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Walking for Transportation or Leisure Among U.S. Women and Men — National Health Interview Survey, 2005–2015

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Physical activity confers considerable health benefits, but only half of U.S. adults report participating in levels of aerobic physical activity consistent with guidelines (*1*,*2*). *Step It Up! The Surgeon General's Call to Action to Promote Walking and Walkable Communities* identified walking as an important public health strategy to increase physical activity levels (*3*). A previous report showed that the self-reported prevalence of walking for transportation or leisure increased by 6 percentage points from 2005 to 2010 (*4*), but it is unknown whether this increase has been sustained. CDC analyzed National Health Interview Survey (NHIS) data from 2005 (26,551 respondents), 2010 (23,313), and 2015 (28,877) to evaluate trends in the age-adjusted prevalence of self-reported walking among adults aged ≥18 years. The prevalence of walking increased steadily among women, from 57.3% in 2005, to 62.5% in 2010, and to 65.1% in 2015 (significant linear trend). Among men, a significant linear increase in reported walking was observed, from 54.3% in 2005, to 61.8% in 2010, and to 62.8% in 2015, although the increase stalled between 2010 and 2015 (significant linear and quadratic trends). Community design policies and practices that encourage pedestrian activity and programs tailored to the needs of specific population subgroups remain important strategies for promoting walking (*3*).

NHIS is a continuous in-person survey of U.S. households designed to be representative of the civilian, noninstitutionalized population (*5*). NHIS consists of a core questionnaire that collects basic health and demographic information for all family members in a sampled household and supplements that collect information about specialized topics. Questions specific to walking for leisure and transportation were asked of one adult aged ≥18 years per sampled household in the 2005, 2010, and 2015 Cancer Control Supplements. Sample adult response rates were 69.0% (2005), 60.8% (2010), and 55.2% (2015) (*6*).

Walking was defined as engaging in at least one 10-minute period of transportation or leisure walking in the past 7 days at the time of survey. To assess transportation walking, respondents in all 3 years were asked, "During the past 7 days, did you walk to get someplace that took you at least 10 minutes?" To assess leisure-time walking, respondents in 2005 were asked, "During the past 7 days, did you walk for at least 10 minutes at a time [for fun, relaxation, exercise, or to walk the dog]?" and in 2010 and 2015, "During the past 7 days, did you walk for at least 10 minutes [for fun, relaxation, exercise, or to walk the dog]?"

Demographic characteristics (sex, age, race/ethnicity, and education level) and health-related characteristics (height, weight, walking assistance status, and physical activity) were also assessed. Meeting the aerobic physical activity guideline of at least 150 minutes of moderate-intensity equivalent aerobic activity per week was assessed using responses on the usual

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frequency and duration of light- to moderate-intensity and vigorous-intensity leisure-time physical activity (*1*).

From the initial total sample of 92,257 (31,428 [2005]; 27,157 [2010]; and 33,672 [2015]), 13,516 (15%) persons were excluded, including 2,280 who were unable to walk and 11,236 for whom data were missing for walking (6,044), physical activity (1,054), health-related characteristics (3,708), or demographic characteristics (430). Thus, the final analytic sample consisted of 78,741 respondents (26,551 [2005]; 23,313 [2010]; and 28,877 [2015]).

The proportion (with 95% confidence intervals) of adults who reported walking each year was calculated. Linear and quadratic trends in walking prevalence from 2005 to 2015 were tested using logistic regression, controlling for age group. For three time points, a temporal change that includes significant linear and quadratic trend terms indicates an overall increase or decrease over time as well as a deviation from linearity. For example, if the linear trend is positive and quadratic trend is negative, this indicates an increase from 2005 to 2015 with a stalling or leveling off between 2010 and 2015. Because significant interactions between sex and trend terms were observed, sex-specific results are presented. Subgroup analyses were conducted by age group, race/ethnicity, education level, U.S. Census region, body mass index category, walking assistance status, and meeting the aerobic physical activity guideline, and pairwise differences between subgroups and across years were tested using adjusted Wald tests. Statistically significant ($p<0.05$) results are reported. All analyses accounted for the complex survey design. Reported estimates are weighted and age-standardized to the 2000 U.S. standard population (*7*).

In 2015, women were significantly more likely to report walking (65.1%) than were men (62.8%) (Figure). Among women in 2015, the lowest reported prevalence of walking was among those aged ≥65 years, non-Hispanic blacks (blacks), and residents of the South, compared with their respective counterparts (Table 1). Among men in 2015, the lowest prevalence of walking was among blacks and Hispanics and the highest prevalence was among men in the West, compared with their respective counterparts (Table 2). Among males, there were no significant age group differences in walking prevalence. The prevalence of walking was lower among men and women with a high school education or less, who had obesity, who needed walking assistance, or who did not meet aerobic physical activity guidelines than among their respective counterparts.

Among women, the prevalence of walking demonstrated a significant linear increase from 2005 to 2015, with no significant quadratic trend (Figure) (Table 1). This trend remained when stratified by selected characteristics, with two exceptions: both linear and quadratic trends were significant among women who were overweight or lived in the Midwest. The increase in walking prevalence among women between 2010 and 2015 was significant overall (2.7 percentage points) and among select strata (age 45–64 years, age ≥65 years, non-Hispanic whites, college graduates, residents of the Northeast and South regions, those who were underweight or normal weight, those with obesity, and those not needing walking assistance).

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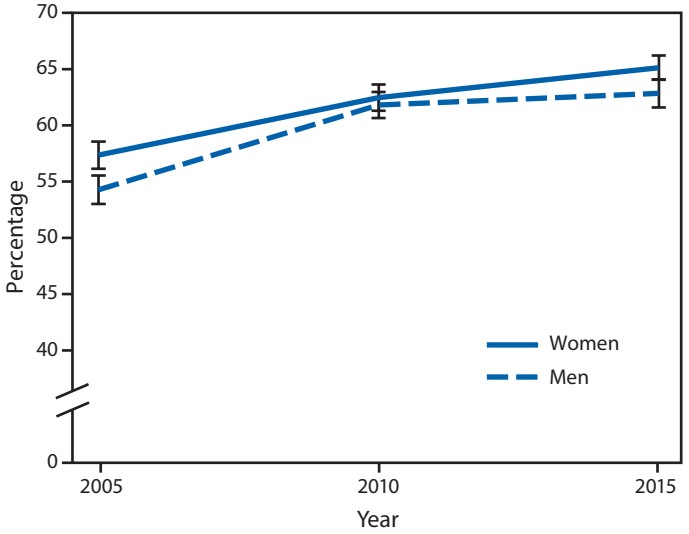
FIGURE. Percentage* of U.S. women† and men§ aged ≥18 years who reported recent walking for transportation or leisure — National Health Interview Survey, 2005–2015



* Weighted percentages, age-standardized to the 2000 U.S. standard population. Error bars represent upper and lower bounds of 95% confidence intervals.
† Significant linear trend from 2005 to 2015 only ($p<0.05$), based on trend analyses using logistic regression controlling for age category.
§ Significant linear trend from 2005 to 2015 ($p<0.05$) and a significant deviation from linear trend ($p<0.05$), based on trend analyses using logistic regression controlling for age category.

Among men, a significant positive linear and negative quadratic trend in reported walking from 2005 to 2015 was observed overall and for most subgroups, with the increase stalling from 2010 to 2015 (Figure) (Table 2). The change in walking prevalence among men from 2010 to 2015 was not significant overall or when estimates were stratified by selected characteristics, with one exception: among men aged ≥65 years, the prevalence of walking increased by 3.8 percentage points from 2010 to 2015.

Discussion

The prevalence of reported walking for transportation or leisure among men and women increased between 2005 and 2015; however, for men, the increase stalled between 2010 and 2015. This trend among males is similar to trends for leisure time physical activity, with the reported prevalence of meeting physical activity guidelines increasing steadily from 2008 to 2012 and stalling between 2012 and 2015 (*2*).* However, even given this increase, nearly one third of women and men report that they did not walk for at least 10 minutes in the past week.

Walking is an easy way for most adults to incorporate more physical activity into their daily routines. Women are less likely than men to achieve physical activity levels sufficient to meet guidelines (*2*). However, this study found that walking has become increasingly common among women since 2005, representing a potential opportunity for addressing the gender difference in overall physical activity. Efforts to sustain the observed increase in the percentage of adults who walk could contribute to more adults meeting guidelines, potentially reducing the burden of chronic diseases and premature death associated with low levels of physical activity. For example, communities can create additional opportunities for walking by implementing walking programs tailored to the interests and abilities of specific subgroups of the population (*3*). In addition, policies and practices that improve the safety of communities and promote walkable design can help make walking a convenient option for almost all persons.

For both women and men, walking was least prevalent among blacks and persons with lower educational attainment, groups that have been shown to report lower levels of physical activity compared to their counterparts (*8*). In some cases, differences in walking appear to be widening over time. For example, among men, walking increased at a steady rate among college graduates from 2005 to 2015 (significant linear

Summary

What is already known about this topic?

Only half of U.S. adults report achieving physical activity levels consistent with published guidelines. Walking is an easy way for most persons to be more physically active. Self-reported walking among adults increased by 6 percentage points from 2005 to 2010, but it is unknown whether this increase has continued.

What is added by this report?

The prevalence of self-reported walking among women significantly increased from 2005 to 2015 (2005: 57.4%; 2010: 62.5%; 2015: 65.1%); among men, the prevalence increased overall but stalled between 2010 and 2015 (2005: 54.3%; 2010: 61.8%; 2015: 62.8%). Sociodemographic disparities in walking prevalence exist, with the lowest prevalences among non-Hispanic blacks and persons with a high school education or less. Moreover, differences by education level appear to have widened over time among men, with walking prevalence increasing steadily among college graduates but leveling off among men with lower education levels.

What are the implications for public health practice?

To promote walking, streets and communities can be designed so that walking is a safe and convenient option for all persons. Communities can also implement walking programs that are tailored to the interests and abilities of specific population subgroups. Focused approaches to overcome barriers to walking in low socioeconomic status and minority communities, such as policies and practices that improve the safety and quality of community supports for physical activity (e.g. trails and sidewalks), might help reduce the observed disparities in walking.

* https://www.cdc.gov/physicalactivity/downloads/trends-in-the-prevalence-of-physical-activity.pdf.

