.6–16.3)	<0.001	-1.2
6–13	37.3 (32.5–42.3)	34.0 (28.5–40.0)	24.2 (20.0–29.0)	<0.001	-1.6
Gestational age and birthweight††					
Preterm	19.0 (16.6–21.6)	15.4 (13.4–17.7)	11.7 (9.8–13.8)	<0.001	-0.9
Term, low birthweight	20.4 (16.0–25.5)	19.1 (15.4–23.5)	17.6 (13.4–22.8)	0.412	—¶
Term, normal birthweight	14.2 (13.4–15.2)	12.0 (11.0–13.0)	9.5 (8.7–10.4)	<0.001	-0.6
Infant admission to NICU at birth					
No	14.0 (13.1–14.9)	11.7 (10.8–12.7)	9.5 (8.7–10.4)	<0.001	-1.0
Yes	20.5 (17.9–23.4)	18.6 (15.6–22.0)	12.5 (10.4–14.9)	<0.001	-0.5

Abbreviations: CI = confidence interval; NICU = neonatal intensive care unit.

* Included 13 states that had data for all three periods: Alaska, Colorado, Georgia, Hawaii, Maine, Maryland, Minnesota, Nebraska, Oregon, Rhode Island, Utah, Vermont, and Washington.

† State-specific linear trends were assessed using logistic regression models among states with all 3 periods using year of birth as the predictor.

§ Unadjusted average annual percentage-point change in prevalence within selected characteristic during 2004–2012 was calculated using the beta coefficient of the infant's birth year from the linear model and the average percentage during 2004–2012.

¶ Average annual percentage-point change was not computed because linear trend was not significant.

** Vermont data do not include race/ethnicity, and were excluded from subgroup analysis.

†† Preterm birth: <37 weeks' gestation; Term, low birthweight: ≥37 weeks' gestation and <2,500 g; Term, normal birthweight: ≥37 weeks' gestation and ≥2,500 g.

These questions with similar categorization schemes have a sensitivity of 58% and specificity of 85%, compared with clinical assessments of major depressive episodes (*10*); thus, the results in this report might underestimate the true prevalence of postpartum depression. Second, data might not be generalizable to states not included in this analysis or pregnancies that did not result in a live birth. Finally, PRAMS has limited data on mental health treatment, including antidepressant use; thus, mental health treatment over time could not be assessed in this report.

PRAMS data can be used to monitor progress toward meeting the *Healthy People 2020* objective to decrease the proportion of women delivering a live birth who experience PDS. Despite the observed decline in prevalence, approximately one in nine women experience PDS, with higher prevalence in certain states and subgroups of women. Ongoing surveillance and activities to promote appropriate screening, referral, and treatment are needed

to reduce PDS among U.S. women. In addition, more research is needed to understand the etiology of postpartum depression.

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Update: Influenza Activity — United States, October 2, 2016–February 4, 2017

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This report summarizes U.S. influenza activity* during October 2, 2016–February 4, 2017,† and updates the previous summary (*1*). Influenza activity in the United States began to increase in mid-December, remained elevated through February 4, 2017, and is expected to continue for several more weeks. To date, influenza A (H3N2) viruses have predominated overall, but influenza A (H1N1)pdm09 and influenza B viruses have also been identified.

Virologic Surveillance

U.S. World Health Organization (WHO) and National Respiratory and Enteric Virus Surveillance System laboratories, which include both public health and clinical laboratories throughout the United States, contribute to virologic surveillance for influenza.

During October 2, 2016–February 4, 2017, clinical laboratories in the United States tested 392,901 respiratory specimens for influenza viruses, 38,244 (9.7%) of which were positive (Figure 1). During the week ending February 4, 2017 (week 5), 27,409 specimens were tested, 5,722 (20.9%) of which were positive for influenza. Among these, 5,017 (87.7%) were positive for influenza A viruses and 705 (12.3%) were positive for influenza B viruses.

Public health laboratories in the United States tested 38,141 respiratory specimens collected during October 2, 2016–February 4, 2017. Among these, 15,781 were positive for influenza (Figure 2), 14,606 (92.6%) were positive for influenza A viruses, and 1,174 (7.4%) were positive for influenza B viruses. Among the 14,335 (98.1%) influenza A viruses subtyped, 13,973 (97.5%) were influenza A (H3N2) and 362 (2.5%) were influenza A (H1N1)pdm09 virus. Among the 851 (72.5%) influenza B viruses for which lineage was determined, 460 (54.1%) belonged to the B/Yamagata lineage and 391 (45.9%) belonged to the B/Victoria lineage.

Age was reported for 13,306 influenza-positive patients, among whom 1,048 (7.9%) were aged 0–4 years, 4,041 (30.4%) were aged 5–24 years, 4,029 (30.3%) were aged 25–64 years, and 4,188 (31.5%) were aged ≥65 years. Influenza A (H3N2) viruses predominated in each age group, representing a range of 82.3% of influenza-positives in persons aged 0–4 years to 93.6% in persons aged ≥65 years. The largest number of influenza B viruses were reported in persons aged 5–24 years.

Novel Influenza A Viruses

Two human infections with a novel influenza A virus were reported during October 2, 2016–February 4, 2017. One patient from Iowa with exposure to swine in the week preceding illness was infected with an influenza A (H1N2) variant [(H1N2)v] virus.§ Another patient was infected with an avian lineage influenza A (H7N2) virus and reported close, prolonged unprotected exposure to the respiratory secretions of sick cats known to be infected with this virus at a New York City animal shelter. Neither patient was hospitalized; both recovered fully, and there was no evidence of human-to-human transmission in either instance.

Antigenic and Genetic Characterization of Influenza Viruses

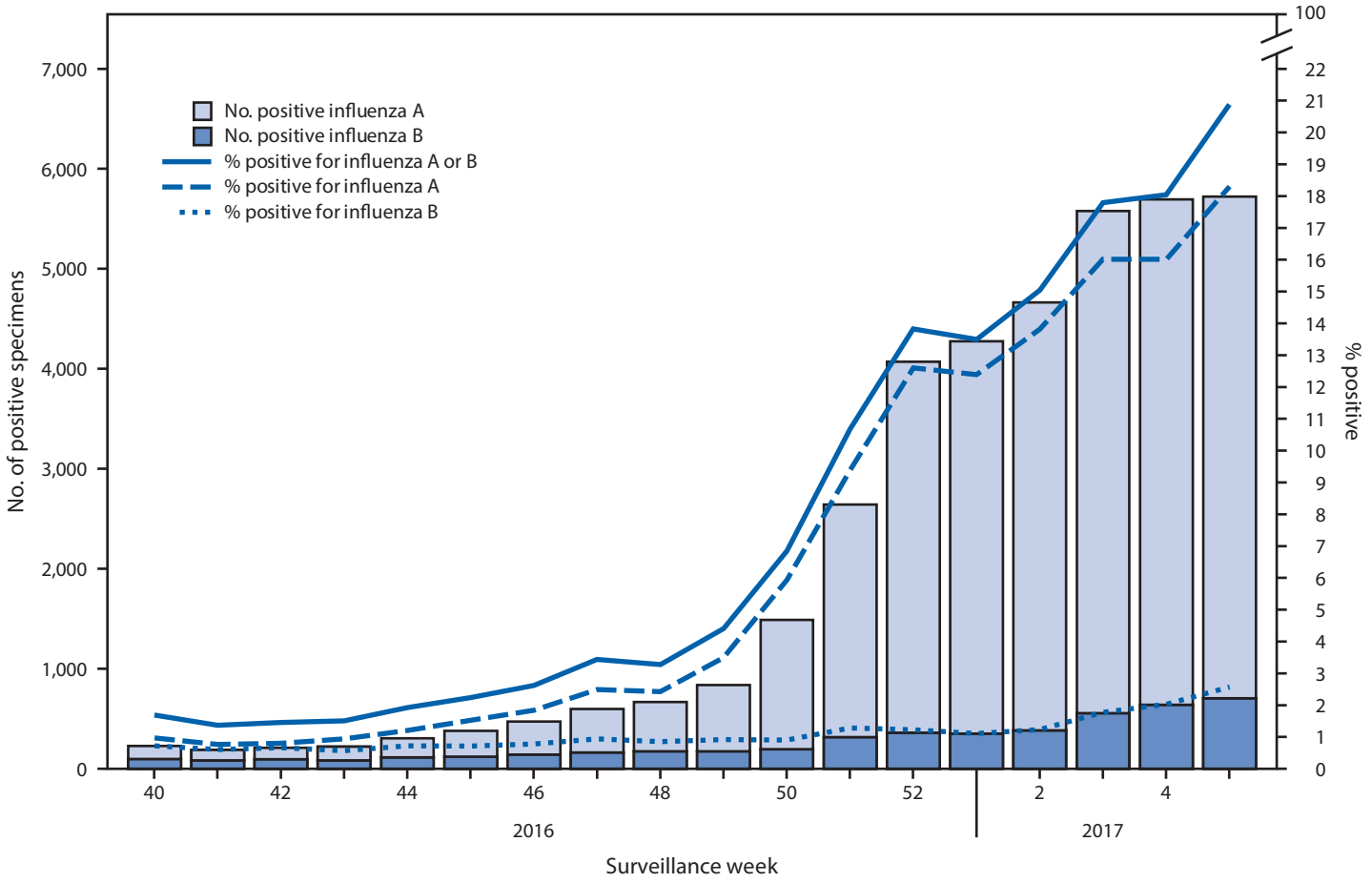
WHO collaborating laboratories in the United States are requested to submit a subset of influenza-positive respiratory specimens to CDC for further virus characterization. CDC characterizes influenza viruses through one or more laboratory tests, including genomic sequencing, antigenic characterization by hemagglutination inhibition (HI), and neutralization assays. Historically, HI data have been used most commonly to assess the similarity between vaccine viruses and circulating viruses to infer how well the vaccine might work until

* The CDC influenza surveillance system collects five categories of information from eight data sources: 1) viral surveillance (U.S. World Health Organization collaborating laboratories, the National Respiratory and Enteric Virus Surveillance System, and novel influenza A virus case reporting); 2) outpatient illness surveillance (U.S. Outpatient Influenza-Like Illness Surveillance Network); 3) mortality (the National Center for Health Statistics Mortality Surveillance System and influenza-associated pediatric mortality reports); 4) hospitalizations (FluSurv-NET, which includes the Emerging Infections Program and surveillance in three additional states); and 5) summary of the geographic spread of influenza (state and territorial epidemiologist reports). https://www.cdc.gov/flu/weekly/fluactivitysurv.htm.

† Data as of February 10, 2017.

§ Influenza viruses that circulate in swine are called swine influenza viruses when isolated from swine, but are called variant influenza viruses when isolated from humans. Seasonal influenza viruses that circulate worldwide in the human population have important antigenic and genetic differences from influenza viruses circulating in swine.

FIGURE 1. Number* and percentage of respiratory specimens testing positive for influenza reported by clinical laboratories, by influenza virus type and surveillance week — United States, October 2, 2016–February 4, 2017



* 38,244 (9.7%) of 392,907 tested were positive during October 2, 2016–February 4, 2017.

