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National, Regional, State, and Selected Local Area Vaccination Coverage Among Adolescents Aged 13–17 Years — United States, 2020

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The Advisory Committee on Immunization Practices (ACIP) recommends that adolescents aged 11–12 years routinely receive tetanus, diphtheria, and acellular pertussis (Tdap); meningococcal conjugate (MenACWY); and human papillomavirus (HPV) vaccines. Catch-up vaccination is recommended for hepatitis B (HepB); hepatitis A (HepA); measles, mumps, and rubella (MMR); and varicella (VAR) vaccines for adolescents whose childhood vaccinations are not current. Adolescents are also recommended to receive a booster dose of MenACWY vaccine at age 16 years, and shared clinical decision-making is recommended for the serogroup B meningococcal vaccine (MenB) for persons aged 16–23 years (*1*). To estimate coverage with recommended vaccines, CDC analyzed data from the 2020 National Immunization Survey–Teen (NIS-Teen) for 20,163 adolescents aged 13–17 years.* Coverage with ≥1 dose of HPV vaccine increased from 71.5% in 2019 to 75.1% in 2020. The percentage of adolescents

* Eligible participants were born during January 2002–January 2008. Tetanus toxoid, reduced diphtheria toxoid, and acellular pertussis vaccine represents coverage with ≥1 Tdap dose at age ≥10 years. Meningococcal conjugate vaccine represents coverage with the quadrivalent meningococcal conjugate vaccine or meningococcal-unknown type vaccine. HPV vaccination coverage includes receipt of any HPV vaccine and does not distinguish between nine-valent (9vHPV), quadrivalent (4vHPV), or bivalent (2vHPV) vaccines. Some adolescents might have received more than the 2 or 3 recommended HPV vaccine doses. Hepatitis A, hepatitis B, varicella, and measles, mumps, and rubella vaccines are considered childhood vaccinations and are recommended for adolescents who are not up to date with these vaccinations. Estimates in this report include those who might have received vaccinations on-time or as catch-up. Except as noted, coverage estimates for ≥1 and ≥2 varicella vaccine doses were obtained among adolescents with no history of varicella disease. Influenza vaccination coverage data are not included in this report but are available at https://www.cdc.gov/flu/fluvaxview/index.htm.

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who were up to date[†] with HPV vaccination (HPV UTD) increased from 54.2% in 2019 to 58.6% in 2020. Coverage with ≥1 dose of Tdap, ≥1 dose (and among adolescents aged 17 years, ≥2 doses) of MenACWY remained similar to coverage in 2019 (90.1%, 89.3%, and 54.4% respectively). Coverage increased for ≥2 doses of HepA among adolescents aged 13–17 years and ≥1 dose of MenB among adolescents aged 17 years. Adolescents living below the federal poverty level[§] had higher HPV vaccination coverage than adolescents living at or above the poverty level. Adolescents living outside a metropolitan statistical area (MSA)[¶] had lower coverage with ≥1 MenACWY and ≥1 HPV dose, and a lower proportion being HPV UTD than adolescents in MSA principal cities. In 2020, the COVID-19 pandemic disrupted routine immunization services. Results from the 2020 NIS-Teen reflect adolescent vaccination coverage before the COVID-19 pandemic. The 2020 NIS-Teen data could be used to assess the impact of the COVID-19 pandemic on catch-up vaccination but not on routine adolescent vaccination because adolescents included in the survey were aged ≥13 years, past the age when most routine adolescent vaccines are recommended, and most vaccinations occurred before March 2020. Continued efforts to reach adolescents whose routine medical care has been affected by the COVID-19 pandemic are necessary to protect persons and communities from vaccine-preventable diseases and outbreaks.

NIS-Teen is an annual random-digit–dialed telephone survey[**] that monitors vaccination coverage in adolescents aged 13–17 years in all 50 states, the District of Columbia, selected local areas, and some U.S. territories.[††] Parents or guardians of

[†] Adolescents were considered to be up to date with HPV vaccination if they had received ≥3 doses, or if each of the following applied: 1) they had received 2 doses; 2) the first dose was received before their 15th birthday; and 3) the difference between dates of first and second doses was ≥5 months minus 4 days, the absolute minimum interval between the first and second doses. https://www.cdc.gov/vaccines/programs/iis/cdsi.html

[§] Adolescents were classified as being below the federal poverty level if their total family income was less than the level specified for the applicable family size and number of children aged <18 years. All others were classified as at or above the poverty level (https://www.census.gov/data/tables/time-series/demo/income-poverty/historical-poverty-thresholds.html). Poverty status was unknown for 711 adolescents.

[¶] MSA status was determined from household reported city and county of residence and was grouped into three categories: MSA principal city, MSA nonprincipal city, and non-MSA. MSA and MSA principal city were as defined by the U.S. Census Bureau (https://www.census.gov/programs-surveys/metro-micro.html). Non-MSA areas include urban populations not located within an MSA and completely rural areas.

[**] Persons living in all identified mobile-telephone households were eligible for interview. Sampling weights were adjusted for single frame (mobile telephone), nonresponse, noncoverage, and overlapping samples of mixed telephone users. A description of NIS-Teen single-frame survey methodology and its effect on reported vaccination estimates is available at https://www.cdc.gov/vaccines/imz-managers/coverage/teenvaxview/pubs-presentations/dual-to-single-frame-teen.html.

[††] Local areas that received federal immunization funds under Section 317 of the Public Health Service Act were sampled separately. Those included Chicago, Illinois; New York, New York; Philadelphia County, Pennsylvania; Bexar County, Texas; and Houston, Texas. Two territories were sampled separately in 2020: Guam and Puerto Rico.

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eligible adolescents are interviewed to gather sociodemographic information about the household, and consent to contact the adolescent's vaccination provider (or providers) is requested; if permission is granted, a questionnaire is mailed to the provider (or providers) to obtain the adolescent's vaccination history. Vaccination coverage estimates are based on provider-reported immunization records and include any vaccines administered before the 2020 NIS-Teen interview date. This report provides vaccination coverage estimates for 20,163 adolescents aged 13–17 years.[§§] The overall household response rate[¶¶] was 20.7%; 45.2% of adolescents with completed interviews had adequate provider data. Data were weighted and analyzed to account for the complex survey design, and T-tests using Taylor-series variance estimates were used to assess vaccination coverage differences by survey year (2020 versus 2019) and between sociodemographic groups.[***] P-values <0.05 were considered statistically significant. Analyses were conducted using SAS-callable SUDAAN (version 11; RTI International). This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.[†††]

National Vaccination Coverage

In 2020, HPV vaccination coverage (≥1 dose) among adolescents was 75.1%, and 58.6% were HPV UTD (Figure) (Table 1). Coverage with ≥1 dose of Tdap and MenACWY remained high and stable (90.1% and 89.3% respectively). Among adolescents aged 17 years, coverage with ≥2 doses of MenACWY was 54.4%, similar to 2019 (53.7%); coverage increased for ≥1 dose of Men B among adolescents aged 17 years and catchup vaccination with ≥2 doses of HepA among adolescents 13–17 years from 2019. Coverage surpassed 90% for ≥2 doses of MMR, ≥3 doses of HepB, and ≥1 and ≥2 doses of varicella vaccine among adolescents without a history of varicella disease.[§§§]