TABLE 1. Proportion of U.S. women aged ≥18 years who reported recent walking for transportation or leisure, by selected demographic and health characteristics — National Health Interview Survey, 2005–2015

Characteristic	%* (95% CI) 2005 (n = 14,609)	2010 (n = 12,734)	2015 (n = 15,562)	Absolute change from 2010 to 2015
Total	**57.4 (56.1–58.6)**	**62.5 (61.3–63.6)**	**65.1 (64.0–66.2)†**	**2.7§**
Age group (yrs)				
18–24	61.4 (58.0–64.7)	65.4 (62.1–68.6)	66.2 (62.5–69.8)	0.8
25–34	59.7 (57.3–62.1)	66.6 (64.1–69.0)	69.0 (66.7–71.2)†	2.4
35–44	62.1 (59.9–64.3)	66.2 (63.8–68.5)	68.4 (65.9–71.0)†	2.2
45–64	56.7 (54.9–58.6)	62.8 (61.0–64.6)	65.7 (63.8–67.5)†	2.9§
≥65	46.8 (44.6–49.0)	50.6 (48.1–53.0)	55.0 (52.8–57.2)†	4.4§
Race/Ethnicity				
White, non-Hispanic	59.5 (58.0–60.9)	64.0 (62.6–65.5)	66.6 (65.2–68.1)†	2.6§
Black, non-Hispanic	47.5 (45.0–50.1)	53.8 (51.2–56.5)	55.5 (52.4–58.5)†	1.7
Hispanic	54.0 (51.0–57.0)	60.6 (58.2–63.0)	63.9 (61.5–66.3)†	3.3
Other race¶	59.2 (55.2–63.3)	66.9 (63.8–69.9)	69.9 (66.6–73.3)†	3.0
Education level				
Less than high school graduate	47.0 (44.3–49.7)	51.2 (48.4–54.0)	55.1 (52.2–58.0)†	3.9
High school graduate	49.8 (47.8–51.9)	55.6 (53.4–57.9)	56.4 (54.1–58.7)†	0.8
Some college	59.9 (57.9–61.8)	63.4 (61.3–65.4)	63.7 (61.9–65.6)†	0.3
College graduate	68.5 (66.3–70.7)	72.4 (70.3–74.4)	76.0 (74.2–77.8)†	3.6§
U.S. Census region				
Northeast	66.1 (63.8–68.5)	65.7 (62.8–68.5)	70.4 (68.0–72.8)†	4.7§
Midwest	56.7 (54.3–59.0)	62.6 (60.4–64.9)	62.9 (60.8–65.1)†,**	0.3
South	50.8 (48.6–52.9)	56.4 (54.3–58.4)	59.9 (57.9–61.9)†	3.6§
West	61.8 (59.4–64.2)	69.2 (66.9–71.5)	71.8 (69.8–73.8)†	2.6
Body mass index category††				
Underweight/Normal weight	61.4 (59.9–62.9)	66.6 (65.0–68.2)	70.3 (68.8–71.8)†	3.7§
Overweight	56.7 (54.6–58.7)	63.8 (62.0–65.6)	65.0 (63.1–66.9)†,**	1.2
Has obesity	50.0 (47.9–52.0)	54.6 (52.5–56.8)	57.8 (55.9–59.7)†	3.1§
Walking assistance status§§				
Does not need assistance	59.7 (58.5–61.0)	65.3 (62.6–64.9)	67.9 (63.1–65.6)†	2.6§
Needs assistance	25.8 (20.5–31.0)	23.6 (19.3–34.2)	30.3 (23.1–35.6)	6.7
Meets aerobic physical activity guideline¶¶				
No	44.6 (43.2–46.1)	49.1 (47.6–50.7)	51.0 (49.5–52.6)†	1.9
Yes	76.8 (75.4–78.1)	79.3 (78.0–80.7)	80.6 (79.3–82.0)†	1.3

Abbreviation: CI = confidence interval.

* Weighted percentages, age-standardized to the 2000 U.S. standard population.

† Significant linear trend from 2005 to 2015 (p<0.05), based on trend analyses using logistic regression controlling for age category.

§ Significant change from 2010 to 2015 (p<0.05).

¶ "Other race" category includes non-Hispanic Asian, non-Hispanic American Indian/Alaskan Native, and persons reporting more than one race.

** Significant deviation from linear trend from 2005 to 2015 (p<0.05), based on trend analyses using logistic regression controlling for age category.

†† Body mass index (weight [kg]/height [m^2]) estimates were calculated from self-reported weight and height. Underweight and normal weight: <25.0, overweight: 25.0–29.9, and has obesity: ≥30.

§§ Needing walking assistance was defined as being unable or finding it very difficult "to walk one-quarter mile without special equipment."

¶¶ Meeting the 2008 aerobic physical activity guideline was defined as participating in ≥150 minutes of moderate-intensity equivalent aerobic activity per week (light- to moderate-intensity minutes plus two times vigorous-intensity minutes).

trend only), but stalled between 2010 and 2015 among those who did not graduate from high school (significant linear and quadratic trends). Low socioeconomic status (SES) and minority neighborhoods are often perceived as less attractive and less safe because of traffic or crime when compared with higher SES and majority white neighborhoods (*9*). Efforts to overcome such environmental barriers to walking in these communities, like policies and practices that improve the safety and quality of community supports for physical activity (e.g., trails and sidewalks), might help to reduce the observed disparities in walking (*3*).

The findings in this report are subject to at least four limitations. First, this analysis relies on self-reported data, and social desirability bias might result in overestimates of walking (*10*). Second, the wording of the question about leisure walking changed slightly between 2005 and 2010; to improve comparability between years, participants in all years who reported that a typical walking period lasted <10 minutes

TABLE 2. Proportion of U.S. men aged ≥18 years who reported recent walking for transportation or leisure, by selected demographic and health characteristics — National Health Interview Survey, 2005–2015

Characteristic	%* (95% CI) 2005 (n = 11,942)	2010 (n = 10,579)	2015 (n = 13,315)	Absolute change from 2010 to 2015
Total	54.3 (53.0–55.5)	61.8 (60.6–63.0)	62.8 (61.6–64.1)†,§	1.0
Age group (yrs)				
18–24	56.0 (52.5–59.4)	65.7 (62.2–69.3)	63.6 (59.8–67.5)†,§	-2.1
25–34	52.5 (50.0–55.0)	63.7 (61.0–66.3)	64.5 (61.9–67.2)†,§	0.8
35–44	54.4 (52.1–56.7)	61.3 (58.7–63.9)	62.3 (59.2–65.3)†	1.0
45–64	54.5 (52.7–56.4)	61.8 (60.0–63.7)	62.8 (60.8–64.8)†,§	1.0
≥65	54.3 (51.6–56.9)	57.4 (54.6–60.2)	61.2 (58.9–63.5)†	3.8¶
Race/Ethnicity				
White, non-Hispanic	55.1 (53.6–56.6)	62.9 (61.5–64.3)	64.1 (62.4–65.8)†,§	1.2
Black, non-Hispanic	50.8 (47.9–53.7)	55.5 (52.3–58.7)	58.3 (55.2–61.4)†	2.8
Hispanic	52.5 (49.6–55.3)	60.1 (57.4–62.8)	59.6 (56.7–62.5)†,§	-0.5
Other race**	53.8 (48.5–59.1)	64.5 (60.6–68.4)	67.6 (64.2–71.1)†	3.1
Education level				
Less than high school graduate	46.1 (43.6–48.7)	53.8 (51.1–56.5)	53.3 (50.0–56.6)†,§	-0.5
High school graduate	46.5 (44.4–48.5)	55.5 (53.3–57.6)	56.2 (53.7–58.6)†,§	0.7
Some college	55.7 (53.7–57.8)	61.6 (59.5–63.7)	61.0 (58.8–63.2)†,§	-0.6
College graduate	64.8 (62.4–67.2)	71.5 (69.3–73.7)	72.8 (70.8–74.9)†	1.3
U.S. Census region				
Northeast	61.8 (58.9–64.6)	66.2 (63.5–69.0)	63.7 (60.8–66.6)§	-2.6
Midwest	54.2 (51.7–56.6)	60.4 (58.0–62.7)	61.0 (58.5–63.5)†,§	0.6
South	47.8 (45.7–50.0)	57.5 (55.4–59.6)	59.6 (57.5–61.7)†,§	2.2
West	58.8 (56.0–61.6)	66.3 (64.0–68.7)	68.7 (66.0–71.5)†	2.4
Body mass index category††				
Underweight/Normal weight	54.8 (52.7–56.9)	63.9 (62.0–65.9)	64.3 (62.0–66.5)†,§	0.4
Overweight	55.8 (54.0–57.6)	62.8 (61.0–64.6)	63.0 (61.3–64.8)†,§	0.2
Has obesity	51.8 (49.5–54.1)	58.2 (56.1–60.4)	60.8 (58.4–63.2)†	2.6
Walking assistance status§§				
Does not need assistance	55.8 (54.5–57.1)	63.8 (62.6–64.9)	64.4 (63.1–65.6)†,§	0.6
Needs assistance	26.6 (19.5–33.8)	26.7 (19.3–34.2)	29.3 (23.1–35.6)†	2.6
Meets aerobic physical activity guideline¶¶				
No	41.0 (39.3–42.6)	48.4 (46.7–50.1)	47.5 (45.5–49.4)†,§	-0.9
Yes	70.5 (69.0–71.9)	74.5 (73.1–76.0)	76.2 (74.8–77.5)†	1.7

Abbreviation: CI = confidence interval.

* Weighted percentages, age-standardized to the 2000 U.S. standard population.

† Significant linear trend from 2005 to 2015 (p<0.05), based on trend analyses using logistic regression controlling for age category.

§ Significant deviation from linear trend from 2005 to 2015 (p<0.05), based on trend analyses using logistic regression controlling for age category.

¶ Significant change from 2010 to 2015 (p<0.05).

** "Other race" category includes non-Hispanic Asian, non-Hispanic American Indian/Alaskan Native, and persons reporting more than one race.

†† Body mass index (weight [kg]/height [m^2]) estimates were calculated from self-reported weight and height. Underweight and normal weight: <25.0, overweight: 25.0–29.9, and has obesity: ≥30.

§§ Needing walking assistance was defined as being unable or finding it very difficult "to walk one-quarter mile without special equipment."

¶¶ Meeting the 2008 aerobic physical activity guideline was defined as participating in ≥150 minutes of moderate-intensity equivalent aerobic activity per week (light- to moderate-intensity minutes plus two times vigorous-intensity minutes).

(1,076 respondents) were categorized as nonwalkers. Third, survey response rates could contribute to response bias if nonresponders differed systematically from responders, although weighting procedures should reduce the impact of survey nonresponse. Finally, approximately 6% of respondents were missing walking data each year; the application of sample weights would not be expected to mitigate any potential bias associated with missing data.