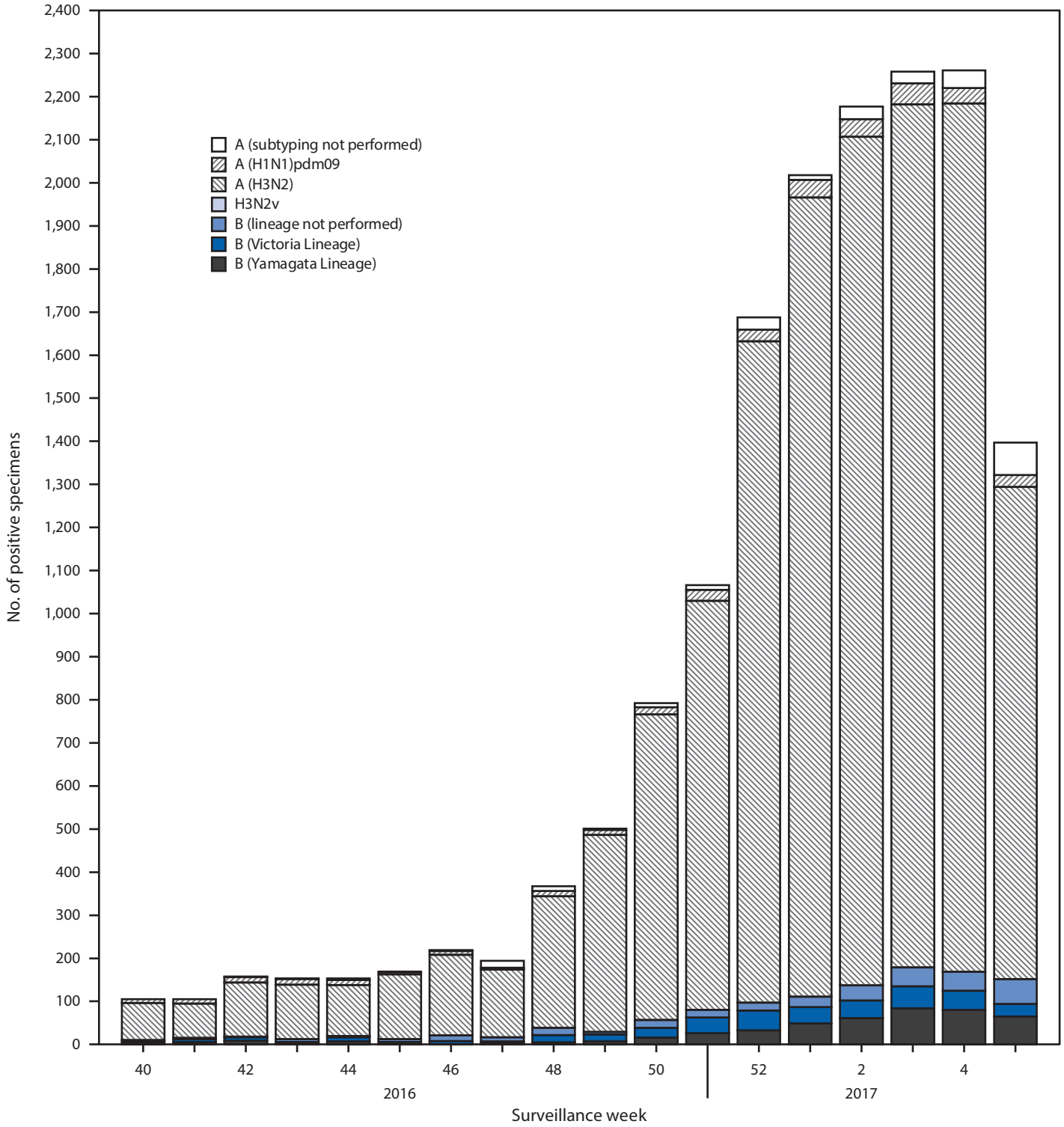
vaccine effectiveness estimates are available.¶ For all viruses characterized at CDC laboratories, next-generation sequencing is performed to determine the genetic identity of circulating viruses. The antigenic properties of viruses that cannot be characterized are inferred from viruses with matching genes whose antigenic profile is known.

CDC has genetically characterized 892 viruses (101 influenza A (H1N1)pdm09; 593 influenza A (H3N2); and 198 influenza B viruses) collected from October 1, 2016, through February 4, 2017. The hemagglutinin (HA) gene segment of all influenza A (H1N1)pdm09 viruses analyzed belonged to genetic group 6B.1. Influenza A (H3N2) virus HA gene segments analyzed belonged to genetic groups 3C.2a (567 viruses) or 3C.3a (26 viruses). Genetic group 3C.2a includes an emerging subgroup defined as 3C.2a1. The HA of influenza B/Victoria-lineage viruses all belonged to genetic group V1A. The HA of all influenza B/Yamagata-lineage viruses analyzed belonged to genetic group Y3.

During October 1, 2016–February 4, 2017, CDC antigenically characterized 484 influenza viruses (74 influenza A (H1N1) pdm09, 267 influenza A (H3N2), and 143 influenza B viruses). All 74 (100%) influenza A (H1N1)pdm09 viruses were antigenically similar to A/California/7/2009, the recommended influenza A (H1N1) component of the 2016–17 Northern Hemisphere vaccine. Among 267 influenza A (H3N2) viruses, 258 (96.6%) were antigenically similar to the A/Hong Kong/4801/2014–like cell propagated reference virus belonging to genetic group 3C.2a, which is the recommended influenza A (H3N2) component of the 2016–17 Northern Hemisphere vaccine. Seventy (90.9%) of 77 influenza B/Victoria-lineage viruses were antigenically similar to B/Brisbane/60/2008, which is the recommended influenza B component of the 2016–17 Northern Hemisphere trivalent and

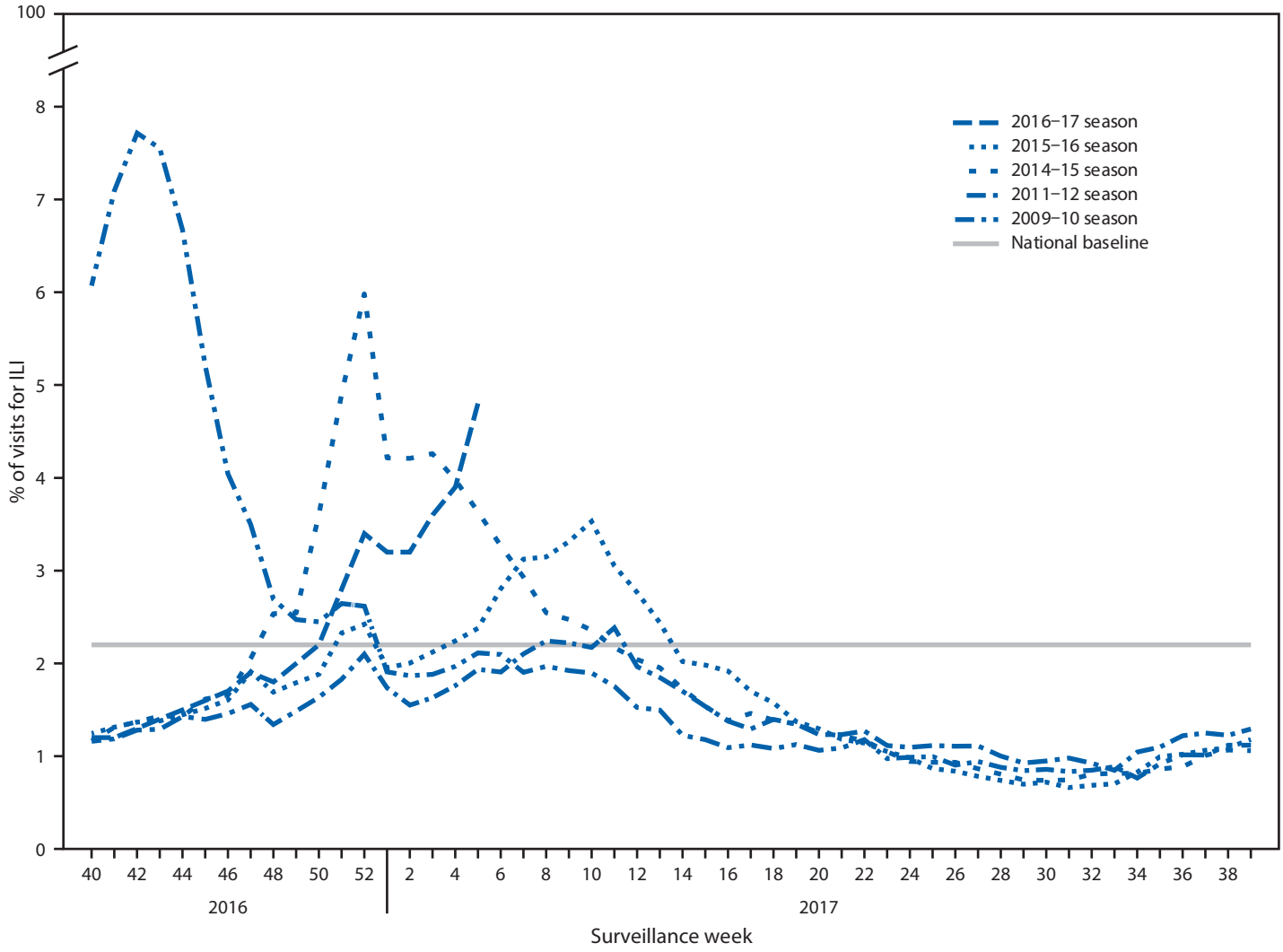
¶ A virus is considered "reference virus-like" if its hemagglutination inhibition (HI) or neutralization focus reduction assay (FRA) titer is within fourfold of the homologous HI/FRA titer of the reference strain. A virus is considered as low to the reference virus if there is an eightfold or greater reduction in the HI or FRA titer when compared with the homologous HI or FRA titer of the reference strain.

FIGURE 2. Number* of respiratory specimens testing positive for influenza reported by public health laboratories, by influenza virus type, subtype/lineage, and surveillance week — United States, October 2, 2016–February 4, 2017†



* N = 15,781.
† As of February 10, 2017.

FIGURE 3. Percentage of visits for influenza-like illness (ILI)* reported to CDC, by surveillance week — Outpatient Influenza-Like Illness Surveillance Network, United States, 2016–17 influenza season and selected previous influenza seasons



* Defined as fever (≥100°F [≥37.8°C]), oral or equivalent, and cough and/or sore throat, without a known cause other than influenza.

quadrivalent vaccines. All 66 (100%) influenza B/Yamagata-lineage viruses were antigenically similar to B/Phuket/3073/2013, the recommended influenza B component of the 2016–17 Northern Hemisphere quadrivalent vaccine.

Antiviral Resistance of Influenza Viruses

The WHO Collaborating Center for Surveillance, Epidemiology, and Control of Influenza at CDC tested 807 influenza virus specimens (94 influenza A (H1N1)pdm09, 519 influenza A (H3N2), and 194 influenza B viruses) collected in the United States from October 1, 2016, through February 4, 2017, for resistance to the influenza neuraminidase inhibitor antiviral medications oseltamivir, zanamivir, and peramivir, drugs currently approved for use against seasonal influenza. All 807 influenza viruses tested were found to be sensitive to all three antiviral medications. An additional 114 influenza A (H3N2) viruses were tested for resistance to oseltamivir and zanamivir, and were found to be sensitive to both antiviral medications.

Outpatient Illness Surveillance

From October 2, 2016, through February 4, 2017, the weekly percentage of outpatient visits for influenza-like illness (ILI)** reported by approximately 2,000 U.S. Outpatient ILI Surveillance Network (ILINet) providers in 50 states, New York City, Chicago, the U.S. Virgin Islands, Puerto Rico, and the District of Columbia, has ranged from 1.2% to 4.8%.

** Defined as a fever (temperature ≥100°F [≥37.8°C]), oral or equivalent, and cough and/or sore throat, without a known cause other than influenza.

The percentage exceeded the national baseline[††] of 2.2% for 8 consecutive weeks, from the weeks ending December 17, 2016–February 4, 2017 (weeks 50–5) (Figure 3). During the previous five influenza seasons, the peak weekly percentages of outpatient visits for ILI ranged from 2.4%–6.1% and remained above baseline levels for an average of 13 weeks (range = 1–20 weeks). For the week ending February 4, 2017 (week 5), the percentage of outpatient visits for ILI was 4.8%, and all 10 U.S. Department of Health and Human Services (HHS) regions[§§] reported ILI activity at or above region-specific baseline levels.