Vaccination Coverage by Selected Characteristics

Among adolescents living in non-MSA areas, vaccination coverage was lower compared with those living in MSA principal cities with ≥1 dose MenACWY (85.7% versus 90.2% [–4.5 percentage points]), ≥1 dose HPV (68.0% versus 77.8% [–9.8 percentage points]), and ≥2 doses HepA (76.2% versus 83.6% [–7.4 percentage points])], and being HPV UTD (49.2% versus 60.4% [–11.2 percentage points]) (Table 2). These MSA disparities persisted among adolescents at or above the poverty level but were not significant among those below the poverty level for HPV UTD status and ≥2 dose–HepA coverage. The coverage disparity in non-MSA areas compared with MSA principal cities among adolescents living at or above the poverty level were largest for HPV UTD status (46.0% versus 59.8% [–13.8 percentage points]), ≥1-dose HPV coverage (64.9% versus 76.2% [–11.3 percentage points], and ≥2-dose HepA coverage (74.4% versus 83.6% [–9.2 percentage points]). Coverage varied by jurisdiction (Supplementary Table, https://stacks.cdc.gov/view/cdc/109214), race and ethnicity,[¶¶¶] and health insurance status.[****]

COVID-19 Pandemic Effects on HPV Vaccination

The COVID-19 pandemic was declared a national emergency on March 13, 2020. To evaluate the impact of the pandemic on HPV vaccination, CDC conducted two analyses comparing the 2019 and 2020 NIS-Teen samples. Historically, HPV vaccination coverage has been lower than coverage with most other routine vaccines, allowing for more catch-up vaccinations among adolescents aged 13–17 years. Most adolescents had initiated HPV vaccination before March 1 in both survey

[§§] The 2020 NIS-Teen sample included 9,576 females and 10,587 males. Adolescents from Guam (300), and Puerto Rico (169) were excluded from the national estimates.

[¶¶] The Council of American Survey Research Organizations response rate is the product of three other rates: 1) the resolution rate (the proportion of telephone numbers that can be identified as either for business or residence), 2) the screening rate (the proportion of qualified households that complete the screening process), and 3) the cooperation rate (the proportion of contacted eligible households for which a completed interview is obtained).

[***] The NIS-Teen methodology for weighting and synthesizing provider-reported vaccination histories has been previously described. https://www.cdc.gov/vaccines/imz-managers/nis/downloads/NIS-TEEN-PUF19-DUG.pdf

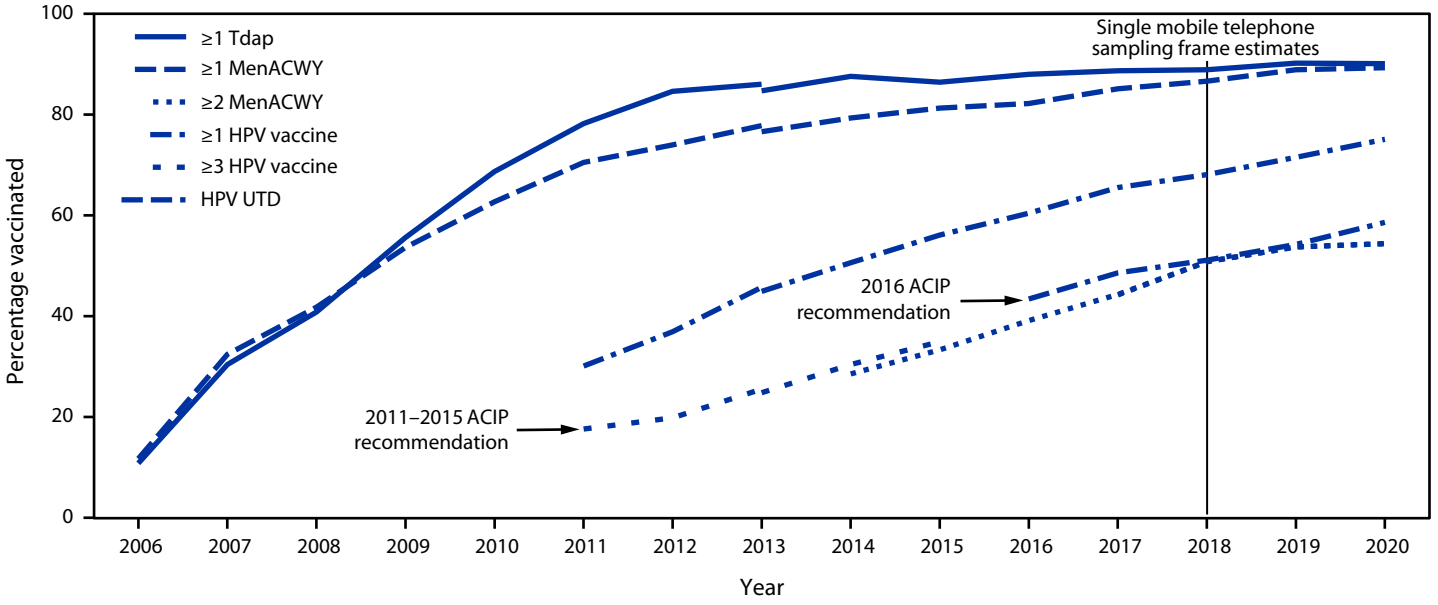
[†††] 45 C.F.R. part 46.102(l)(2); 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

[§§§] HepA, HepB, VAR, and MMR vaccines are considered childhood vaccinations and are recommended for adolescents who are not up to date with these vaccinations. Estimates in this report include those who might have received vaccinations on-time or as catch-up.

[¶¶¶] Hispanic adolescents had lower coverage for ≥1 Tdap (–3.9 percentage points), ≥2 MMR (–4.0 percentage points), ≥3 HepB (–4.3 percentage points), ≥1 Var (–2.6 percentage points), and ≥2 Var (–3.2 percentage points) than White adolescents. Black adolescents had lower coverage for ≥2 MenACWY (–2.5 percentage points) than White adolescents. Results showed higher HPV vaccine coverage (≥1 dose) for Black, Hispanic, American Indian or Alaska Native, Asian, and multiracial adolescents than White adolescents. Results also showed higher HPV UTD for Black, Hispanic, and multiracial adolescents. The higher HPV coverage has been observed for Black and Hispanic adolescents compared with White adolescents for several years. https://www.cdc.gov/vaccines/imz-managers/coverage/teenvaxview/pubs-presentations/NIS-teen-vac-coverage-estimates-2020-tables.html#table-01

[****] Adolescents with any Medicaid insurance had lower coverage for ≥1 Tdap (–3.1 percentage points) but higher coverage with ≥1 HPV (6.1 percentage points) compared with adolescents with private health insurance. Adolescents who were uninsured had lower coverage for all routine vaccinations (Tdap, MenACWY, and HPV vaccines) compared with adolescents with private health insurance. https://www.cdc.gov/vaccines/imz-managers/coverage/teenvaxview/pubs-presentations/NIS-teen-vac-coverage-estimates-2020-tables.html#table-02

FIGURE. Estimated vaccination coverage with selected vaccines and doses* among adolescents aged 13–17 years, by survey year† — National Immunization Survey–Teen,§,¶ United States, 2006–2020



Abbreviations: ACIP = Advisory Committee on Immunization Practices; HPV = human papillomavirus; MenACWY = quadrivalent meningococcal conjugate vaccine; NIS-teen = National Immunization Survey–Teen; Tdap = tetanus toxoid, reduced diphtheria toxoid, and acellular pertussis vaccine; UTD = up to date.

* ≥1 dose Tdap at age ≥10 years; ≥1 dose MenACWY or meningococcal-unknown type vaccine; ≥2 doses MenACWY or meningococcal-unknown type vaccine, calculated only among adolescents aged 17 years at time of interview. Does not include adolescents who received their first and only dose of MenACWY at age ≥16 years; HPV vaccine, nine-valent (9vHPV), quadrivalent (4vHPV), or bivalent (2vHPV). The routine ACIP recommendation for HPV vaccination was made for females in 2006 and for males in 2011. Because HPV vaccination was recommended for males in 2011, coverage for all adolescents was not measured before that year; HPV UTD includes those with ≥3 doses, and those with 2 doses when the first HPV vaccine dose was initiated at age <15 years and at least 5 months minus 4 days elapsed between the first and second dose.