The reported prevalence of transportation or leisure walking among women and men increased from 2005 to 2015, although among men, the increase has stalled in recent years. By implementing community and street scale design strategies that encourage pedestrian activity and by supporting walking programs where persons spend their time, communities can improve walkability and make walking a safer and easier option for increasing physical activity (*3*).

Conflict of Interest

No conflicts of interest were reported.

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Multistate Outbreak of *Salmonella* Anatum Infections Linked to Imported Hot Peppers — United States, May–July 2016

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Foodborne salmonellosis causes an estimated 1 million illnesses and 400 deaths annually in the United States (*1*). *Salmonella* Anatum is one of the top 20 *Salmonella* serotypes in the United States. During 2013–2015 there were approximately 300–350 annual illnesses reported to PulseNet, the national molecular subtyping network for foodborne disease surveillance. In June 2016, PulseNet identified a cluster of 16 *Salmonella* Anatum infections with an indistinguishable pulsed-field gel electrophoresis (PFGE) pattern from four states.* In April 2016, the same PFGE pattern had been uploaded to PulseNet from an isolate obtained from an Anaheim pepper, a mild to medium hot pepper. Hot peppers include many pepper varieties, such as Anaheim, jalapeño, poblano, and serrano, which can vary in heat level from mild to very hot depending on the variety and preparation. This rare PFGE pattern had been seen only 24 times previously in the PulseNet database, compared with common PFGE patterns for this serotype which have been seen in the database hundreds of times. Local and state health departments, CDC, and the Food and Drug Administration (FDA) investigated to determine the cause of the outbreak. Thirty-two patients in nine states were identified with illness onsets from May 6–July 9, 2016. Whole-genome sequencing (WGS) was performed to characterize clinical isolates and the Anaheim pepper isolate further. The combined evidence indicated that fresh hot peppers were the likely source of infection; however, a single pepper type or source farm was not identified. This outbreak highlights challenges in reconciling epidemiologic and WGS data, and the difficulties of identifying ingredient-level exposures through epidemiologic investigations alone.

Epidemiologic Investigation

During June, local and state health departments in seven states interviewed patients with standard foodborne illness questionnaires. By June 29, 14 patients had been interviewed; commonly reported foods eaten in the week preceding illness included tomatoes (71% of respondents); pork (64%); avocado/guacamole (57%); jalapeños, a hot pepper that can vary from mild to hot heat (36%); and cantaloupe (36%). These exposures were compared with the 2006–2007 FoodNet Population Survey, which summarizes data on foods eaten by a sample of healthy persons.† The only food exposure reported significantly more frequently than expected among patients was avocado/guacamole (p = 0.01); however, because the FoodNet Population Survey does not include questions on jalapeños, it was not possible to make a comparison for that exposure. Seven of the 14 interviewed patients reported eating at Mexican-style restaurants in the week preceding illness onset.

The lack of a strong hypothesis for the outbreak source led CDC to propose open-ended interviews by a single interviewer. Open-ended interviews are unstructured, conversational interviews that sometimes identify uncommon exposures because they gather more detailed information than that typically obtained from standard interviews.§ CDC completed open-ended interviews with nine patients, including seven from Texas, one from Colorado, and one from Illinois. Concurrently, Minnesota investigators conducted open-ended interviews with eight patients in Minnesota and shared exposure information with CDC.

A case of *Salmonella* Anatum gastroenteritis was defined as infection with an outbreak strain of *Salmonella* Anatum in a person with onset of diarrheal illness during May 6–July 9, 2016. In total, 32 cases from nine states were identified¶ (Figure 1). The median patient age was 36 years (range = 4–79 years); 19 (59%) were female. Illness onset dates ranged from May 6 to July 9 (Figure 2). Among 25 patients for whom information on hospitalization was available, eight (32%) were hospitalized; no deaths were reported. Among 18 patients for whom information from initial or open-ended interviews was available, 14 reported eating, or possibly eating fresh hot peppers, or reported eating an item containing fresh hot peppers. Nine patients reported eating peppers at restaurants, two reported eating peppers both at restaurants and at home, and three did not specify a location. Among the 14 patients who had eaten peppers, 11 reported eating, or possibly eating jalapeños. No patient reported eating Anaheim peppers; most had never heard of an Anaheim pepper.

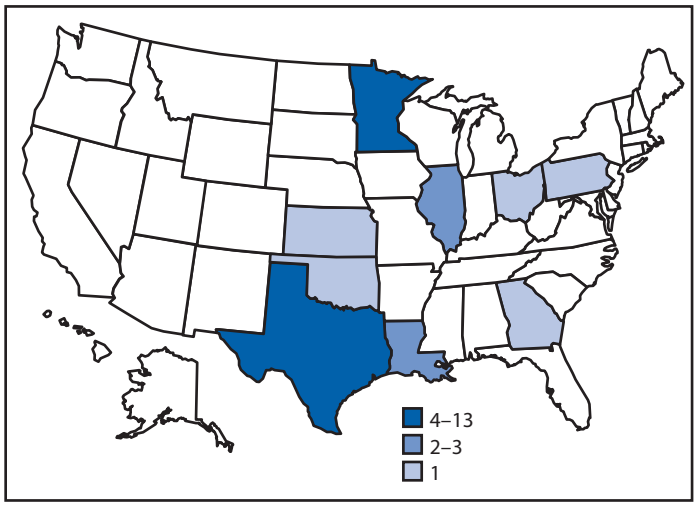
* https://www.cdc.gov/pulsenet.

† https://www.cdc.gov/foodnet/surveys/population.html.

§ https://www.cdc.gov/foodsafety/outbreaks/investigating-outbreaks/investigations/sources.html.

¶ Georgia (one case), Illinois (two), Kansas (one), Louisiana (one), Minnesota (10), Ohio (one), Oklahoma (one), Pennsylvania (one), Texas (13)

FIGURE 1. Number of persons (N = 32) infected with the outbreak strain of *Salmonella* Anatum, by state — United States, May 6–July 9, 2016



One illness subcluster was identified consisting of two patients who did not know one another and ate at the same Mexican-style restaurant in Texas in the week preceding illness. Both dined there on the same day and consumed multiple common food items, including steak, eggs, rice, beans, mild salsa, and pico de gallo (a fresh salsa made with chopped tomatoes), hot peppers, and other fresh ingredients. The only fresh hot peppers included in reported meal items were jalapeños, used in both the pico de gallo and mild salsa. The restaurant used serrano and poblano peppers in other dishes, but neither patient reported eating these items. Because the epidemiologic evidence supported hot peppers in general, but not Anaheim peppers specifically, investigators explored multiple hot pepper types as possible outbreak vehicles.

Traceback Investigation

Local and state investigators visited restaurants where patients reported consuming peppers. They collected recipes for reported menu items, including salsa, and reviewed invoices to identify common ingredients. To identify the source of hot peppers, FDA conducted traceback (the process of tracing a food from point-of-service to its origin or manufacturer source) from three restaurants in Minnesota and Texas where patients reported eating. Two of the three restaurants received peppers from a consolidator/grower in Mexico (consolidator/grower B) (Figure 3), which exported Anaheim peppers to the United States in April 2016. Consolidators pool foods from different growers or growing locations; this designation is also used if some growers/growing locations are unknown.** The third restaurant received peppers from various firms in Mexico; however, this restaurant had received peppers from consolidator/grower B before this outbreak. Because of the complicated supply chain for peppers and the extensive mixing of peppers from different suppliers, repacking, and reselling of product, FDA was unable to identify a single source farm or point of contamination for peppers.

In April 2016, before the identification of cases and as part of routine surveillance cultures of produce, the FDA isolated this strain of *Salmonella* Anatum from an Anaheim pepper sample. This Anaheim pepper was collected from consolidator/grower B, which supplied two restaurants reported to have been visited by patients in this outbreak. FDA collected seven additional samples of hot peppers, including serrano, habanero, jalapeño, and bell peppers, from consolidator/grower B as part of the outbreak investigation; none yielded *Salmonella*.

Laboratory Investigation

Representative clinical isolates and the Anaheim pepper isolate were further characterized by WGS.†† High-quality single-nucleotide polymorphism (hqSNP) analysis indicated

Summary

What is already known about this topic?

Salmonellosis is the most common bacterial cause of foodborne illness in the United States. *Salmonella* Anatum is one of the top 20 *Salmonella* serotypes in the United States, with approximately 300–350 illnesses reported to PulseNet annually during 2013–2015. Fresh hot peppers have previously been linked to foodborne outbreaks, including a large 2008 *Salmonella* Saintpaul outbreak that sickened 1,500 persons.

What is added by this report?

In June 2016, a nine-state outbreak of *Salmonella* Anatum infections was detected, involving 32 patients, with onset of diarrheal illness during May 6–July 9, 2016. The outbreak strain was isolated from an imported Anaheim pepper. The combined epidemiologic, laboratory, and traceback evidence indicated that fresh hot peppers were the likely source of infection, but a single pepper type or source farm could not be identified.