Data collected in ILINet are used to produce a measure of ILI activity[¶¶] by jurisdiction. During the week ending February 4, 2017, New York City and 23 states (Alabama, Arkansas, Connecticut, Georgia, Hawaii, Indiana, Kansas, Louisiana, Minnesota, Mississippi, Missouri, New Jersey, New Mexico, New York, North Carolina, Oklahoma, Pennsylvania, South Carolina, South Dakota, Tennessee, Texas, Virginia, and Wyoming) experienced high ILI activity; 10 states (California, Colorado, Florida, Illinois, Iowa, Michigan, Nebraska, North Dakota, Oregon, and Wisconsin) experienced moderate ILI activity; Puerto Rico and eight states (Alaska, Arizona, Kentucky, Maryland, Massachusetts, Nevada, Rhode Island, and West Virginia) experienced low ILI activity; nine states (Delaware, Idaho, Maine, Montana, New Hampshire, Ohio, Utah, Vermont, and Washington) experienced minimal ILI activity; and the District of Columbia had insufficient data to calculate an ILI activity level.

Geographic Spread of Influenza Activity

Influenza activity levels reported by state and territorial epidemiologists indicate the geographic spread of influenza viruses. For the week ending February 4, 2017 (week 5), Puerto Rico and 43 states (Alabama, Alaska, Arkansas, California, Connecticut, Delaware, Florida, Georgia, Idaho, Illinois, Iowa, Kansas, Kentucky, Louisiana, Maine, Maryland, Massachusetts, Michigan, Minnesota, Mississippi, Missouri, Montana, Nebraska, Nevada, New Hampshire, New Jersey, New Mexico, New York, North Carolina, North Dakota, Ohio, Oklahoma, Oregon, Pennsylvania, Rhode Island, South Carolina, South Dakota, Texas, Vermont, Virginia, Washington, Wisconsin, and Wyoming) reported widespread activity.[***] Guam and six states (Arizona, Colorado, Indiana, Tennessee, Utah, and West Virginia) reported regional activity. The District of Columbia and one state (Hawaii) reported local activity, and the U.S. Virgin Islands reported no influenza activity. During the previous five influenza seasons, the peak number of jurisdictions reporting widespread activity in a single week during each season has ranged from 20 in the 2011–12 season to 48 during the 2012–13 season.

Influenza-Associated Hospitalizations

CDC monitors hospitalizations associated with laboratory-confirmed influenza infection in adults and children through the Influenza Hospitalization Surveillance Network (FluSurv-NET),[†††] which covers approximately 27 million persons (9% of the U.S. population). From October 1, 2016, through February 4, 2017, 6,804 laboratory-confirmed

[††] The national and regional baselines are the mean percentage of visits for influenza-like illness (ILI) during noninfluenza weeks for the previous three seasons plus two standard deviations. Noninfluenza weeks are defined as periods of ≥2 consecutive weeks in which each week accounted for <2% of the season's total number of specimens that tested positive for influenza. National and regional percentages of patient visits for ILI are weighted based on state population. Use of the national baseline for regional data is not appropriate.

[§§] The 10 regions include the following jurisdictions: *Region 1*: Connecticut, Maine, Massachusetts, New Hampshire, Rhode Island, and Vermont; *Region 2*: New Jersey, New York, Puerto Rico, and the U.S. Virgin Islands; *Region 3*: Delaware, District of Columbia, Maryland, Pennsylvania, Virginia, and West Virginia; *Region 4*: Alabama, Florida, Georgia, Kentucky, Mississippi, North Carolina, South Carolina, and Tennessee; *Region 5*: Illinois, Indiana, Michigan, Minnesota, Ohio, and Wisconsin; *Region 6*: Arkansas, Louisiana, New Mexico, Oklahoma, and Texas; *Region 7*: Iowa, Kansas, Missouri, and Nebraska; *Region 8*: Colorado, Montana, North Dakota, South Dakota, Utah, and Wyoming; *Region 9*: Arizona, California, Hawaii, Nevada, American Samoa, Commonwealth of the Northern Mariana Islands, Federated States of Micronesia, Guam, Marshall Islands, and Republic of Palau; *Region 10*: Alaska, Idaho, Oregon, and Washington.

[¶¶] Activity levels are based on the percentage of outpatient visits in a jurisdiction attributed to ILI and are compared with the average percentage of ILI visits that occur during weeks with little or no influenza virus circulation. Activity levels range from minimal, corresponding to ILI activity from outpatient clinics at or below the average, to high, corresponding to ILI activity from outpatient clinics much higher than the average. Because the clinical definition of ILI is nonspecific, not all ILI is caused by influenza; however, when combined with laboratory data, the information on ILI activity provides a clearer picture of influenza activity in the United States.

[***] Levels of activity are 1) no activity; 2) sporadic: isolated laboratory-confirmed influenza cases or a laboratory-confirmed outbreak in one institution, with no increase in activity; 3) local: increased ILI, or two or more institutional outbreaks (ILI or laboratory-confirmed influenza) in one region of the state, with recent laboratory evidence of influenza in that region; virus activity no greater than sporadic in other regions; 4) regional: increased ILI activity or institutional outbreaks (ILI or laboratory-confirmed influenza) in two or more outbreaks, but less than half of the regions in the state with recent laboratory evidence of influenza in those regions; and 5) widespread: increased ILI activity or institutional outbreaks (ILI or laboratory-confirmed influenza) in at least half the regions in the state, with recent laboratory evidence of influenza in the state.

[†††] FluSurv-NET conducts population-based surveillance for laboratory-confirmed, influenza-associated hospitalizations in children and adolescents aged <18 years (since the 2003–04 influenza season) and adults aged ≥18 years (since the 2005–06 influenza season). The FluSurv-NET covers approximately 70 counties in the 10 Emerging Infections Program states (California, Colorado, Connecticut, Georgia, Maryland, Minnesota, New Mexico, New York, Oregon, and Tennessee) and additional Influenza Hospitalization Surveillance Project (IHSP) states. IHSP began during the 2009–10 season to enhance surveillance during the 2009 H1N1 pandemic. IHSP sites included Iowa, Idaho, Michigan, Oklahoma, and South Dakota during the 2009–10 season; Idaho, Michigan, Ohio, Oklahoma, Rhode Island, and Utah during the 2010–11 season; Michigan, Ohio, Rhode Island, and Utah during the 2011–12 season; Iowa, Michigan, Ohio, Rhode Island, and Utah during the 2012–13 season; and Michigan, Ohio, and Utah during the 2013–14, 2014–15, 2015–16, and 2016–17 seasons. Cumulative unadjusted incidence rates are calculated using CDC's National Center for Health Statistics population estimates for the counties included in the surveillance catchment area. Laboratory confirmation is dependent on clinician-ordered influenza testing, and testing for influenza often is underutilized because of the poor reliability of rapid test results and greater reliance on clinical diagnosis for influenza. Therefore, cases identified as part of influenza hospitalization surveillance likely are an underestimation of the actual number of persons hospitalized with influenza.

influenza-associated hospitalizations were reported, with a cumulative incidence for all age groups of 24.3 per 100,000 population. Persons aged ≥65 years had the highest rate of laboratory-confirmed influenza-associated hospitalization and accounted for approximately 60% of reported influenza-associated hospitalizations.

The cumulative hospitalization rate (per 100,000 population) during October 1, 2016–February 4, 2017 was 13.6 among children aged 0–4 years, 4.8 among children and adolescents aged 5–17 years, 7.3 among adults aged 18–49 years, 23.5 among adults aged 50–64 years, and 113.4 among adults aged ≥65 years. Among all hospitalizations reported during October 1, 2016–February 4, 2017, a total of 6,367 (93.6%) were associated with influenza A virus, 395 (5.8%) with influenza B virus, 21 (0.3%) with influenza A and B virus coinfection, and 21 (0.3%) with influenza virus for which the type was not determined. Among 1,729 patients with influenza A subtype information, 1,701 (98.4%) were infected with influenza A (H3N2) virus and 28 (1.6%) were infected with influenza A (H1N1)pdm09 virus.

Complete medical chart abstraction data were available for 796 (11.7%) hospitalized patients with laboratory-confirmed influenza as of February 4, 2017. Among 744 hospitalized adults with complete medical chart abstraction, 703 (94.5%) had at least one underlying medical condition that placed them at high risk for influenza-associated complications. The most commonly reported medical conditions were cardiovascular disease (47.1%), metabolic disorders (39.7%), and obesity (38.3%). Among 52 hospitalized children with complete medical chart abstraction, 28 (53.8%) had at least one underlying medical condition, the most commonly reported being asthma (15.4%), chronic lung disease (15.4%), and neurologic disorder (15.4%). Among 59 hospitalized women of childbearing age (15–44 years), 20 (33.9%) were pregnant.

Pneumonia and Influenza-Attributed Mortality

CDC tracks pneumonia and influenza (P&I)-attributed deaths through the National Center for Health Statistics (NCHS) Mortality Reporting System. The percentages of deaths attributed to P&I are released 2 weeks after the week of death to allow for collection of sufficient data to produce a stable P&I mortality percentage. Weekly mortality surveillance data includes a combination of machine coded and manually coded causes of death collected from death certificates. There is a backlog of data requiring manual coding within the NCHS mortality surveillance data. The percentages of deaths attributable to P&I are higher among manually coded records than the more rapidly available machine coded records and might result in initially reported P&I percentages that are lower than percentages calculated from final data. Initiatives continue to reduce and monitor the number of records awaiting manual coding.

Based on data from NCHS available on February 9, 2017, 7.9% (2,691 of 33,868) of all U.S. deaths occurring during the week ending January 21, 2017 (week 3) were attributed to P&I. This percentage is above the epidemic threshold[§§§] of 7.4% for week 3. Since October 2, 2016 the weekly percentage of deaths attributed to P&I has ranged from 5.6% to 7.9% and has exceeded the epidemic threshold for three consecutive weeks, from the weeks ending January 7–21 (weeks 1–3), this season. During the previous five influenza seasons, the peak weekly percentage of deaths attributable to P&I ranged from 8.2% in the 2015–16 season to 11.1% in the 2012–13 season.

Influenza-Associated Pediatric Mortality

As of February 4, 2017 (week 5), 20 laboratory-confirmed influenza-associated pediatric deaths that occurred during the 2016–17 season were reported to CDC. Of the 20 deaths, nine were associated with an influenza A (H3N2) virus infection, one was associated with an influenza A (H1N1)pdm09 virus infection, five were associated with an influenza A virus infection for which no subtyping was performed, four were associated with an influenza B virus infection, and one was associated with an influenza virus for which the type was not determined. Since influenza-associated pediatric mortality became a nationally notifiable condition in 2004, the total number of influenza-associated pediatric deaths per season has ranged from 37 to 171; excluding the 2009 pandemic, when 358 pediatric deaths were reported to CDC from April 15, 2009, through October 2, 2010.

Discussion

Influenza activity in the United States began to increase in mid-December and remained elevated as of February 4, 2017. During the most recent weeks, decreases in activity have been observed in the Northwest (HHS Region 10), while activity has continued to increase in the remainder of the country. During October 2, 2016–February 4, 2017, influenza A (H3N2) viruses accounted for the majority of circulating influenza viruses, but influenza A (H1N1)pdm09 and influenza B viruses also were identified. Influenza activity has been moderate so far this season, and severity indicators are within the range of what has been observed during previous seasons when influenza A (H3N2) viruses predominated. Elevated influenza activity in parts of the United States is expected for several more weeks.

[§§§] The seasonal baseline proportion of pneumonia and influenza (P&I) deaths is projected using a robust regression procedure, in which a periodic regression model is applied to the observed percentage of deaths from P&I that were reported by the National Center for Health Statistics Mortality Surveillance System during the preceding 5 years. The epidemic threshold is set at 1.645 standard deviations above the seasonal baseline.