† NIS-Teen implemented a revised adequate provider data definition in 2014 and retrospectively applied the revised definition to 2013 data. Estimates using a revised definition might not be directly comparable.

§ NIS-Teen moved in 2018 to a single-sample frame.

¶ ACIP revised the recommended HPV vaccination schedule in late 2016. The schedule changed from a 3-dose to 2-dose series with appropriate spacing between receipt of the first and second dose for immunocompetent adolescents initiating the series before the 15th birthday. Three doses are still recommended for adolescents initiating the series at age ≥15 years. Because of the change in definition, the graph includes estimates for ≥3 doses of HPV during 2011–2015 and the HPV UTD estimate for 2016–2020. Because HPV vaccination was recommended for males in 2011, coverage for all adolescents was not measured before that year.

years (69.1% in 2019 and 73.6% in 2020). An additional 2.4% and 1.5% of adolescents initiated the series after this date in 2019 and 2020, respectively.

The second analysis evaluated adolescents in the 2020 NIS-Teen sample who had not received HPV vaccine before March 1 and whose parent or guardian was interviewed on or after that date. This cohort was compared with a similarly constructed cohort using 2019 NIS-Teen data. Cumulative daily HPV vaccination initiation estimates from March through December for these cohorts were calculated using the Kaplan-Meier method.†††† Among the 4,918 adolescents who had not received HPV vaccine as of March 1, 2019 (26.2% of the total sample), 452 (15.0%) initiated the series by mid-December 2019. Among the 4,527 adolescents who had not received HPV vaccine as of March 1, 2020, (22.5% of total sample), 282 (15.2%) initiated the series by mid-December 2020. HPV vaccination initiation in the 2020 cohort was lower than that in the 2019 cohort by April. The difference between the two cohorts was largest in August and September (4.9 percentage points lower in 2020 in both months) but narrowed in subsequent months and was no longer significant by end of November (Supplementary Figure, https://stacks.cdc.gov/view/cdc/109215).

†††† Kaplan-Meier methods were used to calculate cumulative daily vaccination estimates from March–December 2019 and from March–December 2020. In 2019, 4,918 adolescents had not received a dose of HPV vaccine and had not been interviewed as of March 1, 2019; 452 were vaccinated between March–December 2019. In 2020, 4,527 adolescents had not received a dose of HPV vaccine and had not been interviewed as of March 1, 2020; 282 were vaccinated between March–December 2020.

TABLE 1. Estimated vaccination coverage with selected vaccines and doses among adolescents aged 13–17* years, by age at interview — National Immunization Survey–Teen, United States, 2020

	Age at interview (yrs), % (95% CI)†					Total, % (95% CI)†	
	13	14	15	16	17	2020	2019
Vaccine	(n = 4,276)	(n = 4,173)	(n = 3,998)	(n = 4,028)	(n = 3,688)	(N = 20,163)	(N = 18,788)
Tdap§ ≥1 dose	88.9 (87.0–90.6)	89.4 (87.1–91.3)	90.7 (88.7–92.5)	90.4 (88.3–92.1)	91.1 (88.7–93.0)	**90.1 (89.2–90.9)**	**90.2 (89.2–91.1)**
MenACWY¶							
≥1 dose	87.5 (85.3–89.4)	87.6 (85.0–89.8)	90.4 (88.6–92.0)**	89.1 (86.9–91.0)	92.3 (90.3–93.9)**	**89.3 (88.4–90.2)**	**88.9 (88.0–89.8)**
≥2 doses††	NA	NA	NA	NA	54.4 (51.2–57.5)	**54.4 (51.2–57.5)**	**53.7 (49.9–57.4)**
HPV§§ vaccine							
All adolescents							
≥1 dose	69.4 (66.6–72.1)	72.3 (69.4–75.0)	77.6 (75.3–79.8)**	77.2 (74.7–79.6)**	79.0 (76.4–81.4)**	**75.1 (73.9–76.2)¶¶**	**71.5 (70.1–72.8)**
HPV UTD***	45.6 (42.7–48.5)	56.0 (53.0–58.9)**	61.9 (58.9–64.7)**	65.5 (62.6–68.2)**	64.5 (61.5–67.4)**	**58.6 (57.3–60.0)¶¶**	**54.2 (52.7–55.8)**
Females							
≥1 dose	71.3 (67.7–74.7)	72.9 (68.4–77.0)	78.1 (74.6–81.3)**	80.3 (76.3–83.8)**	83.5 (80.8–85.9)**	**77.1 (75.4–78.7)¶¶**	**73.2 (71.3–75.0)**
HPV UTD	48.4 (44.3–52.5)	57.2 (52.6–61.7)**	63.7 (59.4–67.8)**	68.5 (64.0–72.6)**	70.4 (66.6–73.9)**	**61.4 (59.5–63.3)¶¶**	**56.8 (54.6–59.0)**
Males							
≥1 dose	67.5 (63.2–71.5)	71.7 (67.9–75.2)	77.1 (73.9–80.1)**	74.5 (71.1–77.6)**	74.8 (70.4–78.6)**	**73.1 (71.5–74.8)¶¶**	**69.8 (67.9–71.7)**
HPV UTD	42.7 (38.6–46.9)	54.8 (50.9–58.6)**	60.0 (56.1–63.9)**	62.8 (58.9–66.4)**	59.0 (54.4–63.5)**	**56.0 (54.1–57.8)¶¶**	**51.8 (49.7–53.9)**
MenB ≥1 dose†††	NA	NA	NA	NA	28.4 (25.5–31.5)	**28.4 (25.5–31.5)¶¶**	**21.8 (18.9–24.9)**
MMR ≥2 doses	92.5 (90.7–94.0)	92.1 (90.3–93.5)	92.5 (90.4–94.2)	93.2 (91.5–94.7)	91.6 (89.2–93.5)	**92.4 (91.6–93.2)**	**91.9 (90.8–92.8)**
Hepatitis A vaccine ≥2 doses§§§	86.5 (84.1–88.5)	84.9 (82.6–86.9)	81.5 (79.1–83.6)**	79.8 (77.5–81.8)**	77.7 (75.0–80.1)**	**82.1 (81.1–83.1)¶¶**	**77.1 (75.8–78.4)**
Hepatitis B vaccine ≥3 doses	91.8 (89.8–93.4)	93.5 (92.1–94.8)	92.5 (90.7–94.0)	93.6 (92.0–94.8)	91.4 (89.1–93.3)	**92.6 (91.8–93.3)**	**91.6 (90.6–92.6)**
Varicella							
History of varicella¶¶¶	6.8 (5.4–8.5)	6.9 (5.7–8.3)	8.7 (7.1–10.6)	7.6 (6.4–9.1)	12.0 (9.7–14.8)**	**8.4 (7.6–9.2)**	**9.1 (8.4–9.9)**
No history of varicella disease							
≥1 dose vaccine	96.2 (94.8–97.2)	95.9 (94.4–97.0)	95.3 (93.5–96.7)	95.3 (93.3–96.7)	95.2 (93.6–96.5)	**95.6 (94.9–96.2)**	**95.2 (94.3–95.9)**
≥2 doses vaccine	93.6 (92.0–95.0)	91.6 (89.6–93.2)	92.8 (90.6–94.5)	90.8 (88.3–92.9)**	90.5 (88.1–92.5)**	**91.9 (91.0–92.7)**	**90.6 (89.5–91.7)**
History of varicella or received ≥2 doses varicella vaccine	94.1 (92.6–95.3)	92.1 (90.3–93.6)	93.4 (91.4–95.0)	91.5 (89.2–93.4)	91.6 (89.5–93.4)**	**92.6 (91.7–93.3)**	**91.5 (90.4–92.4)**

Abbreviations: CI = confidence interval; HPV = human papillomavirus; MenACWY = quadrivalent meningococcal conjugate vaccine; MenB = serogroup B meningococcal vaccine; MMR = measles, mumps, and rubella vaccine; NA = not applicable; NIS-Teen = National Immunization Survey–Teen; Tdap = tetanus toxoid, reduced diphtheria toxoid, and acellular pertussis vaccine; UTD = up to date.