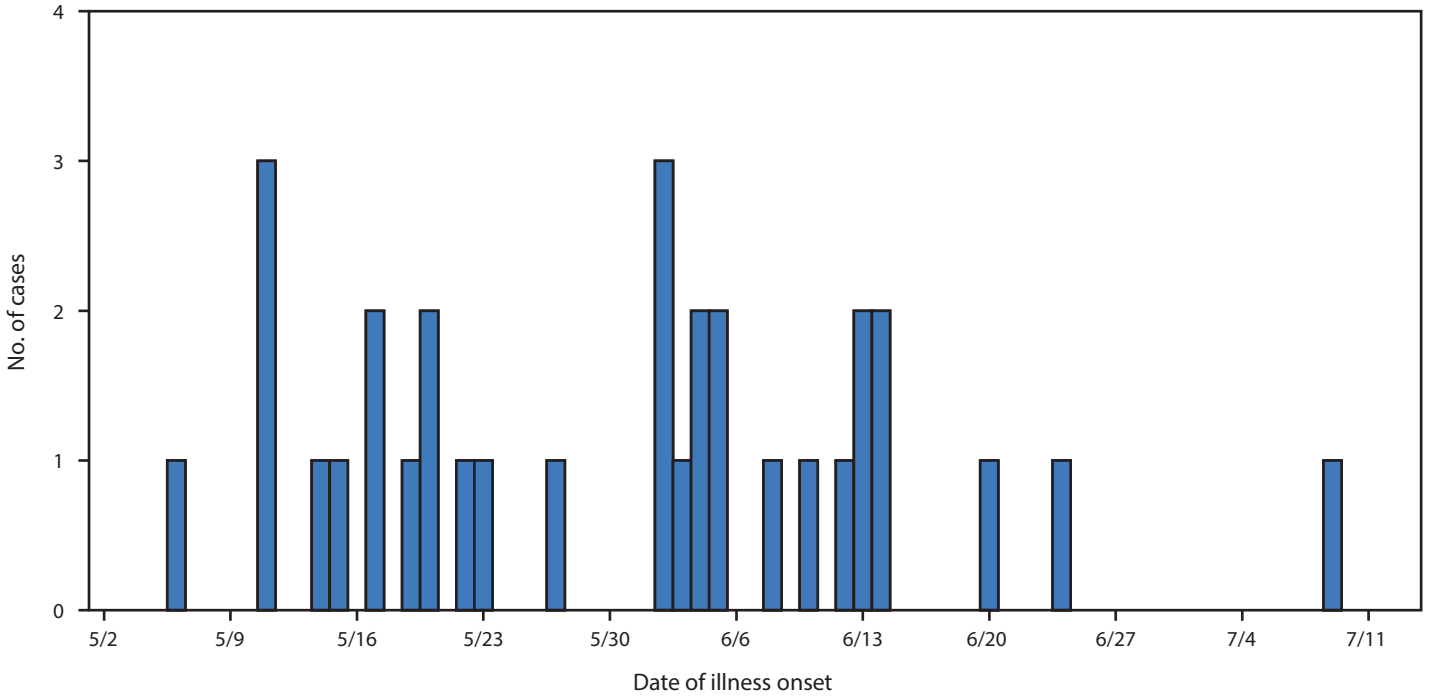
What are the implications for public health practice?

This investigation highlights the importance of using epidemiologic and traceback data in concert with whole-genome sequencing results during the course of foodborne outbreak investigations, as well as the utility of open-ended interviews and restaurant-specific recipe review in identifying ingredient-level exposures. Fresh hot peppers are a potential vehicle for *Salmonella* infections; both the complexity of the hot pepper supply chain, as well as the difficulties of identifying specific pepper types through epidemiologic investigations create challenges to investigating outbreaks linked to fresh hot peppers.

** https://www.fda.gov/ForIndustry/ImportProgram/default.htm.

†† https://www.ncbi.nlm.nih.gov/bioproject/369523.

FIGURE 2. Number of persons (N = 32) infected with the outbreak strain of *Salmonella* Anatum, by date of illness onset — nine states,* May 6–July 9, 2016



* Georgia, Illinois, Kansas, Louisiana, Minnesota, Ohio, Oklahoma, Pennsylvania, and Texas.

that 19 clinical isolates and the Anaheim pepper isolate differed by 0–3 hqSNPs, suggesting they were highly related genetically. This strong laboratory evidence was key to aiding in interpretation of the epidemiologic data.

Public Health Response

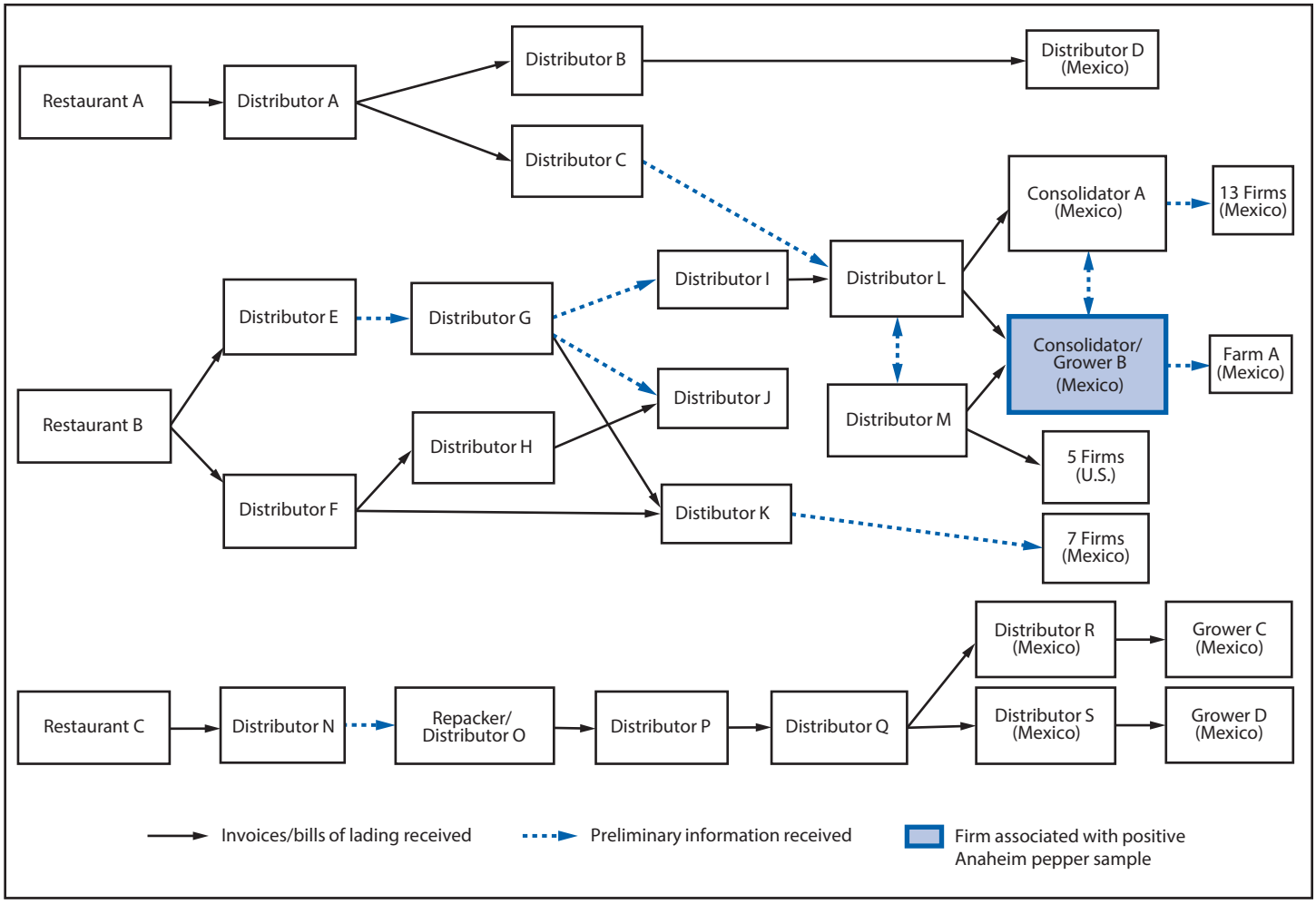
On June 21, 2016, before the epidemiologic investigation began, FDA placed consolidator/grower B on import alert for Anaheim peppers because they could be contaminated with *Salmonella.* (A product under an import alert is held at the port of entry before being allowed to enter the country. The importer must provide FDA evidence that the product is free from *Salmonella* within 10 business days of detention of the product; otherwise, the product cannot be imported.) There were only two outbreak-associated illnesses reported after the import alert was issued.

Discussion

In this outbreak, the only food sample yielding *Salmonella* matching the outbreak strain was an Anaheim pepper, which patients did not report consuming, perhaps because they were unfamiliar with this pepper variety or could not identify the pepper variety they consumed at restaurants in salsas or other dishes with chopped peppers. Although only two of the three restaurants included in the informational traceback investigation received peppers from the same consolidator/grower, it is possible that contaminated peppers cross-contaminated other foods or materials along the supply chain, providing a mechanism for the outbreak strain to reach the third restaurant. In addition, it is possible that the third restaurant did receive contaminated peppers during the outbreak timeframe, but the traceback was unable to uncover this because the companies involved kept incomplete records. However, no observations were made to support or refute either of these hypotheses. The strong genetic relationship between the clinical and food isolates, in combination with the epidemiologic and traceback evidence, indicated that fresh hot peppers were the likely source of the outbreak. Nevertheless, it was not possible to implicate one pepper type or source farm.

The epidemiologic investigation relied on review of restaurant-specific recipes, because pepper varieties were difficult to identify when used as ingredients in foods, particularly when prepared at restaurants. In addition, because many common ingredients are consumed in Mexican-style meals, it was difficult to narrow a hypothesis based on epidemiologic information alone. Similar challenges were documented in previous investigations, including a 2008 *Salmonella* Saintpaul outbreak that sickened 1,500 people; investigators ultimately determined

FIGURE 3. *Salmonella* Anatum outbreak informational traceback flow diagram for fresh hot peppers — United States, May–July 2016



that both fresh jalapeño and serrano peppers were outbreak sources after initial evidence indicated tomatoes might have been the source (*2*).

This outbreak highlights the importance of preventing produce contamination to reduce the risk for foodborne illness, especially for foods that are often consumed raw. Many patients consumed peppers at restaurants, often in dishes like fresh salsa, which are served raw. A 2009 study of *Salmonella* in fresh salsa found that chopped jalapeños were more supportive of *Salmonella* growth than some other raw vegetable ingredients when stored at 53°F–69°F (12°C–21°C) (*3*). *Salmonella* survival and growth varied with salsa formulation and were inhibited only in recipes containing both fresh garlic and lime juice (*3*); further research is needed to assess the microbiologic effects of these formulations. For all recipes, no growth was detected at 39°F (4°C), underscoring the importance of proper temperature controls at restaurants (*3*). All fresh produce, including hot peppers, should be thoroughly washed before preparation and consumption, and refrigerated as soon as possible to prevent the proliferation of bacteria such as *Salmonella*.

This outbreak also highlights new challenges in outbreak investigations when trying to reconcile epidemiologic data with WGS results indicating that clinical and food isolates are genetically closely related to one another. Although WGS can provide additional resolution of the relatedness of isolates, it should not be used as the sole source of evidence (*4*). Careful review of all available epidemiologic, traceback, and laboratory data is critical to determining the source of foodborne outbreaks as enhanced molecular techniques are implemented.

Conflict of Interest

No conflicts of interest were reported.

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Update: Influenza Activity in the United States During the 2016–17 Season and Composition of the 2017–18 Influenza Vaccine

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During the 2016–17 influenza season (October 2, 2016–May 20, 2017) in the United States, influenza activity* was moderate. Activity remained low through November, increased during December, and peaked in February nationally, although there were regional differences in the timing of influenza activity. Influenza A(H3N2) viruses predominated through mid-March and were predominant overall for the season, but influenza B viruses were most commonly reported from late March through May. This report summarizes influenza activity in the United States during October 2, 2016–May 20, 2017† and updates the previous summary (*1*).