Interim estimates of vaccine effectiveness based on data collected from November 28, 2016, through February 4, 2017, indicate that overall the influenza vaccine has been 48% (95% confidence interval [CI] = 37%–57%) effective in preventing influenza-related medical visits across all age groups, and specifically was 43% (CI = 29%–54%) and 73% (CI = 54%–84%) effective in preventing medical visits associated with influenza A (H3N2) and influenza B, respectively (*2*). Annual influenza vaccination is the first and best defense to protect against influenza infection. Depending on the vaccine formulation (trivalent or quadrivalent), influenza vaccines can protect against three or four different influenza viruses. Even during seasons when vaccine effectiveness is reduced, vaccination can offer substantial benefit and might reduce the likelihood of severe outcomes such as hospitalization and death.

Although health care providers should continue to offer and encourage vaccination to all unvaccinated persons aged ≥6 months as long as influenza viruses are circulating, influenza antiviral medications are an important adjunct to vaccination in the treatment and prevention of influenza. No antiviral resistance to oseltamivir, zanamivir, or peramivir has been identified among influenza viruses collected since October 1, 2016. Treatment as soon as possible with influenza antiviral medications 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 influenza complications.¶¶¶ Antiviral treatment should not be withheld from high-risk or severely ill patients with suspected influenza infection, even if rapid antigen-detection influenza diagnostic test results are negative (*3*). Generic oseltamivir was approved by the Food and Drug Administration on August 3, 2016 (*4*), and became available in December 2016.

An unusual outbreak of avian lineage influenza A (H7N2) virus infection among cats in an animal shelter in New York City was first reported to public health officials on December 14, 2016. Approximately 350 persons with exposure to infected cats during this outbreak were screened or tested for infection and only one human infection with avian influenza A (H7N2) was identified (*5*). This is the first influenza A (H7N2) virus infection in humans identified in the United States since 2003 and the first known human infection with an influenza A virus likely acquired through exposure to an ill cat. The finding of an avian lineage influenza virus in an unexpected host, such as a domestic cat, or any human infection with a nonhuman influenza virus is concerning. Early identification and investigation of human infections with novel influenza A viruses are critical so that the risk of infection can be more fully understood and appropriate public health measures can be taken. If clinical laboratories test a respiratory specimen that they cannot type or subtype using commercially available rapid or molecular influenza diagnostic tests, they should contact their state public health laboratory to facilitate transport of specimens for additional testing. Public health laboratories should immediately send virus specimens that they cannot type or subtype using standard methods to CDC and submit all specimens that are otherwise unusual as soon as possible after identification.

Influenza surveillance reports for the United States are posted online weekly (https://www.cdc.gov/flu/weekly). Additional information regarding influenza viruses, influenza surveillance, influenza vaccine, influenza antiviral medications, and novel influenza A infections in humans is online (https://www.cdc.gov/flu).

Summary

What is already known about this topic?

CDC collects, compiles, and analyzes data on influenza activity year round in the United States. Timing of influenza activity and predominant circulating influenza viruses vary by season.

What is added by this report?

Influenza activity in the United States began to increase in mid-December, remained elevated through February 4, 2016, and is expected to continue for several more weeks. During October 2, 2016–February 4, 2017, influenza A (H3N2) viruses were identified most frequently, but influenza A (H1N1)pdm09 and influenza B viruses were also reported. No antiviral resistance to oseltamivir, zanamivir, or peramivir has been identified among influenza viruses tested to date.

What are the implications for public health practice?

Elevated influenza activity in parts of the United States is expected for several more weeks. Influenza vaccination remains the most effective way to prevent influenza illness. Antiviral medications are an important adjunct to vaccination in the treatment and prevention of influenza. Early treatment with neuraminidase inhibitor antiviral medications is recommended for patients with severe, complicated, or progressive influenza illness and those at higher risk for influenza complications, including adults aged ≥65 years.

¶¶¶ Persons at higher risk include 1) children aged <2 years; 2) adults aged ≥65 years; 3) persons with chronic pulmonary conditions (including asthma), cardiovascular disease (except hypertension alone), renal, hepatic, hematologic (including sickle cell) disease, metabolic disorders (including diabetes mellitus), or neurologic and neurodevelopmental conditions (including disorders of the brain, spinal cord, peripheral nerves, and muscles, such as cerebral palsy, epilepsy [seizure disorders], stroke, intellectual disability [mental retardation], moderate to severe developmental delay, muscular dystrophy, or spinal cord injury); 4) persons with immunosuppression, including that caused by medications or by human immunodeficiency virus infection; 5) women who are pregnant or postpartum (within 2 weeks after delivery); 6) persons aged ≤18 years who are receiving long-term aspirin therapy; 7) American Indians/Alaska Natives; 8) persons with extreme obesity (i.e., body mass index ≥40); and 9) residents of nursing homes and other chronic care facilities.

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Interim Estimates of 2016–17 Seasonal Influenza Vaccine Effectiveness — United States, February 2017

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In the United States, annual vaccination against seasonal influenza is recommended for all persons aged ≥6 months (*1*). Each influenza season since 2004–05, CDC has estimated the effectiveness of seasonal influenza vaccine to prevent influenza-associated, medically attended, acute respiratory illness (ARI). This report uses data, as of February 4, 2017, from 3,144 children and adults enrolled in the U.S. Influenza Vaccine Effectiveness Network (U.S. Flu VE Network) during November 28, 2016–February 4, 2017, to estimate an interim adjusted effectiveness of seasonal influenza vaccine for preventing laboratory-confirmed influenza virus infection associated with medically attended ARI. During this period, overall vaccine effectiveness (VE) (adjusted for study site, age group, sex, race/ethnicity, self-rated general health, and days from illness onset to enrollment) against influenza A and influenza B virus infection associated with medically attended ARI was 48% (95% confidence interval [CI] = 37%–57%). Most influenza infections were caused by A (H3N2) viruses. VE was estimated to be 43% (CI = 29%–54%) against illness caused by influenza A (H3N2) virus and 73% (CI = 54%–84%) against influenza B virus. These interim VE estimates indicate that influenza vaccination reduced the risk for outpatient medical visits by almost half. Because influenza activity remains elevated (*2*), CDC and the Advisory Committee on Immunization Practices recommend that annual influenza vaccination efforts continue as long as influenza viruses are circulating (*1*). Vaccination with 2016–17 influenza vaccines will reduce the number of infections with most currently circulating influenza viruses. Persons aged ≥6 months who have not yet been vaccinated this season should be vaccinated as soon as possible.

Methods used by the U.S. Flu VE Network have been published previously (*3*). At five study sites, patients aged ≥6 months seeking outpatient medical care for an ARI with cough, within 7 days of illness onset, were enrolled.* Study enrollment began after ≥1 laboratory-confirmed cases of influenza were identified through local surveillance for ≥2 consecutive weeks. Patients were eligible for enrollment if they 1) were aged ≥6 months on September 1, 2016, and thus eligible for vaccination; 2) reported an ARI with cough and onset ≤7 days earlier; and 3) had not been treated with influenza antiviral medication (e.g., oseltamivir) during this illness. After obtaining informed consent from patients or parents/guardians for their children, participants or their proxies were interviewed to collect demographic data, general and current health status, symptoms, and 2016–17 influenza vaccination status. Respiratory specimens were collected from each patient using nasal and oropharyngeal swabs, which were placed together in a single cryovial with viral transport medium. Only nasal swabs were collected for patients aged <2 years. Specimens were tested at U.S. Flu VE Network laboratories using CDC's real-time reverse transcription – polymerase chain reaction (rRT-PCR) protocol for detection and identification of influenza viruses. Participants (including children aged <9 years who require 2 vaccine doses during their first vaccination season) were considered vaccinated if they received ≥1 dose of any seasonal influenza vaccine ≥14 days before illness onset, according to medical records and registries (at Wisconsin site), medical records and self-report (at Texas and Washington sites), or self-report only (Michigan and Pennsylvania sites). VE was estimated as 100% x (1 - odds ratio).† Estimates were adjusted for study site, age group, sex, race/ethnicity, self-rated general health, and number of days from illness onset to enrollment using logistic regression. Interim VE estimates for the 2016–17 season were based on patients enrolled through February 4, 2017.

Among the 3,144 children and adults with ARI enrolled at the five study sites from November 28, 2016, through February 4, 2017, 744 (24%) tested positive for influenza virus by rRT-PCR; 656 (88%) of these viruses were influenza A, and 90 (12%) were influenza B viruses (Table 1). Among 606 subtyped influenza A viruses, 595 (98%) were A (H3N2) viruses. The proportion of patients with influenza differed by study site, sex, age group, race/ethnicity, and interval from illness onset to enrollment (Table 1). The proportion vaccinated ranged

* The U.S. Flu VE Network sites and the date enrollment began are as follows: Group Health Cooperative (Seattle, Washington) (November 28, 2016); Marshfield Clinic Research Foundation (Marshfield, Wisconsin) (January 3, 2017); University of Michigan School of Public Health (the School of Public Health partnered with the University of Michigan Health System, Ann Arbor, and the Henry Ford Health System, Detroit, Michigan) (January 3, 2017); University of Pittsburgh Schools of the Health Sciences (the Schools of the Health Sciences partnered with the University of Pittsburgh Medical Center, Pittsburgh, Pennsylvania) (December 5, 2016); and Baylor Scott and White Health, Texas A&M University Health Sciences Center College of Medicine (Temple, Texas) (December 13, 2016).

† 100% x (1 - odds ratio [ratio of odds of being vaccinated among outpatients with influenza-positive test results to the odds of being vaccinated among outpatients with influenza-negative test results]).

TABLE 1. Selected characteristics for enrolled patients with medically attended acute respiratory illness, by influenza test result and seasonal influenza vaccination status — U.S. Influenza Vaccine Effectiveness Network, United States, November 28, 2016–February 4, 2017

Characteristic	Influenza test result			Vaccination status		
	No. positive (%)	No. negative (%)	p-value†	No. enrolled	No. vaccinated*(%)	p-value†
Overall	**744 (24)**	**2,400 (76)**		**3,144**	**1,650 (52)**	
State of study site						
Michigan	92 (26)	267 (74)	<0.001	359	206 (57)	<0.001
Pennsylvania	176 (30)	416 (70)		592	271 (46)	
Texas	56 (8)	646 (92)		702	341 (49)	
Washington	374 (38)	613 (62)		987	598 (61)	
Wisconsin	46 (9)	458 (91)		504	234 (46)	
Sex						
Male	350 (26)	990 (74)	0.005	1,340	665 (50)	0.006
Female	394 (22)	1410 (78)		1,804	985 (55)	
Age group						
6 mos–8 yrs	97 (14)	614 (86)	<0.001	711	362 (51)	<0.001
9–17 yrs	122 (33)	247 (67)		369	128 (35)	
18–49 yrs	208 (21)	783 (79)		991	452 (46)	
50–64 yrs	189 (31)	425 (69)		614	337 (55)	
≥65 yrs	128 (28)	331 (72)		459	371 (81)	
Race/Ethnicity§						
White	532 (23)	1,744 (77)	<0.001	2,276	1,231 (54)	0.001
Black	81 (35)	153 (65)		234	99 (42)	
Other race	72 (24)	222 (76)		294	163 (55)	
Hispanic	47 (15)	274 (85)		321	150 (47)	
Self-rated health status						
Fair or poor	55 (22)	200 (78)	0.52	255	142 (56)	0.04
Good	179 (23)	599 (77)		778	436 (56)	
Very good	301 (25)	902 (75)		1,203	622 (52)	
Excellent	209 (23)	699 (77)		908	450 (50)	
Illness onset to enrollment (days)						
<3	284 (29)	693 (71)	<0.001	977	473 (48)	0.003
3–4	304 (25)	933 (75)		1,237	654 (53)	
5–7	156 (17)	774 (83)		930	523 (56)	
Influenza test result						
Negative	—	2,400	—	2,400	1,317 (55)	—
Influenza B positive¶	90	—		90	23 (26)	
B/Yamagata	83	—		83	20 (24)	
B/Victoria	4	—		4	1 (25)	
B lineage pending	3	—		3	2 (67)	
Influenza A positive¶	656	—		656	310 (47)	
A (H1N1)pdm09	11	—		11	3 (27)	
A (H3N2)	595	—		595	282 (47)	
A subtype pending	50	—		50	25 (50)	

* Defined as having received ≥1 dose of influenza vaccine ≥14 days before illness onset. A total of 89 participants who received the vaccine ≤13 days before illness onset were excluded from the study sample.