* Adolescents (20,163) in the 2020 NIS-Teen were born during January 2002–January 2008.

† Estimates with 95% CI widths >20 might be unreliable.

§ Includes percentages receiving Tdap vaccine at age ≥10 years.

¶ Includes percentages receiving MenACWY or meningococcal-unknown type vaccine.

** Statistically significant difference (p<0.05) in estimated vaccination coverage by age: reference group was adolescents aged 13 years.

†† ≥2 doses of MenACWY or meningococcal-unknown type vaccine. Calculated only among adolescents who were aged 17 years at interview. Does not include adolescents who received 1 dose of MenACWY vaccine at age ≥16 years.

§§ HPV vaccine, nine-valent (9vHPV), quadrivalent (4vHPV), or bivalent (2vHPV). For ≥1 HPV dose measure and HPV-UTD measure, percentages are reported among females and males combined (20,163) and among females only (9,576) and among males only (10,587).

¶¶ Statistically significant difference (p<0.05) compared with 2019 NIS-Teen estimates.

*** HPV UTD includes those with ≥3 doses, and those with 2 doses when the first HPV vaccine dose was initiated before age 15 years and there was at least 5 months minus 4 days between the first and second dose. This update to the HPV recommendation occurred in December 2016.

††† ≥1 dose of MenB. Calculated only among adolescents who were aged 17 years at interview. Administered based on individual clinical decision.

§§§ In July 2020, ACIP revised recommendations for HepA vaccination to include catch-up vaccination for children and adolescents aged 2–18 years who have not previously received HepA vaccine at any age. https://www.cdc.gov/mmwr/volumes/69/rr/rr6905a1.htm?s_cid

¶¶¶ By parent or guardian report or provider records.

Discussion

NIS-Teen 2020 data indicate that although ≥1 dose HPV coverage and HPV UTD status continue to increase, they remain lower than coverage with most other routinely recommended vaccines. Improvements in HPV vaccination coverage are crucial to lowering rates of HPV-attributable cancers in the United States. Coverage with ≥1 dose of Tdap and MenACWY vaccines remains high and stable, while coverage with ≥2 doses of MenACWY remains low, indicating the need for increased awareness of the importance of the booster dose.

TABLE 2. Estimated vaccination coverage with selected vaccines and doses among adolescents aged 13–17* years, by metropolitan statistical area† and by poverty level — National Immunization Survey–Teen, United States, 2020

	MSA, % (95% CI)§			Below poverty level, % (95% CI)§			At or above poverty level, % (95% CI)§		
Vaccine	Non-MSA (n = 3,678)	MSA nonprincipal city (n = 8,409)	MSA principal city (n = 8,076)	Non-MSA (n = 631)	MSA nonprincipal city (n = 865)	MSA principal city (n = 1,352)	Non-MSA (n = 2,938)	MSA nonprincipal city (n = 7,246)	MSA principal city (n = 6,420)
Tdap¶ ≥1 dose	90.7 (88.7–92.3)	90.6 (89.3–91.8)	89.3 (87.7–90.7)	93.1 (89.7–95.5)	89.0 (84.7–92.1)	89.6 (86.3–92.2)	89.8 (87.4–91.9)	91.1 (89.7–92.3)	89.2 (87.3–90.9)
MenACWY**									
≥1 dose	85.7 (83.7–87.5)††	89.4 (87.9–90.7)	90.2 (88.7–91.5)	86.1 (81.8–89.5)††	87.2 (82.6–90.6)	91.6 (88.8–93.7)	85.6 (83.2–87.7)††	90.2 (88.6–91.5)	89.4 (87.5–91.0)
≥2 doses§§	50.1 (43.4–56.9)	58.5 (54.0–62.8)††	50.6 (45.2–56.1)	47.4 (33.5–61.7)	47.6 (33.0–62.7)	48.6 (35.8–61.7)	50.2 (42.3–58.0)	61.2 (56.6–65.6)††	50.2 (44.1–56.4)
HPV¶¶ vaccine									
All adolescents									
≥1 dose	68.0 (65.3–70.6)††	74.2 (72.5–75.9)††	77.8 (75.8–79.6)	73.6 (67.8–78.7)††	83.6 (79.5–87.0)	85.7 (82.0–88.7)	64.9 (61.7–67.9)††	73.1 (71.3–74.9)††	76.2 (74.0–78.3)
HPV UTD***	49.2 (46.3–52.1)††	59.1 (57.2–61.0)	60.4 (58.2–62.6)	56.7 (50.3–62.9)	63.8 (58.1–69.2)	64.4 (59.2–69.3)	46.0 (42.9–49.3)††	58.4 (56.4–60.4)	59.8 (57.4–62.2)
Females									
≥1 dose	67.8 (63.7–71.7)††	76.7 (74.5–78.8)	79.8 (76.9–82.4)	75.2 (66.4–82.2)††	84.4 (78.9–88.6)	87.2 (82.0–91.0)	63.6 (58.6–68.2)††	75.7 (73.3–78.0)	78.8 (75.7–81.7)
HPV UTD	50.3 (46.0–54.6)††	62.2 (59.6–64.7)	63.2 (59.9–66.4)	56.9 (47.6–65.8)	65.3 (56.8–72.9)	66.0 (58.2–73.0)	46.8 (42.0–51.6)††	61.9 (59.1–64.5)	63.5 (60.0–67.0)
Males									
≥1 dose	68.1 (64.6–71.5)††	71.9 (69.3–74.4)††	75.8 (73.2–78.3)	71.6 (63.7–78.4)††	82.9 (76.5–87.8)	84.3 (78.8–88.6)	66.1 (61.9–70.0)††	70.7 (68.0–73.3)	73.7 (70.5–76.6)
HPV UTD	48.1 (44.3–52.0)††	56.2 (53.4–58.9)	57.8 (54.8–60.7)	56.4 (47.8–64.7)	62.5 (54.5–69.8)	62.9 (55.8–69.4)	45.4 (41.2–49.7)††	55.2 (52.2–58.1)	56.2 (52.8–59.5)
MMR ≥2 doses	92.8 (91.0–94.2)	92.4 (91.2–93.5)	92.3 (90.9–93.5)	93.6 (89.4–96.2)	89.5 (83.8–93.3)	90.8 (86.2–94.0)	92.3 (90.2–94.0)	92.9 (91.6–93.9)	92.4 (90.9–93.6)
Hepatitis A vaccine ≥2 doses†††	76.2 (73.7–78.5)††	82.0 (80.6–83.4)	83.6 (81.9–85.2)	80.4 (75.0–84.9)	82.1 (77.1–86.3)	83.0 (78.1–87.0)	74.4 (71.5–77.0)††	81.8 (80.2–83.3)	83.6 (81.7–85.3)
Hepatitis B vaccine ≥3 doses	92.4 (90.6–93.9)	92.9 (91.7–93.9)	92.3 (90.9–93.5)	92.8 (89.0–95.4)	91.0 (86.3–94.2)	89.9 (85.5–93.2)	92.0 (89.8–93.8)	93.1 (91.9–94.1)	92.9 (91.5–94.1)

See table footnotes on the next page.