Viral Surveillance

CDC receives influenza test results from public health and clinical laboratories located in all 50 states, Puerto Rico, and the District of Columbia through U.S. World Health Organization (WHO) Collaborating Laboratories and the National Respiratory and Enteric Virus Surveillance System. During October 2, 2016– May 20, 2017, clinical laboratories tested 865,168 specimens for influenza virus: 121,223 (14.0%) specimens tested positive for influenza virus (Figure 1), including 84,854 (70.0%) that tested positive for influenza A viruses and 36,369 (30.0%) that tested positive for influenza B viruses. Nationally, the percentage of specimens tested by clinical laboratories that were positive for influenza peaked during the 3 weeks ending February 11, February 18, and February 25, 2017 (weeks 6, 7, and 8) at 23.6%, 24.2%, and 24.3%, respectively. At a U.S. Department of Health and Human Services regional§ level, the timing of peak percent positivity varied. In regions 8 and 10, the percentage of viruses testing positive for influenza peaked during the week ending December 31, 2016 (week 52) and in region 9, the peak occurred during the week ending January 14, 2017 (week 2). In each of regions 1, 2, 3, 5, 6, and 7 the peak occurred from the week ending February 11 to February 25, 2017 (weeks 6–8). Region 4 also had peaks in influenza activity during the week ending February 11 through the week ending February 25, 2017 (weeks 6–8), and experienced a second peak during the week ending March 25, 2017 (week 12).

Public health laboratories tested a total of 84,303 specimens during October 2, 2016–May 20, 2017, and 40,728 were positive for influenza, including 31,736 (77.9%) influenza A and 8,992 (22.1%) influenza B viruses (Figure 2). Among the 31,411 influenza A viruses subtyped, 30,519 (97.2%) were influenza A(H3N2) viruses and 892 (2.8%) were influenza A(H1N1)pdm09 viruses. Influenza B lineage information was available for 6,875 (76.5%) influenza B viruses: 4,892 (71.2%) belonged to the B/Yamagata lineage and 1,983 (28.8%) to the B/Victoria lineage.

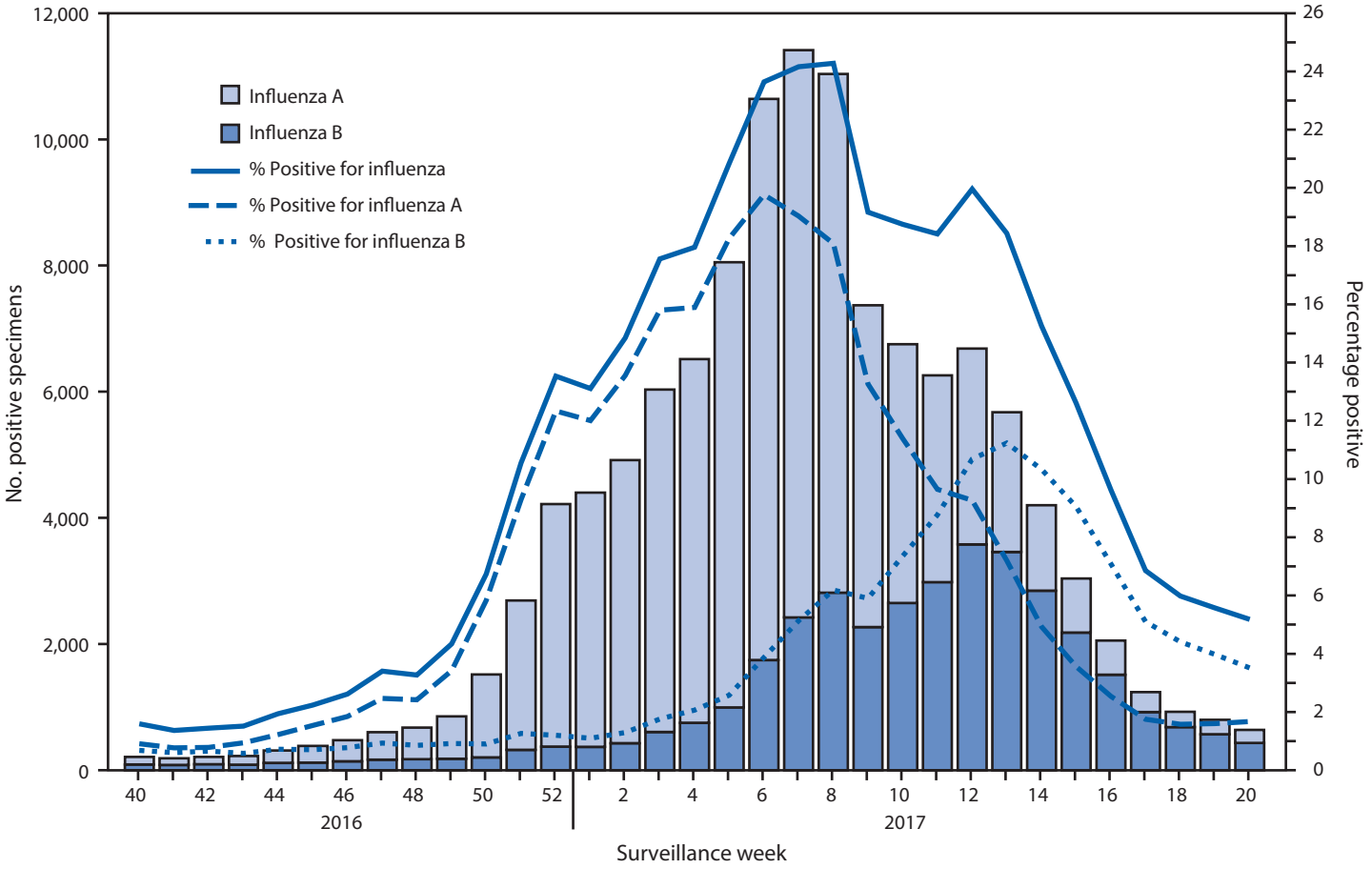
Age data were available for 36,426 of the influenza-positive patients tested by public health laboratories. Overall, 2,912 (8.0%) persons were aged 0–4 years, 11,066 (30.4%) were aged 5–24 years, 10,872 (29.8%) were aged 25–64 years, and 11,576 (31.8%) were aged ≥65 years. Influenza A(H3N2) viruses were predominant among all age groups, accounting for 70% of viruses identified among persons aged 0–4 years and 80% of viruses reported among persons aged ≥65 years. The largest proportion of reported influenza B viruses occurred

*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 June 9, 2017.

§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.

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–May 20, 2017†



* Specimens from 121,223 (14.0%) of 865,168 persons tested positive during October 2, 2016–May 20, 2017.
† As of June 9, 2017.

in persons aged 5–24 years; influenza B viruses accounted for 28% of the viruses reported for that age group.

Novel Influenza A Viruses

Three human infections with novel influenza A viruses were reported to CDC during the 2016–17 influenza season. The first was an infection with an influenza A(H1N2) variant (H1N2v) virus¶ reported by Iowa public health officials during the week ending November 19, 2016 (week 46). The patient was not hospitalized and fully recovered.

The second case, a human infection with a North American lineage avian influenza A(H7N2) virus, was reported to CDC during the week ending December 24, 2016 (week 51). The patient reported close, prolonged unprotected exposure to the respiratory secretions of infected, sick cats at a New York City animal shelter. This is the first avian 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 acquired through exposure to an ill cat. The patient was mildly ill, not hospitalized, and recovered completely.

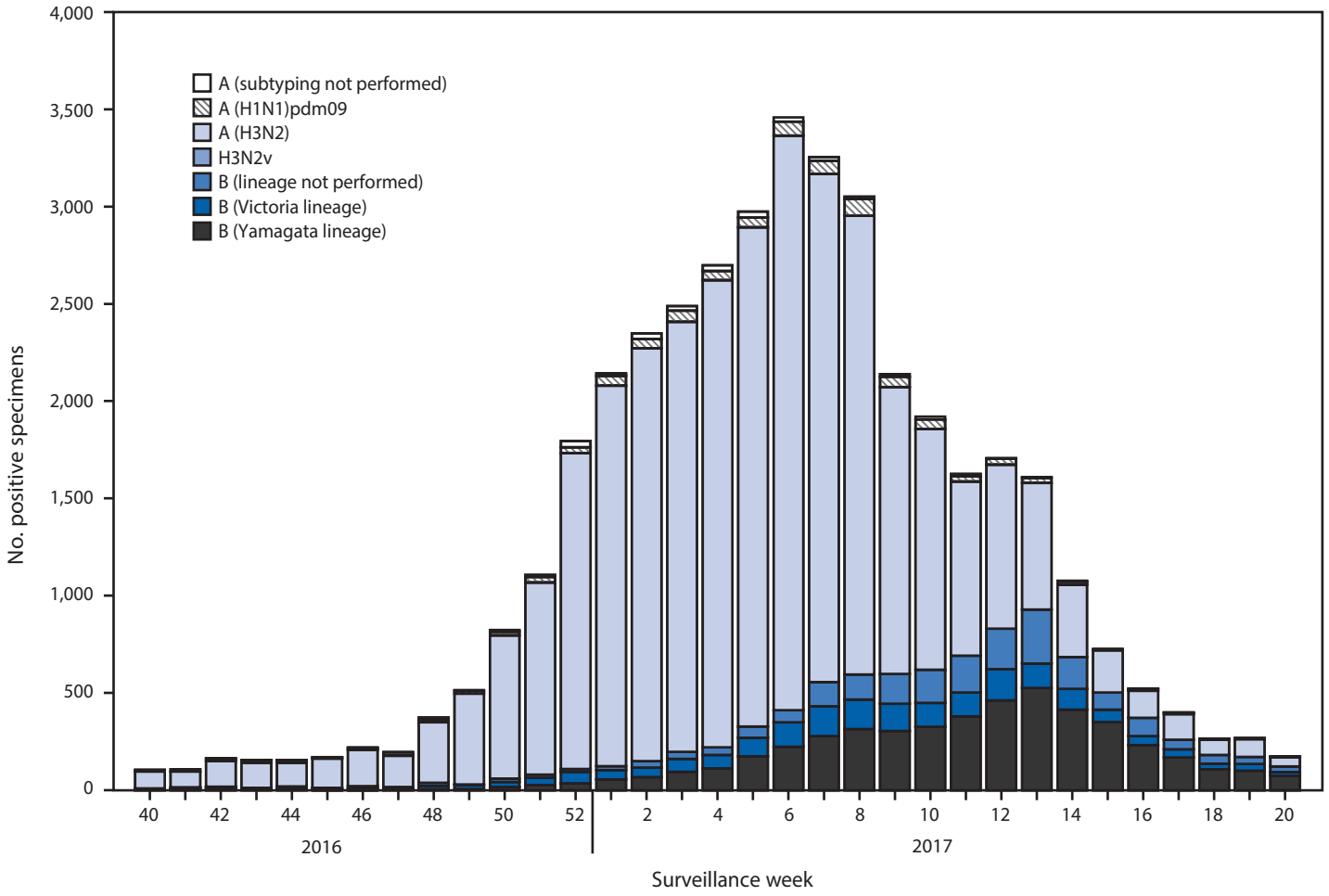
The third case, an infection with an influenza A(H3N2) variant (H3N2v) virus, was detected through the Department of Defense Global Laboratory–based Influenza Surveillance Program and reported by Texas during the week ending April 29, 2017 (week 17). The patient reported contact with swine at an agricultural event the week preceding illness onset, was not hospitalized, and fully recovered.