† The chi-square statistic was used to assess differences between the numbers of persons with influenza-negative and influenza-positive test results, in the distribution of enrolled patient and illness characteristics, and in differences between groups in the percentage vaccinated.

§ Enrollees were categorized into one of four mutually exclusive racial/ethnic populations: white, black, other race, and Hispanic. Persons identified as Hispanic might have been of any race. Persons identified as white, black, or other race were non-Hispanic. Race/ethnicity data were missing for 19 enrollees.

¶ Two patients had coinfection with influenza A and influenza B, making the sum 746, or two greater than the total number of influenza positives.

from 46% to 61% across sites and differed by sex, age group, and interval from illness onset to enrollment.

The proportion of ARI patients vaccinated with 2016–17 seasonal influenza vaccine was 45% among influenza patients compared with 55% among influenza-negative participants (Table 2). After adjusting for study site, age group, sex, race/ethnicity, self-rated general health, and number of days from illness onset to enrollment, VE against medically attended ARI because of influenza was 48% (CI = 37%–57%). VE for all ages was 43% (CI = 29%–54%) against medically attended ARI because of A (H3N2) virus infection and 73% (CI = 54%–84%) against influenza B virus infection. VE point estimates against H3N2-related illness varied by age group; statistically significant protection was found against H3N2-related illness among children aged 6 months through 8 years (VE = 53%; CI = 16%–74%) and adults aged 50–64 years (VE = 50%; CI = 23%–67%), whereas protection in other age groups did not reach statistical significance.

TABLE 2. Number and percentage receiving 2016–17 seasonal influenza vaccine among 3,144 outpatients with acute respiratory illness and cough, by influenza test result status, age group, and vaccine effectiveness against all influenza A and B and against virus types A (H3N2) and B — U.S. Influenza Vaccine Effectiveness Network, United States, November 28, 2016–February 4, 2017

	Influenza-positive		Influenza-negative		Vaccine effectiveness*	
Influenza type/Age group	Total	No. (%) vaccinated	Total	No. (%) vaccinated	Unadjusted % (95% CI)	Adjusted % (95% CI)
Influenza A and B						
Overall	**744**	**333 (45)**	**2,400**	**1,317 (55)**	**33 (21 to 44)†**	**48 (37 to 57)†**
Age group						
6 mos–8 yrs	97	32 (33)	614	330 (54)	58 (33 to 73)†	53 (22 to 72)†
9–17 yrs	122	36 (30)	247	92 (37)	29 (-12 to 56)	32 (-20 to 61)
18–49 yrs	208	89 (43)	783	363 (46)	13 (-18 to 36)	19 (-17 to 43)
50–64 yrs	189	76 (40)	425	261 (61)	58 (40 to 70)†	58 (38 to 72)†
≥65 yrs	128	100 (78)	331	271 (82)	21 (-31 to 52)	46 (4 to 70)†
Influenza A (H3N2)						
Overall	**595**	**282 (47)**	**2,400**	**1,317 (55)**	**26 (11 to 38)†**	**43 (29 to 54)†**
Age group						
6 mos–8 yrs	68	24 (35)	614	330 (54)	53 (21 to 72)†	53 (16 to 74)†
9–17 yrs	94	28 (30)	247	92 (37)	29 (-19 to 57)	23 (–43 to 59)
18–49 yrs	168	73 (43)	783	363 (46)	11 (-24 to 36)	13 (-30 to 41)
50–64 yrs	154	70 (45)	425	261 (61)	48 (24 to 64)†	50 (23 to 67)†
≥65 yrs	111	87 (78)	331	271 (82)	20 (-37 to 53)	44 (-3 to 69)
Influenza B						
Overall	**90**	**23 (26)**	**2,400**	**1,317 (55)**	**72 (54 to 83)†**	**73 (54 to 84)†**

Abbreviation: CI = confidence interval.
* Vaccine effectiveness was estimated as 100% x (1 - odds ratio [ratio of odds of being vaccinated among outpatients with influenza-positive test results to the odds of being vaccinated among outpatients with influenza-negative test results]); odds ratios were estimated using logistic regression.
† Statistically significant at the p<0.05 level.

As of February 10, 2017, a total of 13 influenza A (H3N2) viruses from U.S. Flu VE Network participants had been characterized by CDC; 11 (85%) belonged to genetic group 3C.2a or the related group 3C.2a1, and all of those characterized antigenically were similar to the reference virus representing the 2016–17 A (H3N2) vaccine component.

Discussion

Interim influenza vaccine effectiveness estimates for the 2016–17 season indicate that vaccination reduced the risk for influenza-associated medical visits by approximately half. Influenza activity is likely to continue for several more weeks in the United States, and vaccination efforts should continue as long as influenza viruses are circulating. Persons aged ≥6 months who have not yet received the 2016–17 influenza vaccine should be vaccinated as soon as possible.[§] As of February 3, 2017, approximately 145 million doses of influenza vaccine had been distributed in the United States for the 2016–17 season.

Interim VE estimates indicate improved protection during the 2016–17 influenza season against the predominant influenza A (H3N2) virus belonging to genetic group 3C.2a, which emerged in early 2014 and was predominant during the 2014–15 influenza season in the United States. During 2014–15, these influenza A (H3N2) 3C.2a viruses were antigenically different from the recommended A (H3N2) vaccine component, and this resulted in low (1%) vaccine effectiveness against illness caused by influenza A (H3N2) 3C.2a viruses (*4*). Low effectiveness of the 2014–15 vaccines likely contributed to high rates of influenza-associated hospitalizations that season, especially among adults aged ≥65 years. In contrast, rates of influenza-associated hospitalizations observed to date have been substantially lower during the 2016–17 season (*2*). Virologic surveillance indicates that the majority of influenza A (H3N2) viruses collected by U.S. laboratories during the 2016–17 season remain antigenically similar to the A/Hong Kong/4801/2014–like cell propagated reference virus belonging to genetic group 3C.2a, which is the recommended influenza A (H3N2) component of the 2016–17 Northern Hemisphere vaccine.

Since the 2009 influenza A (H1N1) pandemic, VE estimates for A (H3N2) viruses have been lower than VE estimates against A (H1N1) and influenza B viruses. Interim VE estimates against illness caused by influenza A (H3N2) viruses during the 2016–17 influenza season are similar to U.S. VE estimates against A (H3N2)-related illness during the 2011–12 and 2012–13 seasons (VE = 39%) (*5*,*6*). Also, a meta-analysis of VE studies using the test-negative design conducted from the 2007–08 through the 2014–15 influenza seasons reported a pooled VE estimate against A (H3N2)-related illness of 33% (CI = 26%–39%), compared with 61% (CI = 57%–65%)

[§] A local influenza vaccine provider can be found by accessing the Flu Vaccine Finder website at https://vaccinefinder.org/?address.

against influenza A (H1N1)pdm09 and 54% (CI = 46%–61%) against influenza B virus–related illness (*7*). These results reflect properties unique to A (H3N2) viruses that pose special challenges. Influenza A (H3N2) viruses undergo more frequent and extensive genetic changes than do influenza A (H1N1) and influenza B viruses, and require more frequent updates to the A (H3N2) vaccine virus components to maintain activity against evolving circulating strains. In addition, A (H3N2) viruses continue to undergo changes in their receptor-binding specificity, which might result in genetic changes during growth in eggs. Most influenza vaccines are manufactured using egg-based production processes. These genetic changes (referred to as egg-adapted changes) alter the antigenic properties of candidate vaccine viruses (CVVs) as they are grown in eggs and potentially during the vaccine production process (*8*). The egg-adapted changes might contribute to the lower vaccine effectiveness seen with A (H3N2) viruses compared with A (H1N1) and B viruses. Efforts are ongoing to improve influenza vaccine effectiveness against A (H3N2) viruses in CVV development and in manufacturing.

As of February 10, 2017, influenza activity remained elevated nationally and was widespread across most of the United States. During recent A (H3N2) virus predominant–seasons, persons aged ≥65 years and young children experienced higher rates of severe illness and influenza-associated hospitalization compared with other age groups. With vaccine effectiveness of 48%, some vaccinated persons will become infected with influenza. Clinicians should maintain a high index of suspicion for influenza infection among persons with acute respiratory illness while influenza activity is ongoing, especially among older adults. Early antiviral treatment can reduce severity and complications of influenza-associated illness (*9*). Early antiviral treatment is recommended for persons with suspected influenza with severe or progressive illness (e.g., hospitalized persons) and persons at high risk for complications from influenza, such as children aged <2 years, adults aged ≥65 years and persons with underlying health conditions,[¶] even if illness is less severe. Antiviral medications should be used as recommended for treatment in patients with suspected influenza, regardless of vaccination status. The decision to initiate antiviral treatment should not be delayed while waiting for laboratory confirmation of influenza and should not be dependent on insensitive assays, such as rapid influenza diagnostic tests.

The findings in this report are subject to at least four limitations. First, vaccination status included self-report at four of five sites. End-of-season VE estimates based on updated documentation of vaccination status might differ from interim estimates. Second, information from medical records and immunization registries is needed to evaluate VE by vaccine type and for fully vaccinated compared with partially vaccinated children (children aged <9 years require 2 vaccine doses during their first vaccination season), as well as to evaluate the effects of prior season vaccination and timing of vaccination; end-of-season analysis of VE by vaccine type and effects of partial or prior season vaccination is planned. Third, an observational study design has greater potential for confounding and bias relative to randomized clinical trials. However, the test-negative design is widely used in VE studies and has been used by the U.S. Flu VE Network to estimate VE for the past several influenza seasons. Finally, small sample sizes in some age groups resulted in wide confidence intervals, and end-of-season VE estimates could change as additional patient data become available or if there is a change in circulating viruses late in the season. It is also important to note that the VE estimates in this report are limited to the prevention of outpatient medical visits, rather than more severe illness outcomes, such as hospitalization or death; data from studies measuring VE against more severe outcomes will be available at a later date.

Annual vaccination against circulating influenza viruses remains the best strategy for preventing illness from influenza. As of early November 2016, only 37% of children aged 6 months–17 years, 37% of adults aged 18–64 years, and 57% of adults aged ≥65 years had received influenza vaccine this season (*10*). Among pregnant women, early estimates for 2016–17 indicated that only 47% had been vaccinated by early November 2016 (*10*). In addition to ongoing vaccination efforts, antiviral medications continue to be an important adjunct to the treatment and control of influenza and should be used as recommended, regardless of patient vaccination status.

[¶] A complete summary of guidance for antiviral use is available at https://www.cdc.gov/flu/professionals/antivirals/summary-clinicians.htm. Groups at high risk for influenza complications include the following: children aged <2 years; adults aged ≥65 years; persons with chronic pulmonary conditions (including asthma); cardiovascular disease (except hypertension alone); persons with renal, hepatic, or hematologic (including sickle cell) disease; persons with metabolic disorders (including diabetes mellitus); persons with neurologic and neurodevelopmental conditions (including disorders of the brain, spinal cord, peripheral nerves and muscles, such as cerebral palsy, epilepsy [seizure disorders], stroke, intellectual disability [mental retardation], moderate to severe developmental delay, muscular dystrophy, or spinal cord injury); persons with immunosuppression, including that caused by medications or by human immunodeficiency virus infection; women who are pregnant or postpartum (within 2 weeks after delivery); persons aged <19 years who are receiving long-term aspirin therapy; American Indian/Alaska Natives; persons with morbid obesity (i.e., body-mass index ≥40); and residents of nursing homes and other chronic-care facilities.