Disparities in vaccination coverage by MSA and poverty level persist. Among adolescents living at or above the poverty level, those in non-MSAs had lower HPV UTD status and coverage with ≥2 doses of HepA than adolescents in MSA principal cities. Further investigation is needed to understand this disparity and more generally, the relationship between socioeconomic level, geographic location, barriers to vaccination such as vaccination access, and vaccine confidence. Persons living below the poverty level might have better access to the VFC program,§§§§ which provides vaccines to children whose parents or guardians otherwise might not be able to afford them. Adolescents living below the poverty level have previously been shown to have higher HPV vaccine coverage (*2*–*4*).

Although HPV vaccination continues to increase in the United States, and coverage for most other routine vaccinations remains high and stable, the COVID-19 pandemic threatens these achievements. An analysis of immunization information systems data from 10 U.S. jurisdictions during March–May 2020 compared with the same period in 2018 and 2019 identified a substantial decrease in the number of vaccine doses administered to children and adolescents in 2020. Increases in doses administered were noted during June–September 2020 but did not appear sufficient to offset the decline during

§§§§ Children aged ≤18 years who are Medicaid-eligible, uninsured, or American Indian or Alaska Native (as defined by the Indian Health Care Improvement Act) are eligible to receive vaccines from providers through the Vaccines for Children (VFC) program. Children categorized as "underinsured" because their health plans do not include coverage for recommended vaccinations are eligible to receive VFC vaccines if they are served by a rural health clinic or federally qualified health center or under an approved deputization agreement. https://www.cdc.gov/vaccines/programs/vfc/providers/eligibility.html

TABLE 2. (*Continued*) Estimated vaccination coverage with selected vaccines and doses among adolescents aged 13–17* years, by metropolitan statistical area† and by poverty level — National Immunization Survey–Teen, United States, 2020

	MSA, % (95% CI)§			Below poverty level, % (95% CI)§			At or above poverty level, % (95% CI)§		
	Non-MSA	MSA nonprincipal city	MSA principal city	Non-MSA	MSA nonprincipal city	MSA principal city	Non-MSA	MSA nonprincipal city	MSA principal city
Vaccine	**(n = 3,678)**	**(n = 8,409)**	**(n = 8,076)**	**(n = 631)**	**(n = 865)**	**(n = 1,352)**	**(n = 2,938)**	**(n = 7,246)**	**(n = 6,420)**
Varicella									
History of varicella§§§	10.1 (8.6–11.8)	8.2 (7.2–9.4)	8.0 (6.9–9.4)	9.8 (6.9–13.6)	13.3 (9.4–18.5)	9.3 (6.4–13.3)	10.3 (8.6–12.3)††	7.2 (6.2–8.4)	7.8 (6.5–9.3)
No history of varicella disease									
≥1 dose vaccine	96.1 (94.6–97.1)	95.8 (94.8–96.6)	95.3 (94.1–96.2)	95.9 (91.9–97.9)	96.9 (94.6–98.2)	94.0 (90.0–96.4)	96.1 (94.4–97.3)	95.5 (94.3–96.4)	95.5 (94.2–96.5)
≥2 doses vaccine	92.5 (90.7–94.0)	92.0 (90.6–93.2)	91.6 (90.1–92.9)	94.2 (90.1–96.6)	87.9 (81.2–92.4)	90.7 (85.7–94.0)	91.7 (89.4–93.5)	92.4 (91.0–93.5)	91.6 (90.0–93.0)
History of varicella or received ≥2 doses VAR	93.2 (91.6–94.6)	92.7 (91.4–93.8)	92.3 (90.9–93.5)	94.7 (91.0–97.0)	89.5 (83.6–93.4)	91.5 (87.0–94.6)	92.5 (90.5–94.1)	92.9 (91.6–94.0)	92.2 (90.7–93.5)

Abbreviations: CI = confidence interval; HPV = human papillomavirus; MenACWY = quadrivalent meningococcal conjugate vaccine; MMR = measles, mumps, and rubella vaccine; MSA = metropolitan statistical area; NIS-Teen = National Immunization Survey–Teen; Tdap = tetanus toxoid, reduced diphtheria toxoid, and acellular pertussis vaccine; UTD = up-to-date; VAR= varicella vaccine.

* Adolescents (20,163) in the 2020 NIS-Teen were born during January 2002–January 2008.

† MSA status was determined based on household-reported county of residence and was grouped into three categories: MSA principal city, MSA nonprincipal city, and non-MSA. MSA and principal city were as defined by the U.S. Census Bureau https://www.census.gov/programs-surveys/metro-micro.html). Non-MSA areas include urban populations not located within an MSA as well as completely rural areas.

§ Estimates with 95% CI widths >20 might not be reliable.

¶ Includes percentages receiving Tdap vaccine at age ≥10 years.

** Includes percentages receiving MenACWY and meningococcal-unknown type vaccine.

†† Statistically significant difference (p<0.05) in estimated vaccination coverage by metropolitan statistical area; referent group was adolescents living in MSA principal city areas.

§§ ≥2 doses of MenACWY or meningococcal-unknown type vaccine. Calculated only among adolescents who were aged 17 years at interview. Does not include adolescents who received 1 dose of MenACWY vaccine at age ≥16 years.

¶¶ HPV vaccine, nine-valent (9vHPV), quadrivalent (4vHPV), or bivalent (2vHPV)in females and males combined.

*** HPV UTD includes those with ≥3 doses, and those with 2 doses when the first HPV vaccine dose was initiated before age 15 years and there was at least 5 months minus 4 days between the first and second dose. This update to the HPV recommendation occurred in December 2016.

††† In July 2020, ACIP revised recommendations for HepA vaccination to include catch-up vaccination for children and adolescents aged 2–18 years who have not previously received HepA vaccine at any age. https://www.cdc.gov/mmwr/volumes/69/rr/rr6905a1.htm?s_cid

§§§ By parent or guardian report or provider records.

March–May 2020 (*5*). Analysis of adolescents in the 2019 and 2020 NIS-Teen data who were aged ≥13 years and had not initiated HPV vaccination as of March 1 showed lower series initiation initially from April through the end of October in 2020 compared with 2019; however, initiation of the HPV series in 2019 and 2020 was similar by November–December. Although this is encouraging, the NIS-Teen data cannot yet be used to assess the potential impact of the pandemic on adolescents who were due to receive vaccinations at age 11–12 years. As adolescents aged 11–12 years who were due to receive routine vaccinations during the pandemic age into the NIS-Teen survey sample (13–17 years), the full impact of the COVID-19 pandemic can be assessed.

The findings in this report are subject to at least three limitations. First, the household response rate was 20.7%, and 45.2% of respondents had adequate provider data. Low survey response rates can increase potential biases if survey participants differ from nonrespondents (*6*). Second, bias in estimates might remain after adjustment for household and provider nonresponse and phoneless households. A recent survey error assessment indicated that NIS-Teen estimates might underestimate true coverage, with the largest underestimation for Tdap vaccine (–5.3 percentage points).¶¶¶¶ Little evidence exists of a change in survey accuracy between 2019 and 2020.***** Finally, opportunity is limited to assess the effect of the pandemic on routine coverage using 2020

¶¶¶¶ An assessment of validity of the 2019 NIS-Teen estimates has been reported (https://www.cdc.gov/vaccines/imz-managers/nis/downloads/NIS-TEEN-PUF19-DUG.pdf). NIS-Teen vaccination coverage estimates tended to be slightly low compared with true values derived after adjusting for noncoverage, nonresponse, and vaccination underascertainment, reaching up to 5.3 percentage points too low for Tdap. This was primarily attributed to underascertainment of vaccinations by the NIS provider record check. The validity of estimates did not change from 2018 to 2019.