Antigenic and Genetic Characterization of Influenza Viruses

WHO collaborating laboratories in the United States are requested to submit a subset of influenza-positive respiratory

¶ 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 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–May 20, 2017†



* N = 40,728.
† As of June 9, 2017.

specimens to CDC for further virus characterization. CDC characterizes influenza viruses through one or more laboratory tests, including the following: genomic sequencing, antigenic characterization by hemagglutination inhibition (HI), or neutralization assays. Historically, until vaccine effectiveness estimates are available,** HI data have been used most commonly to assess the antigenic similarity between vaccine reference viruses and circulating viruses to infer how well the vaccine might perform. Since the 2014–15 season, a substantial proportion of influenza A(H3N2) viruses have not yielded sufficient hemagglutination titers for antigenic characterization by HI assay. The focus reduction assay (a neutralization test), has been used to supplement HI testing for antigenic characterization of a subset of influenza A(H3N2) viruses. For nearly all influenza-positive surveillance samples received by CDC, next-generation sequencing†† is performed to determine the genetic identity of circulating viruses.

For the 2016–17 season, CDC genetically characterized 2,476 influenza viruses (311 influenza A(H1N1)pdm09, 1,280 influenza A(H3N2), and 885 influenza B viruses) collected by U.S. laboratories since October 1, 2016. The hemagglutinin (HA) gene of 309 (99%) of the 311

** 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.

†† Next generation sequencing uses advanced molecular detection to identify gene sequences from each virus in a sample and thus reveals the genetic variations among many different influenza virus particles in a single sample; these methods also reveal the entire coding region of the genomes. https://www.cdc.gov/amd/project-summaries/influenza-vaccines.html.

influenza A(H1N1)pdm09 viruses analyzed belonged to the predominant 6B.1 genetic subgroup, and the remaining two (1%) belonged to genetic group 6B. The HA gene of 1,187 (93%) influenza A(H3N2) viruses analyzed belonged to the 3C.2a genetic group, and the remaining 93 (7%) belonged to the 3C.3a genetic group. Of note, the 3C.2a genetic group includes an emerging subgroup known as 3C.2a1. The HA genes of 495 influenza B/Yamagata-lineage viruses analyzed all belonged to genetic group Y3. The HA genes of 390 influenza B/Victoria-lineage viruses all belonged to genetic group V1A. However, 78 (20%) of the 390 B/Victoria-lineage viruses have several amino acid changes, including two amino acid deletions at positions 162 and 163 in the HA gene, which alter the antigenic properties of these viruses. Viruses with these changes are currently being referred to as the "B/Victoria deletion variant subgroup."

CDC has antigenically characterized 1,824 influenza viruses collected by U.S. laboratories since October 1, 2016 (296 influenza A(H1N1)pdm09, 772 influenza A(H3N2), and 756 influenza B viruses). Among the 296 A(H1N1) pdm09 viruses, 294 (99.3%) were antigenically characterized as A/California/7/2009-like, the influenza A(H1N1)pdm09 component of the 2016–17 Northern Hemisphere vaccine. Among the influenza A(H3N2) viruses, 730 (94.9%) were antigenically characterized as A/Hong Kong/4801/2014-like, a genetic group 3C.2a virus recommended as the A(H3N2) component of the 2016–17 Northern Hemisphere vaccine. Among 42 viruses that were antigenically different from A/Hong Kong/4801/2014-like viruses (i.e., reacted poorly with ferret antisera raised against reference viruses representing A/Hong Kong/4801/2014-like vaccine viruses), 36 (85.7%) belonged to genetic group 3C.3a, represented by the A/Switzerland/9715293/2013 reference virus, which was included as the A(H3N2) component of the 2015–16 Northern Hemisphere vaccine.

Among influenza B viruses, 327 B/Victoria-lineage viruses were antigenically characterized using postinfection ferret antisera and among these, 283 (86.5%) were antigenically characterized as B/Brisbane/60/2008-like, a recommended influenza B component of the 2016–17 Northern hemisphere trivalent and quadrivalent influenza vaccines. Among the 44 B/Victoria linage viruses that had reduced titers against B/Brisbane/60/2008-like viruses, 39 (88.6%) belong to the B/Victoria deletion variant subgroup. All 429 (100%) B/Yamagata-lineage viruses tested were antigenically characterized as B/Phuket/3073/2013-like, the recommended influenza B component of the 2016–17 Northern Hemisphere quadrivalent influenza vaccines.

Antiviral Susceptibility of Influenza Viruses

CDC tested 2,569 influenza virus specimens (304 influenza A(H1N1)pdm09, 1,303 influenza A(H3N2), and 962 influenza B viruses) collected in the United States during October 1, 2016–May 20, 2017 for resistance to the influenza neuraminidase inhibitor antiviral medications oseltamivir, zanamivir, and peramivir, which are currently recommended for use against seasonal influenza. All 2,569 influenza viruses tested were found to be susceptible to all three of these antiviral medications. An additional 34 influenza A(H1N1)pdm09 viruses were tested for resistance to oseltamivir and peramivir and an additional 1,083 influenza A(H3N2) viruses were tested for resistance to oseltamivir and zanamivir; all were found to be susceptible to these antiviral medications.

2016–17 Influenza Vaccine Effectiveness

Data collected through the U.S. Influenza Vaccine Effectiveness Network during November 28, 2016–April 14, 2017, indicate that influenza vaccination this season reduced the overall risk for influenza-associated medical visits by 42% (95% CI = 35%–48%). Vaccine effectiveness against the predominant influenza A(H3N2) viruses was 34% (95% CI = 24%–42%) and vaccine effectiveness against influenza B viruses was 56% (95% CI = 47%–64%).

Composition of the 2017–18 Influenza Vaccine

The Food and Drug Administration's Vaccines and Related Biologic Products Advisory Committee (VRBPAC) has recommended that the 2017–18 influenza trivalent vaccine to be used in the United States contain an A/Michigan/45/2015 (H1N1) pdm09-like virus, an A/Hong Kong/4801/2014 (H3N2)-like virus, and a B/Brisbane/60/2008-like (B/Victoria lineage) virus. It is recommended that quadrivalent vaccines, which have two influenza B viruses, contain the viruses recommended for the trivalent vaccines, as well as a B/Phuket/3073/2013-like (B/Yamagata lineage) virus (*2*). This represents an update in the influenza A(H1N1) component compared with the composition of the 2016–17 influenza vaccines. The recommended Northern Hemisphere 2017–18 vaccine viruses are the same as the vaccine viruses recommended for inclusion in the 2017 Southern Hemisphere influenza vaccines. These vaccine recommendations were based on a number of factors, including global influenza virologic and epidemiologic surveillance, genetic and antigenic characterization, human serology studies, antiviral susceptibility, and the availability of candidate influenza viruses.

Outpatient Illness Surveillance

Nationally, the weekly percentage of outpatient visits for influenza-like illness[§§] (ILI) to heath care providers participating in the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet) was at or above the national baseline[¶¶] level of 2.2% from the week ending December 17, 2016 (week 50) and remained at or above baseline for 17 consecutive weeks during the 2016–17 season (Figure 3). Nationally, the peak percentage of outpatient visits for ILI was 5.1% and occurred during the week ending February 11, 2017 (week 6). During the 2011–12 through 2015–16 seasons, peak weekly percentages of outpatient visits for ILI ranged from 3.6% to 6.1% and remained at or above baseline levels for an average of 13 weeks (range = 1–20 weeks).

ILINet data are used to produce a weekly jurisdiction-level measure of ILI activity,[***] ranging from minimal to high. The number of jurisdictions experiencing elevated ILI activity peaked during the week ending February 11, 2017 (week 6) when 31 states experienced high ILI activity. Thirty-seven jurisdictions (36 states and Puerto Rico) experienced high ILI activity during at least 1 week this season. The peak number of jurisdictions experiencing high ILI activity during a single week from 2011 to 2016 has ranged from four during the 2011–12 season to 45 during the 2014–15 season.

Geographic Spread of Influenza Activity

State and territorial epidemiologists report the geographic distribution of influenza in their jurisdictions[†††] through a weekly influenza activity code.[§§§] The geographic distribution of influenza activity was most extensive during the week ending February 11, 2017 (week 6), when 47 jurisdictions reported widespread influenza activity. From 2011 to 2016, the peak number of jurisdictions reporting widespread influenza activity ranged from 20 during the 2011–12 season to 48 during the 2012–13 season.

Influenza-Associated Hospitalizations

CDC monitors hospitalizations associated with laboratory-confirmed influenza infections in adults and children through the Influenza Hospitalization Surveillance Network (FluSurv-NET),[¶¶¶] which covers approximately 27 million persons (9% of the U.S. population). During October 1, 2016–April 30, 2017, a total of 18,184 laboratory-confirmed influenza-related hospitalizations were reported, with a cumulative incidence for all age groups of 65.0 per 100,000 population. The hospitalization rate was highest among persons aged ≥65 years, who accounted for approximately 60% of reported influenza-associated hospitalizations.

[§§] Defined as a fever (temperature ≥100.0°F [≥37.8°C], oral or equivalent) and cough and/or sore throat, without a known cause other than influenza.

[¶¶] The national and regional baselines are the mean percentages 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 during 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.