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Transmission of Zika Virus — Haiti, October 12, 2015–September 10, 2016

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Zika virus disease is caused by infection with a flavivirus with broad geographic distribution and is most frequently transmitted by the bite of an infected mosquito. The disease was first identified in the World Health Organization's Region of the Americas in 2015 and was followed by a surge in reported cases of congenital microcephaly in Brazil; Zika virus disease rapidly spread to the rest of the region and the Caribbean (*1*), including Haiti. Infection with the virus is associated with adverse fetal outcomes (*1*) and rare neurologic complications in adults. The magnitude of public health issues associated with Zika virus led the World Health Organization to declare the Zika virus outbreak a Public Health Emergency of International Concern on February 1, 2016 (*2*). Because many persons with mild Zika virus disease are asymptomatic and might not seek care, it is difficult to estimate the actual incidence of Zika virus infection. During October 12, 2015–September 10, 2016, the Haitian Ministry of Public Health and Population (Ministère de la Santé Publique et de la Population [MSPP]) detected 3,036 suspected cases of Zika virus infection in the general population, 22 suspected cases of Zika virus disease among pregnant women, 13 suspected cases of Guillain-Barré syndrome (GBS), and 29 suspected cases of Zika-associated congenital microcephaly. Nineteen (0.6%) patients with suspected Zika virus disease, residing in Ouest (10 patients), Artibonite (six), and Centre (three) administrative departments,* have been confirmed by laboratory testing, including two among pregnant women and 17 in the general population. Ongoing laboratory-enhanced surveillance to monitor Zika virus disease in Haiti is important to understanding the outbreak and ensuring effective response activities.

Haiti's MSPP first received reports of patients suspected to have Zika virus disease on October 13, 2015, from the Sud Department. MSPP's Directorate of Epidemiology, Laboratory, and Research (DELR) conducted active investigations and collected serum specimens from 19 patients with suspected Zika virus disease during October 2015–January 2016. The National Laboratory† sent these 19 specimens to the Caribbean Public Health Agency (*3*) for Zika virus testing. On January 15, 2016, MSPP reported that five specimens were positive for Zika virus RNA using the Trioplex reverse transcription–polymerase chain reaction (RT-PCR) assay (*3*).

Standard case definitions§ were developed by MSPP in September 2015, and a Zika surveillance module was developed in February 2016; these were disseminated to Haiti's departments and health facilities (*4*). DELR initiated sentinel Zika virus disease surveillance at 357 health facilities in the National Epidemiology Surveillance Network, using trained surveillance officers who reported the number of suspected cases each week, by age and sex. Pregnancy status of females with suspected Zika virus disease began to be reported in March. Immediate notification of suspected cases of microcephaly and GBS was followed by investigations and laboratory testing (*4*). Surveillance officers completed case investigation forms documenting signs and symptoms of Zika virus disease either when collecting laboratory specimens or after disease confirmation. On February 24, 2016, the National Laboratory introduced in-country multiplex dengue, chikungunya, and Zika testing with the Trioplex RT-PCR assay; all viable specimens collected from 1 to 5 days after symptom onset are tested via the Trioplex assay (*5*). Serologic and plaque reduction neutralization testing for Zika virus currently is not available in Haiti. After immediate notification of suspected cases of GBS or congenital microcephaly, blood specimens are collected. Infants and mothers of infants with congenital microcephaly are tested. For pregnant women with symptoms of Zika virus disease, serum and urine specimens collected within 5 days of symptom onset are tested by RT-PCR; specimens collected >5 days after symptom onset are stored for future Zika testing when additional testing technology is available. For symptomatic persons in the general population, only serum specimens are collected 1 to 5 days after symptom onset only if specimens can be delivered within 2 days to the National Laboratory (*5*) using the national Specimen Referral Network.

*Haiti is divided geographically into 10 administrative departments. Each department is further divided into 42 arrondissements.

†The National Public Health Laboratory runs Trioplex reverse transcription–polymerase chain reaction tests. All Zika testing reported from October 2015 to September 2016 was done using Trioplex RT-PCR testing.

§A suspected Zika virus disease case was defined as the occurrence of a temperature >37.2°C (99.0°F) or a rash with one of the following symptoms: headache/discomfort, nonpurulent conjunctivitis (hyperemia), joint pain (arthralgia), or myalgia in any person (excluding newborns). Congenital microcephaly was defined as a head circumference measuring less than the 3rd percentile for gestational age and sex at birth after 24 hours; any newborn with microcephaly is considered to be a suspected case of congenital microcephaly Zika and is investigated. Suspected cases of GBS are defined as symmetric, progressive flaccid paralysis with or without pain or paresthesia, or clinician-diagnosed Guillain-Barré syndrome in a person of any age. A confirmed Zika virus disease case is any suspected Zika case with a positive RT-PCR result or confirmation of Zika by plaque reduction neutralization testing.

Epidemiologic data and laboratory testing results for persons with suspected Zika virus disease and GBS in Haiti presented in this report were obtained from this surveillance system. MSPP personnel were interviewed to describe the Zika virus disease module and response.

Geographic Distribution

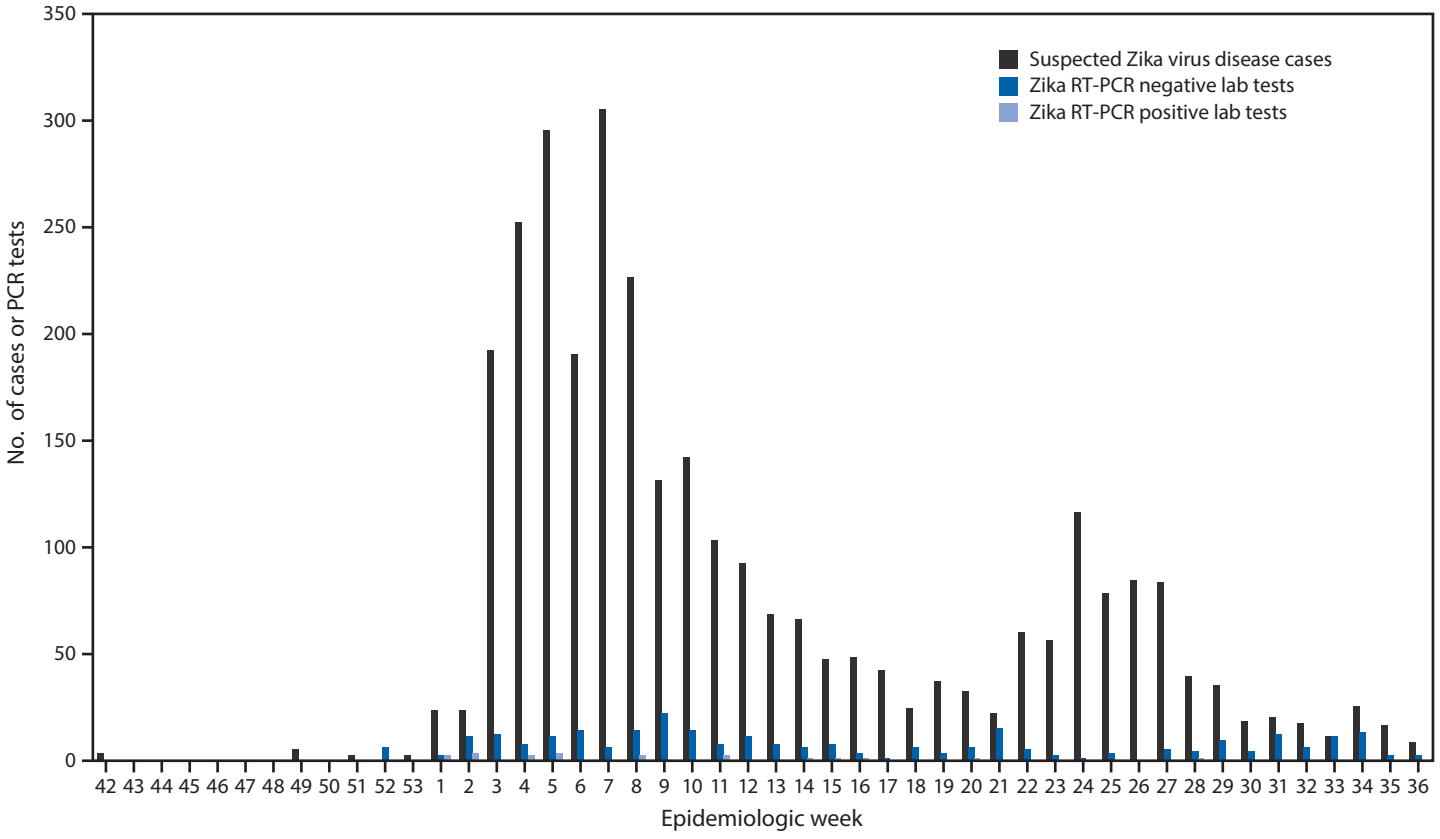
Among 3,036 suspected cases of Zika virus disease (including persons meeting the case definition for Zika virus disease, newborns or stillbirths (including one miscarriage) with suspected congenital microcephaly, and cases of GBS), the highest number originated from Ouest (n = 1,064), Nord (583), and Centre (421) departments. Two peaks occurred in 2016 between epidemiologic weeks 5–7 and weeks 21–27 (Figure). Communes[¶] with the highest suspected Zika virus disease cumulative incidence rates were Plaine du Nord (441 per 100,000 persons), Milot (234), and Fond des Négres (254).

[¶] Communes (n = 145) make up Haiti's third geographic administrative unit within arrondissements.

Laboratory Testing

Among 294 (9.7%) patients with suspected Zika virus disease, congenital microcephaly, or GBS who underwent testing, 19 cases (6.5%) were confirmed by RT-PCR from serum specimens (five at the Caribbean Public Health Agency and 14 at Haiti's National Laboratory). Two cerebrospinal fluid specimens and eight urine specimens from other patients tested negative. The median age of patients with confirmed infection was 34 years (range = 0–69 years; interquartile range [IQR] = 12 years) and 44.4% were male. Nine of the confirmed cases were investigated; among these, eight patients reported symptoms including nonpurulent conjunctivitis (seven cases); maculopapular rash (six); temperature >37.2°C (99.0°F) (four); arthritis (three); headache (three); general pain (three); and digestive pain (one). A male fetus (24 weeks' gestation) had spinal and limb malformations. Blood and urine specimens from the mother were negative, but the umbilical cord blood specimen was positive for Zika virus RNA by RT-PCR.

FIGURE. Reported cases of suspected Zika virus disease and RT-PCR testing results*,† by epidemiologic week — Haiti, October 12, 2015–September 10, 2016



Abbreviation: RT-PCR = reverse transcription polymerase–chain reaction.
* Some persons might have had more than one laboratory test.
† A person with a negative Zika RNA test via RT-PCR might have had recent Zika infection detectable by serology and plaque reduction neutralization testing, both of which are unavailable in Haiti.

Epidemiologic Investigations

DELR completed 148 case investigations; the highest percentage of investigations (90.9%) occurred among pregnant women (Table 1). The most common symptoms reported by patients with suspected Zika virus disease among the general population, pregnant women, and patients with suspected Zika-associated GBS were elevated temperature, headache, and arthralgia (Table 2). Approximately 93% of patients reported mosquitoes in their residences, and 56% reported mosquitoes at work or school. Nine (7.6%) patients reported traveling outside their administrative department in the 2 weeks before symptom onset, indicating potential Zika virus transmission in another department.