***** https://www.cdc.gov/vaccines/imz-managers/coverage/teenvaxview/pubs-presentations/NIS-teen-vac-coverage-estimates-2020-tables.html#table-03

Summary

What is already known about this topic?

Tetanus, diphtheria, and acellular pertussis (Tdap), meningococcal conjugate (MenACWY), and human papillomavirus (HPV) vaccines are routinely recommended for adolescents.

What is added by this report?

In 2020, adolescent coverage with Tdap and the first dose of MenACWY remained high and continued to improve for HPV vaccines, with some disparities. Adolescents living outside a metropolitan statistical area (MSA) had lower vaccination coverage compared with adolescents living in MSA principal cities.

What are the implications for public health?

Results from the 2020 National Immunization Survey–Teen reflect adolescent vaccination coverage before the COVID-19 pandemic. Efforts to reach adolescents whose routine medical care has been affected by the pandemic are necessary to protect adolescents and communities from vaccine-preventable diseases and outbreaks.

NIS-Teen data; because many vaccines are recommended for children aged 11–12 years, most adolescents aged 13–17 years received their routine vaccinations before the pandemic started.

Health care providers should review patient vaccination records and administer any vaccines or doses that are due. Children and adolescents aged 12–17 years are also eligible (those aged 16–17 years as of December 11, 2020 and those aged 12–15 years as of May 10, 2021) for a COVID-19 vaccine, which may be administered with other vaccines at the same visit (*7*). Ensuring that routine vaccination is maintained and that adolescents catch up on any missed doses is essential to protecting persons and communities from vaccine-preventable diseases and outbreaks.

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Evaluation of Syndromic Surveillance Data for Studying Harmful Algal Bloom-Associated Illnesses — United States, 2017–2019

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Harmful algal and cyanobacterial blooms (harmful algal blooms) are large colonies of algae or cyanobacteria that can harm humans, animals, and the environment (*1–3*). The number of algal blooms has been increasing in the United States, augmented by increasing water temperatures and nutrients in water from industry and agricultural run-off (*4,5*). The extent to which harmful algal bloom exposures cause human illness or long-term health effects is unknown. As the number of blooms increases annually, the likelihood of negative health outcomes (e.g., respiratory or gastrointestinal illness) from exposure also increases (*4,5*). To explore the utility of syndromic surveillance data for studying health effects from harmful algal bloom exposures, CDC queried emergency department (ED) visit data from the National Syndromic Surveillance Program (NSSP) for harmful algal bloom exposure–associated administrative discharge diagnosis codes and chief complaint text terms related to harmful algal bloom exposure (*6*). A total of 321 harmful algal bloom-associated ED visits were identified during January 1, 2017–December 31, 2019. An increase in harmful algal bloom–associated ED visits occurred during warmer months (June–October), consistent with seasonal fluctuations of blooms and recent publications (*6,7*). Although syndromic surveillance data are helpful for understanding harmful algal bloom–associated ED visits in the United States, exposures were documented infrequently with discharge diagnosis codes; 67% of harmful algal bloom–associated ED visits were identified through querying chief complaint text. Improving the documentation of harmful algal bloom exposures in medical records would further benefit future health studies.

NSSP is a collaboration among CDC, state, and local health departments, and academic and private sector partners which captures data electronically from EDs throughout the country. As of the end of the study period (December 2019), the national database represented approximately 70% of all ED visits in the United States. Data are queried by creating Boolean search terms of diagnostic codes and chief complaint text. Chief complaint text terms are also used to categorize visits into many broad, medically similar syndromes using prebuilt algorithms.

For the current analysis, a query was created that comprises main terms from the chief complaint (e.g., red tide, algae) along with discharge diagnostic codes associated with exposure to harmful algal blooms (*International Classification of Diseases, Tenth Revision, Clinical Modification* [ICD-CM-10]) codes and their corresponding Systematized Nomenclature of Medicine [SNOMED]* Clinical Terms codes). The final query was reviewed using the NSSP query development tool.† Records identified by this query are defined as harmful algal bloom-associated ED visits. To exclude ED visits associated with the ingestion of contaminated seafood, relevant keywords such as "shellfish" or "ciguatera poisoning" and corresponding ICD-CM-10 codes (e.g., ciguatera poisoning, ICD-CM-10 code T61.0), were omitted from the query. Basic demographic information for patients with harmful algal bloom–associated ED visits was summarized by frequency and percentage. The number of identified harmful algal bloom–associated ED visits during 2017–2019 was described by U.S. Department of Health and Human Services region and visualized using a time series graph. Because the number of facilities reporting to NSSP has increased since 2017, regional and time series comparisons were shown as a percentage of total ED visits within NSSP. The frequencies with which various syndrome categories§ were recorded during the harmful algal bloom-associated ED visits were examined. Variables were created to indicate whether an ED visit was related to neurologic, gastrointestinal, respiratory, or dermatologic conditions.¶ This activity was reviewed by

* http://www.snomed.org/snomed-ct/why-snomed-ct

† The NSSP Chief Complaint Query Validation data source contains chief complaint and discharge diagnosis codes only; to help protect anonymity, it does not include any demographic data. This data subset helps users to iteratively develop queries with inclusion and exclusion terms to capture only the records of interest. Some NSSP sites do not contribute data to this data source. The final query included the following ICD-10-CM codes: T65.82, toxic effect harmful algae and algae toxins; Z77.121, contact with and suspected exposure to harmful algae and algae toxins; SNOMED codes: 137512, 240914003, 10076437, 10076441, 402161005, 702986006, and 81034007; and main terms related to algae and red tide. *International Classification of Diseases, Ninth Edition* (ICD-9) codes were not included because ICD-10-CM codes for HAB exposure were implemented in October 2015 and were similar, but more descriptive than the ICD-9 codes for HAB exposure. Other terms related to HAB exposure, such as "cyanobacteria" and "hab," did not identify additional records and were not included in the final query. The final query did not include ICD-10-CM codes for HAB exposures through seafood or shellfish poisonings.

§ An automated algorithm codes standard symptom categories and subcategories based on text in the chief complaint.

¶ Neurologic conditions include altered mental status, such as dizziness, drowsiness, and muscle weakness; gastrointestinal conditions such as abdominal pain, diarrhea, gastrointestinal bleeding, loss of appetite, nausea, and vomiting; respiratory conditions such as acute bronchitis, chest congestion, difficulty breathing, sore throat, influenza-like illness, nasal congestion, otitis media, shortness of breath, upper respiratory infection, wheezing; and dermatologic conditions (e.g., rash).

CDC and was conducted consistent with applicable federal law and CDC policy.**

A total of 321 harmful algal bloom–associated ED visits were identified during January 1, 2017–December 31, 2019. Among these visits, 106 (33%) were identified through ICD-CM-10 codes only; the addition of chief complaint text key terms to the query identified an additional 215 visits. Harmful algal bloom–associated ED visits increased in the summer months (June–October) in all 3 years (Figure). A notable peak occurred in October 2018, corresponding with a large-scale red tide event in the Gulf of Mexico during August–November 2018; of the 197 ED visits occurring during July-November 2018, 73% occurred in Region 4 (southeastern United States).