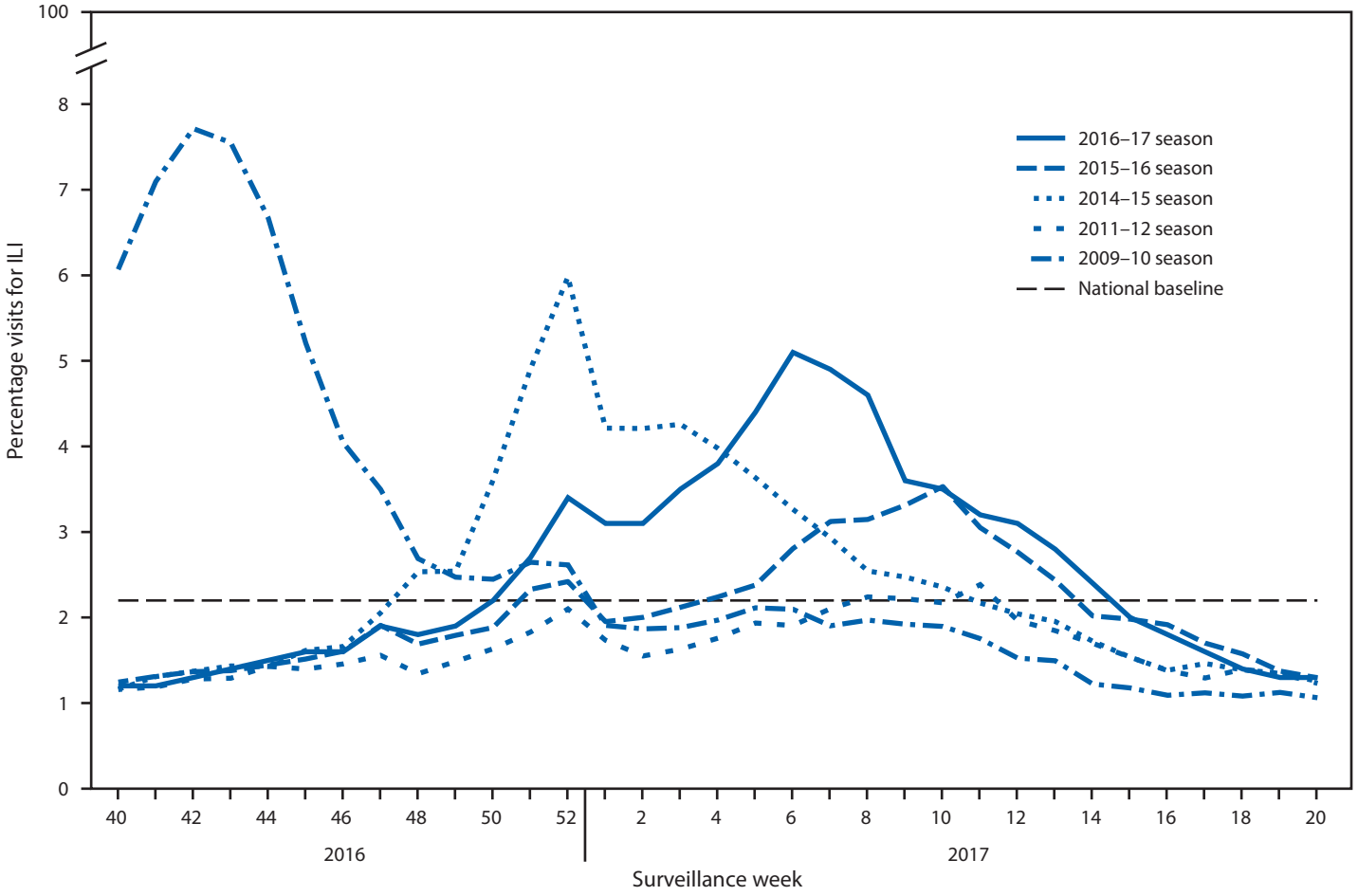
[***] Activity levels are based on the percentage of outpatient visits in a jurisdiction attributed to ILI and are compared with the average percentage of ILI visits that occur during weeks with little or no influenza virus circulation. Activity levels range from minimal, corresponding to ILI activity 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.

[†††] For this surveillance component, 54 jurisdictions participate: the 50 states, the District of Columbia, Guam, Puerto Rico, and U.S. Virgin Islands.

[§§§] 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 Idaho, Iowa, 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.

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 (temperature ≥100.0°F [≥37.8°C], oral or equivalent) and cough and/or sore throat, without a known cause other than influenza.
† As of June 9, 2017.

The cumulative hospitalization rate during October 1, 2016–April 30, 2017, was 44.1 per 100,000 population among children aged 0–4 years, 16.7 among children and adolescents aged 5–17 years, 19.8 among adults aged 18–49 years, 65.1 among adults aged 50–64 years, and 290.5 among adults aged ≥65 years. Among all hospitalizations, 14,185 (78.0%) were associated with influenza A virus infections, 3,873 (21.2%) with influenza B virus infections, 62 (0.3%) with influenza A virus and influenza B virus co-infections, and 64 (0.4%) with an influenza virus for which the type was not determined. Among the 5,383 patients for which influenza A subtype information was available, 5,276 (98.0%) were infected with influenza A(H3N2) viruses and 107 (2.0%) were infected with influenza A(H1N1)pdm09 viruses.

Complete medical chart abstraction data were available for 7,315 (40.2%) hospitalized adults and children with laboratory-confirmed influenza as of June 9, 2017. Among 6,838 hospitalized adults with complete medical chart abstraction, 6,434 (94.1%) had at least one reported underlying medical condition that placed them at high risk**** for influenza-associated complications. The most commonly reported underlying medical conditions among adults were

**** 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.

cardiovascular disease (51.8%), metabolic disorders (44.4%), obesity (34.8%), and chronic lung disease (30.1%). Among 477 hospitalized children with complete medical chart abstraction, 269 (56.4%) had at least one underlying medical condition; the most commonly reported of these were asthma (26.4%) and neurologic disorder (23.2%). Among 447 women of childbearing age (15–44 years) hospitalized with laboratory-confirmed influenza infections, 119 (26.6%) were pregnant.

Pneumonia and Influenza-Associated 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 include a combination of machine-coded and manually coded causes of death collected from death certificates. During the 2016–17 season, there was a backlog of data requiring manual coding within the NCHS mortality surveillance data. Work is underway to reduce and monitor the number of records awaiting manual coding. 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.

During the 2016–17 season, based on data from NCHS, the proportion of deaths attributed to P&I was at or above the epidemic threshold†††† for 12 consecutive weeks from the week ending December 31, 2016 through the week ending March 18, 2017 (weeks 52–11). Mortality attributed to P&I peaked twice, once at 8.2% of all deaths during the week ending January 21, 2017 (week 3) and once at 8.1% during the week ending February 25, 2017 (week 8). During the 2011–12 through 2015–16 seasons, the peak weekly percentages of deaths attributable to P&I ranged from 8.7% during the 2011–12 season to 11.1% during the 2012–13 season.

Influenza-Associated Pediatric Mortality

CDC monitors pediatric influenza deaths through the Influenza-Associated Pediatric Mortality Surveillance System. As of June 9, 2017, a total of 98 laboratory-confirmed influenza-associated pediatric deaths occurring during the 2016–17 season had been reported to CDC from Chicago, New York City, and 28 states. Of these 98 deaths, 46 were associated with an influenza A(H3N2) virus infection, three with an influenza A(H1N1)pdm09 virus infection, 14 with an influenza A virus for which no subtyping was performed, 34 with an influenza B virus infection, and one 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, during which 358 pediatric deaths were reported to CDC during April 15, 2009–October 2, 2010.

Discussion

The 2016–17 influenza season was notable for the predominant circulation of influenza A(H3N2) viruses. Nationally, influenza activity peaked in mid-February, with influenza A(H3N2) viruses predominant early in the season through the week ending March 25, 2017 (week 12). Influenza B viruses became the predominant virus starting during week 13 (the week ending April 1, 2017) and remained the predominant virus through the end of May. The timing of peak influenza activity varied across the United States. Influenza activity peaked at least 1 month earlier (week 52 to week 2) in the western United States (regions 8, 9, and 10) than in the rest of the country. During the 2016–17 season, severity indicators (e.g., hospitalization and mortality rates) were within the range that has been observed during previous seasons when influenza A(H3N2) viruses predominated. Previous influenza A(H3N2)–predominant seasons have been associated with increased hospitalizations and deaths compared with seasons that were not influenza A(H3N2)–predominant, especially among children aged <5 years and adults aged ≥65 years (*3*,*4*). The majority of influenza viruses antigenically characterized at CDC were similar to the reference viruses representing the recommended components for the 2016–17 vaccine. A small subset of antigenically distinct influenza B/Victoria viruses was detected. No antiviral resistance to oseltamivir, zanamivir, or peramivir was identified among tested influenza viruses from the 2016–17 season.

Final vaccine effectiveness estimates of 34% (95% CI = 24%–42%) against illness caused by influenza A(H3N2) viruses and 56% (95% CI = 47%–64%) against illness caused by influenza B viruses were similar to previous seasons when recommended vaccine viruses have been well matched to (i.e.,"like") circulating viruses, including the lower effectiveness observed against well-matched A(H3N2) viruses. Evidence of reduced protection against A(H3N2) viruses, even when vaccine viruses and circulating viruses are well matched, has been observed since the 2011–12 season. In general, vaccination with inactivated influenza vaccine has offered better

†††† 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.

protection against influenza A(H1N1) and influenza B viruses (*5*). Even during seasons when vaccine effectiveness is reduced, vaccination can offer substantial benefit and reduce the likelihood of severe outcomes such as hospitalization and death (*6*,*7*). During the 2012–13 season with estimated vaccination effectiveness against A(H3N2)-related illness of 39% (95% CI = 29%–47%), vaccination averted an estimated 5.6 million illnesses, 2.7 million medical visits, 61,500 hospitalizations, and 1,800 deaths (*8*). Estimates of the number of influenza illnesses, medical visits, and hospitalizations averted by influenza vaccination during the 2016–17 season are scheduled to be published in December 2017.

Influenza antiviral medications are an important adjunct to vaccination in the treatment and prevention of influenza. Treatment with influenza antiviral medications as close to the onset of illness as possible 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 patients who are at high risk for complications or who are severely ill with suspected influenza infection, even if rapid antigen-detection influenza diagnostic test results are negative (*9*).