Congenital Microcephaly, Zika Virus Infection of Pregnant Women, and Guillain-Barré Syndrome

Twenty-nine suspected cases of Zika virus–associated congenital microcephaly (*6*) were detected at 16 health facilities; six infants (20.7%) were delivered in the community. Among the 29 infants with microcephaly, 16 (55%) were female, 26 (90%) were alive at birth, two (3%) were stillborn, and status was not recorded for one. The median number of days from birth until detection of microcephaly was 9 days (range = 0–56 days; IQR = 17 days). Eight live born infants had head circumference measurements at birth, and nine had head circumference measurements 24 hours after birth. Serum specimens were collected for 19 (73%) living infants; all tested negative by RT-PCR. Among 29 infants with microcephaly, 26 (90%) mothers were available for interview. In total, 19 (73%) interviewed mothers reported Zika virus disease symptoms during pregnancy; 14 (54%) reported elevated temperatures, and four (15%) each reported myalgia, rash, and nonpurulent conjunctivitis. The median age of the 26 mothers at delivery was 31 years (range = 16–43 years; IQR = 10 years). The median gestational age at delivery among 13 women for whom this information was available was 37 weeks (range = 18–42 weeks; IQR = 9 weeks).

Among the 22 suspected cases of Zika virus disease identified among women during their pregnancy, field investigations were completed for 20, and 18 women consented to testing. The median age of these women was 32 years (range = 18–39 years; IQR = 6.5 years). On February 24, 2016, two of the 18 women were confirmed to be infected with Zika virus by RT-PCR; they reported rashes, nonpurulent conjunctivitis, and mosquitoes present at home and work.

Thirteen suspected cases of Zika-associated GBS were detected, and 11 patients were hospitalized. The median age was 31 years (range = 2–61 years; IQR = 30 years). Zika-related symptoms included elevated temperature (nine patients) and headache (five). Seven of the 13 GBS cases occurred in females. Among 11 serum specimens submitted to the National Laboratory for testing, two were rejected as inadequate on arrival at the lab; the remaining nine tested negative by RT-PCR. Specimens from these patients might have tested positive for Zika virus by serology and plaque reduction neutralization test, both testing methods that are unavailable in Haiti.

TABLE 1. Suspected, investigated, and laboratory-confirmed cases of Zika virus disease — Haiti, October 12, 2015–September 10, 2016

Classification	No. of suspected cases	No. investigated (%)	No. RT-PCR–confirmed (%)
Adults/Children	2,972	86 (2.9)	17 (0.6)
Pregnant women	22	20 (90.9)	2 (9.1)
Guillian-Barré syndrome	13	13 (100)	0 (0)
Congenital microcephaly	29	29 (100)	0 (0)
Total	**3,036**	**148 (4.8)**	**19 (0.6)**

Abbreviation: RT-PCR = reverse transcription–polymerase chain reaction.

Public Health Response

MSPP implemented a response plan that included epidemiologic monitoring of Zika virus disease and complications, laboratory testing, vector control, social mobilization, and clinical care. MSPP released statements about modes of transmission, testing, strategies to prevent mosquito bites, and potential Zika virus disease complications through their website, fliers, and radio announcements (*7*). Prevention messages included recommending the use of bed nets and DEET repellents, wearing clothing with long sleeves and pants, covering water containers, and maintaining a clean environment (*3*).

The National Malaria Control Program intensified its long-term vector control response targeting mosquitoes responsible for infections of dengue, chikungunya, and Zika viruses and lymphatic filariasis and malaria. Trained personnel applied larvicide to treat 14,280 larval development sites (*8*) and sprayed insecticide via fumigation trucks in 2,833 areas. Door-to-door household inspections were conducted, and 4,404 households were treated (*8*).

DELR rapidly launched a Zika virus disease module, and weekly analysis of microcephaly and GBS cases was instituted several months later. The Pan-American Health Organization and Global Fund financed Zika virus trainings for 60 trainers in August and 126 surveillance officers in September.

Discussion

The MSPP's response to the outbreak has been timely, and the rapid implementation of a Zika virus disease module is reflective of the surveillance system's flexibility; however, Haiti's total suspected cases and testing are lower than expected given the population size and transmission dynamics predicted by a modeled estimate of 2.9 million Haitians infected with Zika

TABLE 2. Reported signs and symptoms* among investigated cases of suspected Zika virus disease (n = 147) — Haiti, October 12, 2015–September 10, 2016

Symptom/Reported co-infection	Total cases (n = 118) No. (%)	RT-PCR–confirmed (n = 8) No. (%)	Adults and children with symptoms of Zika virus disease (n = 85) No. (%)	Pregnant women (n = 20) No. (%)	GBS cases (n = 13) No. (%)
Temperature >37.2°C (99.0°F)	**89 (75.4)**	4 (50.0)	70 (82.4)	10 (50.0)	9 (69.2)
Headache	**80 (67.8)**	3 (37.5)	64 (75.3)	11 (55.0)	5 (38.5)
Nonpurulent conjunctivitis	**59 (50.0)**	7 (87.5)	49 (57.6)	8 (40.0)	2 (15.4)
Myalgia	**58 (49.2)**	3 (37.5)	51 (60.0)	5 (25.0)	2 (15.4)
Rash	**51 (43.2)**	6 (75.0)	41 (48.2)	9 (45.0)	1 (7.7)
Arthralgia	**64 (54.2)**	3 (37.5)	56 (65.9)	8 (40.0)	3 (23.1)
Digestive symptoms	**28 (23.7)**	1 (12.5)	21 (24.7)	5 (25.0)	2 (15.4)
Other†	**26 (22.0)**	2 (25.0)	16 (18.8)	7 (35.0)	0 (0)

Abbreviations: GBS = Guillain-Barré syndrome; RT-PCR = reverse transcription–polymerase chain reaction.
* Excludes the 29 cases of congenital microcephaly and one fetus in the adults and children category.
† Tingling (six patients); sore throat (four); itching (three) fatigue (four); edema (two); abdominal pain (two); hypertension (one); chikungunya infection (one); lymphadenopathy (one); and paraplegia (one).

virus disease (*9*). A strike of health care professionals during March–August 2016 at public health facilities limited the ability to detect and respond to the Zika outbreak. Surveillance for Zika virus disease, congenital microcephaly, and GBS requires clinicians to assess patients systematically for Zika and to recommend testing. In-service national clinical trainings have not been implemented; additional financial resources are needed to increase Zika virus disease testing above 1%, prepare the clinical workforce, and secure Zika serology and PRNT testing.

The findings in this report are subject to at least one limitation. Analysis was limited to Zika confirmation by RT-PCR testing on specimens from persons living at sites from which specimens could be delivered to the National Lab within 2 days. Patients tested after 5 days of the onset of symptoms might have tested negative via RT-PCR, but could have tested positive for Zika through serology and plaque reduction neutralization test. In addition, persons living in Haiti's rural areas are less likely to be tested for Zika. Therefore, the number of cases of Zika virus disease might be underreported.

As awareness, training, and testing capacity increase, providers should continue to report and test for Zika, chikungunya, and dengue as appropriate, using the existing specimen transport network to increase the number of specimens tested. As novel tests are developed, Haiti's testing capacity expands, and algorithms change, Haiti will need to adjust its response accordingly. The MSPP is committed to Zika virus disease prevention, systematic detection, and response; however, resources for training and reagents are needed, and coordination of activities will need to be maintained.

Summary

What is already known about this topic?

Zika virus was first reported in the Region of the Americas in mid-2015 in multiple South American and Caribbean countries and territories. Haiti reported its first confirmed case of Zika virus disease in January 2016.

What is added by this report?

Haiti's Ministry of Public Health and Population has established sentinel Zika surveillance and laboratory testing, and has implemented a public health response to Zika. From October 12, 2015, until mid-September 2016, a total of 3,036 cases of suspected Zika virus infection were identified, including 22 suspected cases in pregnant women, 13 suspected cases of Zika virus–associated Guillain-Barré syndrome, and 29 suspected cases of Zika-associated congenital microcephaly. The National Laboratory tested 294 specimens from suspected Zika virus disease patients; 19 (6.5%) were positive by reverse transcription–polymerase chain reaction testing.

What are the implications for public health practice?

Improving reporting of cases of suspected Zika virus disease to public health authorities by health care workers in Haiti and by providers evaluating patients with recent travel to Haiti is important to ongoing surveillance initiatives. Trained epidemiologists and health care workers are important in ensuring reporting. Although laboratory-confirmed Zika virus disease cases were detected in only three of Haiti's 10 departments (geographic administrative units), testing should continue throughout the country according to Haiti's guidelines. Integrated mosquito control strategies can mitigate disease spread in Haiti. Residents of and visitors to Haiti should follow recommended precautions to protect against Zika virus infection.

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Notes from the Field

Ongoing Cholera Epidemic — Tanzania, 2015–2016

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On August 15, 2015, the Tanzanian Ministry of Health, Community Development, Gender, Elderly and Children (MOHCDGEC) was notified about a case of acute watery diarrhea with severe dehydration in a patient in Dar es Salaam. *Vibrio cholerae* O1, biotype El tor, serotype Ogawa, was isolated from the patient's stool and an investigation was initiated. MOHCDGEC defined a suspected cholera case as the occurrence of severe dehydration or death from acute watery diarrhea in a person aged ≥5 years, or acute, profuse watery diarrhea with or without vomiting in a person aged ≥2 years in a region with an active cholera outbreak. A confirmed cholera case was defined as isolation of *V. cholerae* O1 from the stool of a person with suspected cholera. Tanzania's first reported cholera epidemic was in 1974 with intermittent outbreaks since then; the largest epidemic occurred in 1997, with 40,249 cases and 2,231 deaths (case fatality rate [CFR] was 5.5%) (*1*).

As of November 26, 2016, the current epidemic continues, affecting 23 (92%) of 25 regions in mainland Tanzania (excluding the Zanzibar archipelago), with a cumulative reported case count of 23,258 and a cumulative CFR of 1.5%. The median number of reported cholera cases per week was 271 (range = 5–1,240) (Figure). Approximately half of all reported cases have been from four regions: Dar es Salaam (5,104; 22%), Morogoro (3,177; 14%), Mwanza (2,311; 10%), and Mara (2,299; 10%). Of 511 stool specimens tested during August 17, 2015–March 18, 2016 at the National Health Laboratory-Quality Assurance Training Center in Dar es Salaam, 268 (52%) were positive for *V. cholerae;* all specimens were serogroup O1, biotype El tor, serotype Ogawa. Antimicrobial resistance (AMR) testing revealed sensitivity to cotrimoxazole, ceftriaxone, tetracycline, ciprofloxacin, and chloramphenicol, and resistance to nalidixic acid and ampicillin.