Harmful algal bloom–associated ED visits occurred primarily among patients aged 18–44 years (37%) and 45–64 years (30%) (Table 1); the majority (59%) occurred among females. The largest number of harmful algal bloom–associated ED visits was identified in Region 4 (31.1%). The most frequent syndrome category was respiratory (41%), followed by gastrointestinal (14%), neurologic (10%), and dermatologic (8%) (Table 2).

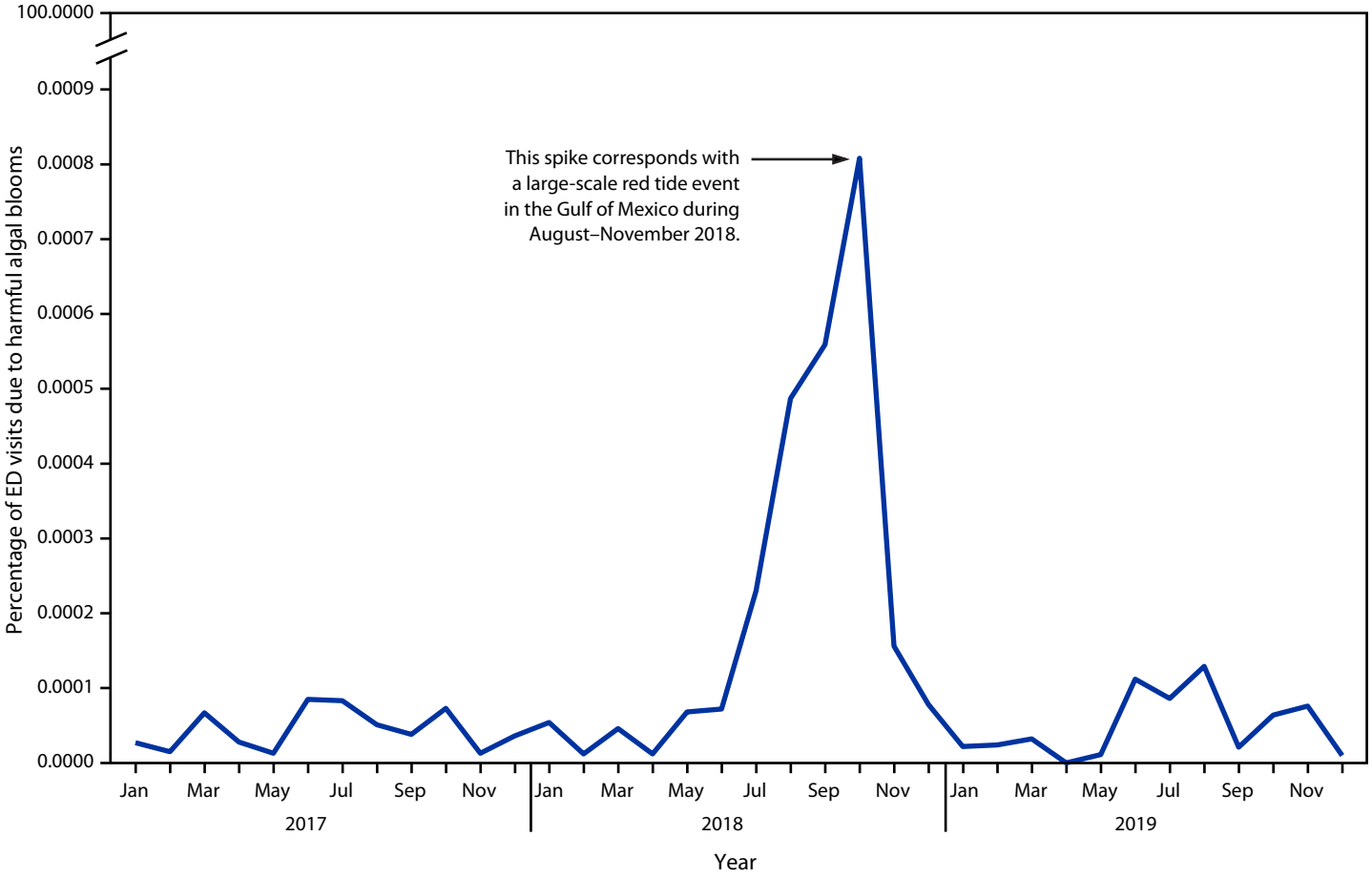
** 45 C.F.R. part 46.102(l)(2), 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

Discussion

This analysis identified approximately 300 harmful algal bloom–associated ED visits during 2017–2019. ED visits increased during the warmer months, consistent with seasonal patterns of harmful algal blooms in the environment, with a notable peak in 2018. Syndrome categories recorded for ED visits were consistent with harmful algal bloom exposures through inhalation (e.g., respiratory and neurologic), ingestion (e.g., gastrointestinal), or skin contact (e.g., dermatologic) (*5*).

Most ED visits were identified through the chief complaint text rather than through the use of ICD-10-CM codes. These

FIGURE. Harmful algal bloom exposure–associated emergency department visits among all emergency department visits, by month — National Syndromic Surveillance Program, United States, 2017–2019*



* Percentage of all emergency department visits in the National Syndromic Surveillance Program was utilized to account for the increasing number of facilities contributing data to the National Syndromic Surveillance Program.

TABLE 1. Demographic characteristics of patients with harmful algal bloom-associated emergency department visits (n = 321) — National Syndromic Surveillance Program, United States, 2017–2019

Characteristic	No. (%)
Age group (yrs)	
0–4	19 (5.9)
5–17	35 (10.9)
18–44	118 (36.8)
45–64	96 (29.9)
≥65	50 (15.6)
Unknown	3 (0.9)
Sex	
Female	190 (59.2)
Male	131 (40.8)
HHS Region*,†	
1	13 (9.7)
2	13 (4.9)
3	11 (4.1)
4	213 (31.1)
5	29 (6.6)
6	8 (4.1)
7	5 (5.3)
8	7 (12.9)
9	11 (7.6)
10	11 (13.7)

Abbreviation: HHS = U.S. Department of Health and Human Services.
* https://www.hhs.gov/about/agencies/iea/regional-offices/index.html
† Percentages for HHS regions are adjusted for the total number of emergency department visits during the time periods to account for the increasing number of facilities reporting to NSSP since 2017.

TABLE 2. Primary syndrome categories associated with harmful algal bloom exposure used among 321 harmful algal bloom-associated emergency department visits

Syndrome type	No. (%)*
Respiratory†	133 (41.4)
Gastrointestinal§	44 (13.7)
Neurologic¶	33 (10.3)
Dermatologic**	27 (8.4)

* Records could contain multiple syndromes. Percentages might not sum to 100% because of missing values or listings of other syndrome types that were not included for this analysis.
† Respiratory symptoms consist of acute bronchitis, chest congestion, cough, difficulty breathing, sore throat, influenza-like illness, nasal congestion, otitis media, shortness of breath, upper respiratory infection, or wheezing.
§ Gastrointestinal symptoms consist of abdominal pain, diarrhea, gastrointestinal bleeding, loss of appetite, nausea, or vomiting.
¶ Neurologic symptoms consist of altered mental status, dizziness, drowsiness, headache, or muscle weakness.
** Dermatologic symptoms consist only of rash.

results corroborate an earlier analysis using a commercial claims data set, which identified few records with harmful algal bloom exposure ICD-10-CM codes (*8*). Searching the chief complaint text in NSSP more than doubled the number of harmful algal bloom–associated visits, compared with the number that would have been identified by searching on ICD-10-CM codes only. The peak in ED visits during 2018 occurred primarily within Region 4, corresponding to a large-scale red tide event in the Gulf of Mexico that persisted during June 2018–November 2018 (*9*). The occurrence of this peak at the time of a red tide event might explain the higher frequency of chief complaints associated with respiratory symptoms because red tide has been linked to respiratory health outcomes (*2*,*3*). Presumably, these types of large-scale events might cause providers to ask patients about recent harmful algal bloom exposures or cause patients to mention them.