Although summer influenza activity in the United States typically is low, influenza cases and outbreaks have occurred during summer months and clinicians should remain vigilant in considering influenza in the differential diagnosis of summer respiratory illnesses. Testing for seasonal influenza viruses and monitoring for novel influenza A virus infections should continue year round. Health care providers also are reminded to consider novel influenza virus infections in persons with influenza-like illness and swine or poultry exposure, or with severe acute respiratory infection after travel to areas where avian influenza viruses have been detected. Providers should alert the local public health department if novel influenza virus infection is suspected. Clinical laboratories using a commercially available influenza diagnostic assay that includes influenza A virus subtype determination should contact their state public health laboratory to facilitate transport and additional testing of any specimen that is positive for influenza A, but for which the subtype cannot be determined. Public health laboratories should immediately send influenza A virus specimens that they cannot 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 available 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?

During the 2016–17 influenza season, influenza activity remained low through November 2016, increased during December, and peaked in February. During October 2, 2016–May 20, 2017, influenza A(H3N2) viruses were identified most frequently, but influenza A(H1N1)pdm09 and influenza B viruses were also reported. Data collected from November 28, 2016 to April 14, 2017, indicate that influenza vaccination this season reduced the overall risk for influenza-associated medical visits by 42% (95% CI = 35%–48%). The composition of the 2017–18 influenza vaccine has been updated to better match circulating influenza viruses.

What are the implications for public health practice?

Annual influenza vaccination is recommended for all persons aged ≥6 months and 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.

Acknowledgments

State, county, city, and territorial health departments and public health laboratories; U.S. World Health Organization collaborating laboratories; National Respiratory and Enteric Virus Surveillance System laboratories; U.S. Outpatient Influenza-Like Illness Surveillance Network sites; FluSurv-NET; National Center for Health Statistics, CDC; FluNet; Stacy Davlin, Lisa Grohskopf, Sonja Olsen, Angie Foust, Elisabeth Blanchard, Priya Budhathoki, Thomas Rowe, Lizheng Guo, Ewelina Lyszkowicz, Shoshona Le, Malania Wilson, Juliana DaSilva, Alma Trujillo, Thomas Stark, Samuel Shepard, Sujatha Seenu, Ha Nguyen, Vasiliy Mishin, Juan De la Cruz, Influenza Division, National Center for Immunization and Respiratory Diseases, CDC.

Conflict of Interest

Jacquline Katz reports U.S. Patent 6,196,175 (issued 01/02/2001) and U.S. Patent 8,163,545 (issued 4/26/2012). No other conflicts of interest were reported.

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Notes from the Field

Late-Onset Infant Group B Streptococcus Infection Associated with Maternal Consumption of Capsules Containing Dehydrated Placenta — Oregon, 2016

Genevieve L. Buser, MDCM[1]; Sayonara Mató, MD[2]; Alexia Y. Zhang, MPH[3]; Ben J. Metcalf, PhD[4]; Bernard Beall, PhD[4]; Ann R. Thomas, MD[3]

In September 2016, the Oregon Health Authority was notified of a case of late-onset group B *Streptococcus agalactiae* (GBS) bacteremia in an infant that began 5 days after completion of treatment for early-onset GBS bacteremia. The infant was born at term following an uncomplicated pregnancy; maternal GBS vaginal/rectal screening culture at 37 weeks' gestation was negative. Shortly after birth, the infant developed signs of respiratory distress and was transferred to the neonatal intensive care unit where blood and cerebrospinal fluid (CSF) were obtained for culture; antibiotics were initiated for presumed sepsis. The blood culture was positive for penicillin-sensitive, clindamycin-intermediate GBS. CSF culture was negative. The infant was discharged and went home after completing an 11-day course of ampicillin (200 mg/kg/day).

Five days later, the infant was taken to the emergency department because of irritability and was admitted to a second hospital. A blood culture yielded penicillin-sensitive, clindamycin-sensitive GBS. CSF was sterile, expressed breast milk did not yield GBS, and serial exams did not reveal a source.

Three days into the infant's admission to the second hospital, the treating physician was notified by a physician from the birth hospital that the mother had requested release of the placenta at the time of delivery. The mother confirmed that she had registered with Company A to pick up and encapsulate her placenta for ingestion. Three days after the infant's birth, the mother had received the dehydrated, encapsulated placenta and began ingesting two capsules three times daily. The physician instructed the mother to stop consuming the capsules. A sample of the capsules was cultured, yielding penicillin-sensitive, clindamycin-sensitive GBS. The infant was treated with ampicillin (300 mg/kg/day) for 14 days and gentamicin (3 mg/kg/daily) for the first 6 days and discharged home.

The three GBS isolates (one from each blood infection, and one from the placenta capsules) were indistinguishable by pulsed-field gel electrophoresis. Whole genome sequencing (WGS) performed at CDC revealed no single nucleotide polymorphisms between strains. WGS predicted serotype III, multilocus sequence type 17 (ST17), and tetM+ (tetracycline resistance). The strains had surface-anchored hypervirulent GBS adhesin Hvga, pilus island PI2b, and serine-rich repeat protein Srr2 (*1*); these virulence factors can facilitate adhesion and invasion from the infant's intestine into the bloodstream and potentially across the blood brain barrier (*2*). Although transmission from other colonized household members could not be ruled out, the final diagnosis was late-onset GBS disease attributable to high maternal colonization secondary to consumption of GBS-infected placental tissue (*3*).

Placenta ingestion has recently been promoted to postpartum women for its physical and psychological benefits, although scientific evidence to support this is lacking (*4*). Placental tissue is consumed raw or prepared by cooking, desiccation, preservation, and other modalities (*5*). Expectant mothers register for Company A's services before delivery and report preexisting infection with human immunodeficiency virus/acquired immunodeficiency syndrome, hepatitis, herpes, chlamydia, syphilis, and Lyme disease; however, the company does not ask about intra- or postpartum infections. According to Company A's website, the placenta is cleaned, sliced, and dehydrated at 115°F–160°F (46°C–71°C), then ground and placed into about 115–200 gelatin capsules, and stored at room temperature.

No standards exist for processing placenta for consumption. Heating at 130°F (54°C) for 121 minutes is required to reduce *Salmonella* bacterial counts by 7 $\log_{10}$ (*6*). In this case, heating for sufficient time at a temperature adequate to decrease GBS bacterial counts might not have been reached. Consumption of contaminated placenta capsules might have elevated maternal GBS intestinal and skin colonization, facilitating transfer to the infant.

The placenta encapsulation process does not per se eradicate infectious pathogens; thus, placenta capsule ingestion should be avoided. In cases of maternal GBS colonization, chorioamnionitis, or early-onset neonatal GBS infection, ingestion of capsules containing contaminated placenta could heighten maternal colonization, thereby increasing an infant's risk for late-onset neonatal GBS infection. Clinicians should inquire about a history of placenta ingestion in cases of late-onset GBS infection and educate mothers interested in placenta encapsulation about the potential risks.

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Valerie Newman, Michael Garcia, Portland, Oregon.

Conflict of Interest

No conflicts of interest were reported.

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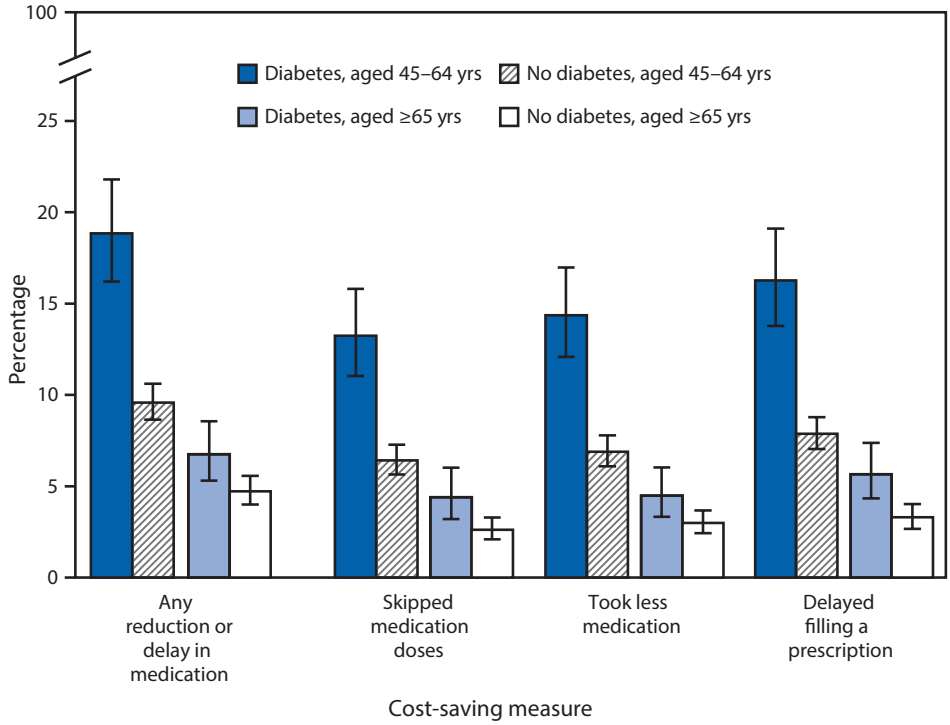
QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Percentage* of Adults Aged ≥45 Years Who Reduced or Delayed Medication to Save Money† in the Past 12 Months Among Those Who Were Prescribed Medication, by Diagnosed Diabetes Status and Age§ — National Health Interview Survey, 2015



* With 95% confidence intervals indicated by error bars.

† Based on responses to the following questions: "During the past 12 months, were any of the following true for you: You skipped medication doses to save money? You took less medicine to save money? You delayed filling a prescription to save money?" These questions were asked of respondents who first answered "yes" to the question "During the past 12 months, were you prescribed medication by a doctor or other health professional?" Any reduction or delay in medication to save money was determined based on a response of "yes" to any of the three questions. Medication refers to any medication prescribed, not just medication for diabetes.

§ Diabetes status was determined by an affirmative response to the survey question "Have you ever been told by a doctor or health professional that you have diabetes or sugar diabetes?" Women were asked not to include diabetes occurring during pregnancy.

In 2015, among adults aged 45–64 years who were prescribed any medication, those with diabetes were more likely than those without diabetes to have reduced or delayed medication (18.8% compared with 9.6%) to save money in the past 12 months, with measures that included skipping medication doses (13.2% compared with 6.4%), taking less medication (14.4% compared with 6.9%), and delaying filling a prescription (16.3% compared with 7.9%). Among adults ≥65, those with diabetes were more likely than those without diabetes to reduce or delay medication (6.8% compared with 4.7%) and to have used each of the specific cost-saving measures. Regardless of diabetes status, among adults who were prescribed medication, those aged 45–64 years were more likely than those aged ≥65 years to reduce or delay taking medication to save money.

Source: National Health Interview Survey, 2015 data. https://www.cdc.gov/nchs/nhis.htm.

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