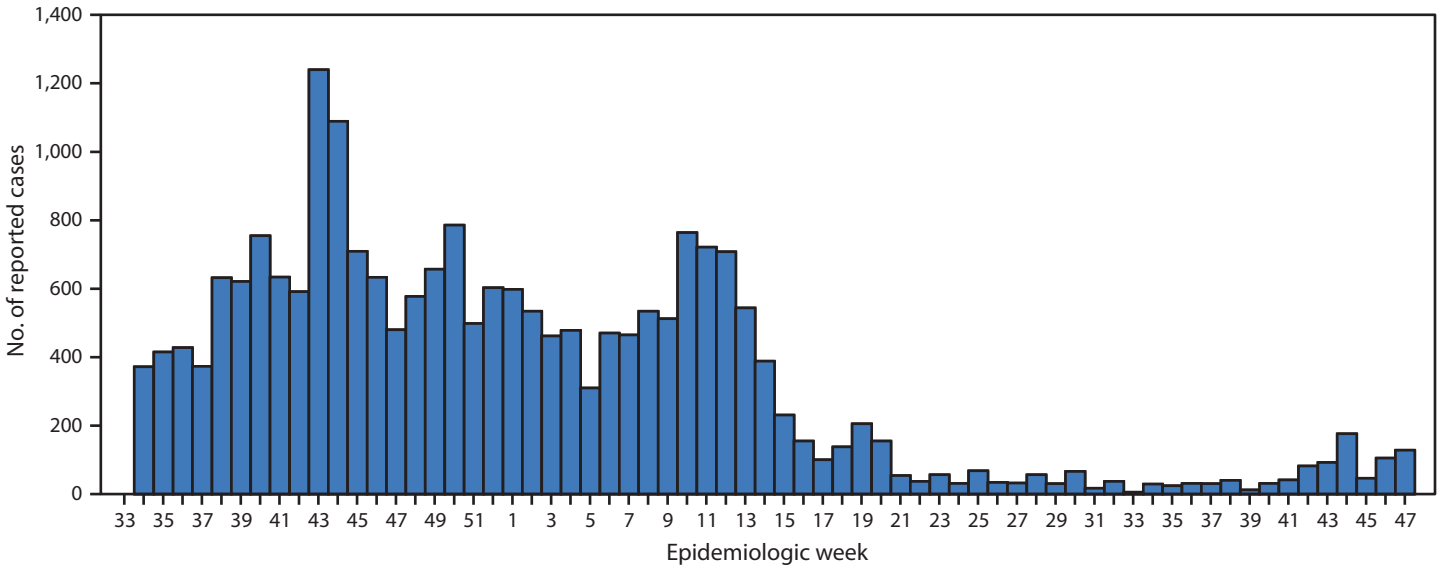
The Tanzania Field Epidemiology and Laboratory Training Program and CDC in the United States and Tanzania evaluated cholera mortality reporting in Dar es Salaam; 81 deaths were identified during August 15–October 28, 2015. Cholera treatment center (CTC) records revealed that 21 (26%) patients died in CTCs. Municipal burial permits recorded 60 (74%) cholera deaths in the community. These results motivated follow-up interviews with decedents' family members to identify characteristics associated with an increased risk for death from cholera in January 2016.

By October 2015, MOHCDGEC collaborated with partner organizations, including Médecins Sans Frontières, Tanzania Red Cross National Society, United Nations Children's Emergency Fund, World Health Organization, and CDC, to enhance cholera response activities. To strengthen cholera surveillance, MOHCDGEC disseminated standardized cholera case definitions, developed reporting tools and communication strategies, produced daily situation reports, and distributed weekly summary reports to national and regional levels. Trainings on isolation, identification, and AMR testing of *V. cholerae* were conducted for regional and district laboratory staff members. MOHCDGEC used AMR test results to develop cholera treatment guidelines that emphasized appropriate antibiotic use in moderate to severe cases, and developed standard operating procedures for appropriate use of rapid diagnostic test kits for *V. cholerae* in regions at risk for cholera importation. A train-the-trainer approach was used to increase the pool of available responders to send to highly affected regions to strengthen cholera case management and infection prevention and control in health care facilities and CTCs. Partner organizations are mapping private water vendors in Dar es Salaam to facilitate chlorination of water tanks, encouraging municipal water authorities in Dar es Salaam and other cities to increase chlorine levels in piped water supplies, and targeting communities at high risk for distribution of household water treatment tablets (*2*). Cholera prevention and treatment materials have been developed and disseminated through mass media, health care facilities, CTCs, and door-to-door.

Tanzania continues to face challenges with epidemic control. Cholera outbreaks have been reported in most countries neighboring Tanzania, including Kenya, Uganda, the Democratic Republic of the Congo, Burundi, Malawi, Mozambique, and Zambia (*3*,*4*). In addition, the El Niño phenomenon, which has exacerbated cholera transmission in the past in the Great Lakes region of Africa (*5*), caused heavy rains throughout East Africa. To help address the challenges of this epidemic,

*These authors contributed equally to this report.

FIGURE. Number of reported cholera cases* — Tanzania,† August 15, 2015–November 26, 2016



* Suspected cholera (severe dehydration or death from acute watery diarrhea in a person aged ≥5 years, or acute, profuse watery diarrhea with or without vomiting in a person aged ≥2 years in a region with an active cholera outbreak) and confirmed cases (isolation of *V. cholerae* O1 from the stool of a person with suspected cholera).
† Excluding the Zanzibar archipelago.

MOHCDGEC established a national Emergency Operations Center in November 2015 and developed a National Cholera Response Plan in February 2016. The Emergency Operations Center is currently coordinating the deployment of multidisciplinary rapid response teams to support affected regions and districts. These activities have improved the ability of Tanzania to respond to this epidemic and serve as a model for responding to future public health emergencies.

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Tanzania regional and district health teams; National Health Laboratory-Quality Assurance Training Center, Dar es Salaam, Tanzania; Médecins Sans Frontières; Population Services International Tanzania; Tanzania Red Cross Society; United Nations Children's Emergency Fund; World Health Organization; United States Embassy, Dar es Salaam, Tanzania; CDC, Dar es Salaam, Tanzania; Enteric Diseases Laboratory Branch, Division of Foodborne, Waterborne, and Environmental Diseases, National Center for Emerging and Zoonotic Infectious Diseases, CDC; Global Disease Detection Operations Center, Division of Global Disease Detection and Emergency Response, Center for Global Health, CDC; Global Rapid Response Team, Emergency Response and Recovery Branch, Center for Global Health, CDC.

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Announcement

American Heart Month — February 2017

Each February, the observance of American Heart Month helps raise awareness of ways to stay heart healthy and prevent heart disease. For 30 years, the number of deaths from heart disease, the number one killer of persons in the United States, declined. However, that progress has stalled in recent years, potentially because of high rates of obesity and hypertension, important risk factors for heart disease (*1*). With increased awareness and education, everyone can work together to prevent the conditions that lead to heart disease.

Heart disease is responsible for one in every four deaths (>630,000) in the United States each year. Approximately 790,000 men and women have a heart attack each year (*2*,*3*). Conditions such as obesity and physical inactivity, and behaviors such as consuming an unhealthy diet or using tobacco, are major contributors to heart disease and heart attacks (*1*). Approximately two thirds of adults are overweight or have obesity (*4*). Obesity can lead to high blood pressure, blood glucose problems (including diabetes), and trouble sleeping, all of which strain the heart (*5*). In addition, just one in five adults meets the current federal recommendations for 150 minutes of moderate activity each week and muscle strengthening two times per week (*6*).

In observance of American Heart Month 2017, CDC is encouraging everyone to have a heart-to-heart with their loved ones and plan to make small changes to their diet and behavior to prevent heart disease. Many of the conditions that contribute to heart disease have a genetic component, so learning a family's health history is an important step toward recognizing a person's risk for developing heart disease. Quitting smoking, avoiding secondhand smoke, eating foods low in sodium and trans fats, and getting appropriate amounts of physical activity are ways families can incorporate heart-healthy behaviors into their lives.

CDC has additional resources to help families improve their heart health at http://millionhearts.hhs.gov/news-media/events/heart-month.html.

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Errata

Vol. 66, No. 1

In the report "Guidance for Assessment of Poliovirus Vaccination Status and Vaccination of Children Who Have Received Poliovirus Vaccine Outside the United States," on page 24, under the section "**Children with documentation of poliovirus vaccination.**" the first paragraph should have read as follows:

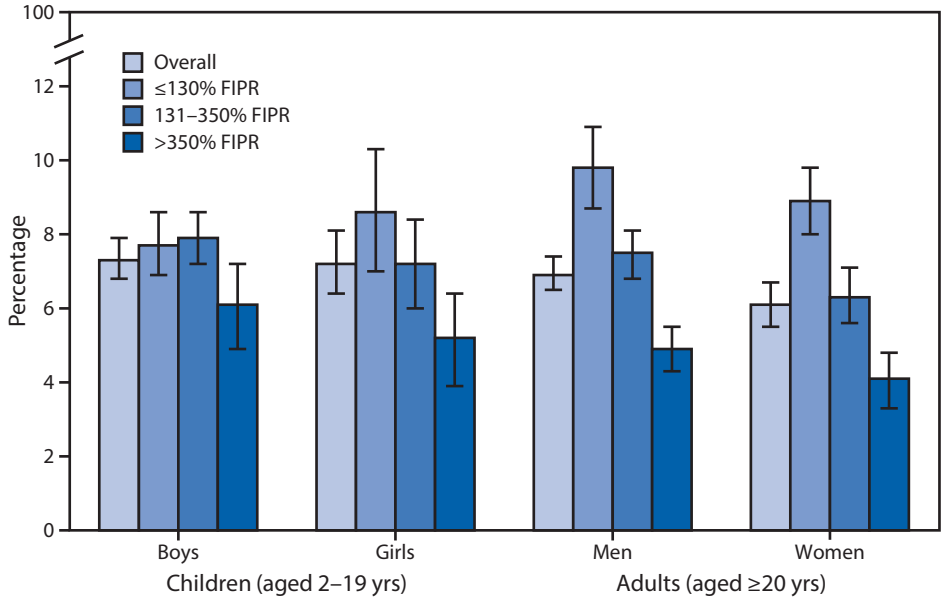
Previous poliovirus vaccination is valid if documentation indicates receipt of IPV or tOPV. tOPV was used for routine poliovirus vaccination before April 1, 2016 in all OPV-using countries. Therefore, if a child has documentation of receipt of an OPV dose (rather than "tOPV") before April 1, 2016, this represents a tOPV dose and should be counted towards the U.S. vaccination schedule, unless specifically notated that it was administered during a vaccination campaign.* Consistent with the polio eradication strategy, doses of OPV administered on or after April 1, 2016 are either bOPV (used in routine vaccination and campaigns), or mOPV (used in a type-specific outbreak response); these doses do not count towards the U.S. vaccination requirements for protection against all three poliovirus types. Persons aged <18 years with doses of OPV that do not count towards the U.S. vaccination requirements should receive IPV to complete the schedule according to the U.S. IPV schedule.

* mOPV or bOPV were often used in vaccination campaigns but doses administered during vaccination campaigns are not typically recorded in parent-held records. These doses do not count towards the U.S. vaccination requirements.

QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Percentage* of Total Daily Kilocalories† Consumed from Sugar-Sweetened Beverages§ Among Children and Adults, by Sex and Income Level¶ — National Health and Nutrition Examination Survey, United States, 2011–2014



Abbreviations: FIPR = family income to poverty ratio; SSBs = sugar-sweetened beverages.
* With 95% confidence intervals indicated with error bars.
† Kilocalories are a measure representing dietary energy or calorie intake. Percentage of daily kilocalories from SSBs is calculated as a percent of total daily calories based on Day 1, 24-hour dietary intake data.
§ SSBs include regular soda, fruit drinks (including sweetened bottled waters and fruit juices and nectars with added sugars), sports and energy drinks, sweetened coffees and teas, and other SSBs. SSBs do not include diet drinks; 100% fruit juice; beverages sweetened by the participant, including coffee and teas; alcohol; or flavored milks.
¶ FIPR is an index based on the ratio of family income to the U.S. Department of Health and Human Services' poverty guidelines.

During 2011–2014, on average, 7.3% of boys' and 7.2% of girls' total daily calories were obtained from SSBs compared with 6.9% for men and 6.1% for women. For men, women, and girls, the percentage of total daily kilocalories from SSBs declined as income level increased. For boys, the percentage of total daily kilocalories was lower for those in the highest income group than in the other income groups. Compared with women, a larger proportion of men's total daily kilocalorie intake came from SSBs.

Source: Rosinger A, Herrick K, Gahche J, Park S. Sugar-sweetened beverage consumption among US adults, 2011–2014. NCHS Data Brief no. 270; 2017. https://www.cdc.gov/nchs/products/databriefs/db270.htm.
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