The NSSP query development tool made it possible to review a sample of the full chief complaint text without linking to other visit data, which helped to protect patient anonymity. Several chief complaints (six) used terms such as, "patient denies red tide exposure." The final query was adjusted to exclude these records; however, this finding implies that providers might have been asking patients if they had been exposed to red tide, or patients might have mentioned that they had not been on the beach or exposed to red tide before their ED visit. Increasing awareness so that more patients know to mention harmful algal bloom exposure and more physicians know to ask about harmful algal blooms would enhance understanding of harmful algal bloom–associated ED visits.

The findings in this report are subject to at least two limitations. First, some records might have been misclassified or miscoded. For example, the query development tool identified some records with a chief complaint that seemed unrelated to harmful algal bloom exposure (e.g., meningitis exposure or vaginal problems) despite the use of the Z77.121 harmful algal bloom exposure ICD-10-CM code. In addition, it is unknown what occurred during the ED visit between when the chief complaint was assigned at triage and when the final diagnosis was determined. Some patients might have described a harmful algal bloom exposure, but medical personnel might have ruled it out as the primary reason for diagnosis. Second, NSSP undercounts the number of harmful algal bloom–associated ED visits that resulted from environmental exposures because 1) only 70% of ED visits nationally are included within the data set, and 2) ICD-10-CM codes are from billing data and codes for harmful algal bloom exposures might not be included if they do not affect reimbursement. Despite these limitations, however, these analyses provide information of how often exposure to a harmful algal bloom is documented during ED visits through diagnostic codes and chief complaints.

These findings provide information about how harmful algal bloom exposure can be identified through syndromic surveillance ED visit data and potentially used to identify the extent of illness from harmful algal bloom exposure in the United States. As the frequency and geographic extent of harmful algal blooms increase, it is important for health care providers to discuss and document harmful algal bloom exposures and health effects during medical visits to ensure proper patient treatment and help patients understand how

Summary

What is already known about this topic?

Harmful algal and cyanobacterial blooms are large colonies of algae or cyanobacteria that can harm humans, animals, and the environment.

What is added by this report?

National syndromic surveillance data identified 321 emergency department visits related to harmful algal bloom exposure during 2017–2019. Frequency of these visits was highest during warmer months.

What are the implications for public health practice?

Syndromic surveillance data are useful for studying the extent of harmful algal bloom–associated illness. Increasing awareness so that more patients know to mention harmful algal bloom exposures and more physicians know to ask about them could improve documentation of health effects and enable further use of health records for health studies.

to prevent exposure in the future. As access to information from electronic medical records for research improves, better documentation of harmful bloom exposures and illnesses can help support a more accurate assessment of their acute public health impact. With better documentation, electronic health record systems with longitudinal data could potentially provide data for monitoring long-term health effects from these exposures, the extent of which are largely unknown.

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Multiple Variants of SARS-CoV-2 in a University Outbreak After Spring Break — Chicago, Illinois, March–May 2021

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To prevent transmission of SARS-CoV-2, the virus that causes COVID-19, colleges and universities have implemented multiple strategies including testing, isolation, quarantine, contact tracing, masking, and vaccination. In April 2021, the Chicago Department of Public Health (CDPH) was notified of a large cluster of students with COVID-19 at an urban university after spring break. A total of 158 cases of COVID-19 were diagnosed among undergraduate students during March 15–May 3, 2021; the majority (114; 72.2%) lived in on-campus dormitories. CDPH evaluated the role of travel and social connections, as well as the potential impact of SARS-CoV-2 variants, on transmission. Among 140 infected students who were interviewed, 89 (63.6%) reported recent travel outside Chicago during spring break, and 57 (40.7%) reported indoor social exposures. At the time of the outbreak, undergraduate-aged persons were largely ineligible for vaccination in Chicago; only three of the students with COVID-19 (1.9%) were fully vaccinated. Whole genome sequencing (WGS) of 104 specimens revealed multiple distinct SARS-CoV-2 lineages, suggesting several nearly simultaneous introductions. Most specimens (66; 63.5%) were B.1.1.222, a lineage not widely detected in Chicago before or after this outbreak. These results demonstrate the potential for COVID-19 outbreaks on university campuses after widespread student travel during breaks, at the beginning of new school terms, and when students participate in indoor social gatherings. To prevent SARS-CoV-2 transmission, colleges and universities should encourage COVID-19 vaccination; discourage unvaccinated students from travel, including during university breaks; implement serial COVID-19 screening among unvaccinated persons after university breaks; encourage masking; and implement universal serial testing for students based on community transmission levels.

University Prevention Measures

In spring 2021, approximately 2,100 students were living on the campus of an urban university in Chicago, Illinois. In response to the COVID-19 pandemic, the university implemented numerous prevention strategies.[†] Students living on- and off-campus were required to report positive SARS-CoV-2 test results to the university. Students living in the dormitories were required to receive testing for SARS-CoV-2 every week (serial screening); testing was offered for free by the university.[§] During March 20–29, 2021, university activities, including classes, paused for spring break, and the university recommended that students avoid all travel during this period; dormitories remained open. After the break, students who lived on campus were advised to stay in their dormitories for 1 week, and all classes were held remotely.[¶] In addition to regular serial screening, students who lived in dormitories were required to receive testing for SARS-CoV-2 before resuming in-person learning.

Investigation and Response

On April 7, 2021, the university notified CDPH of 37 students with positive SARS-CoV-2 test results detected through serial screening conducted during March 29–April 5, 2021. In response to this cluster of COVID-19 cases, the university implemented a stay-at-home order for students living on campus (requiring students to stay in their dormitories), held all classes remotely, and prohibited gatherings. During the stay-at-home order, the university modified the screening schedule to require testing for students living on campus twice during the first 10 days of the order. In consultation with CDPH, after additional testing found few cases, the university lifted the order after 14 days.

A case was defined as receipt of a positive SARS-CoV-2 test result by an undergraduate student living on or near the

[*] These authors contributed equally to this report.

[†] For the 2020–21 academic year, dormitory capacities were reduced, bedrooms were single-occupancy, and numerous changes to physical infrastructure were made. All students were required to sign a health agreement and pledge to avoid social gatherings. The university maintained separate housing space for students with positive SARS-CoV-2 test results; these students were required to follow isolation procedures.

[§] Real-time reverse transcription–polymerase chain reaction testing was performed on anterior nasal swab specimens collected by trained medical assistants.

[¶] Students were permitted to leave their dormitories to take walks, buy food, or pick up meals from the dining halls.

university campus during March 15–May 18, 2021.** For all students with COVID-19, the university provided information on residence (on-campus dormitory or off-campus), age, gender, and positive specimen collection date. CDPH conducted interviews to collect information on demographic characteristics, clinical signs or symptoms, travel history, social activities, attendance at social gatherings, and close contacts. Diagnostic testing history and results were extracted from state surveillance and vaccination records from immunization registry systems. Available specimens were sequenced and assigned a lineage.†† Similar sequences (differing by fewer than five nucleotides) were assumed to represent a single viral introduction.§§ To identify possible geographic sources of importations, outbreak lineages were compared with all contemporaneous sequences of the same lineage available on the Global Initiative on Sharing All Influenza Data (GISAID) platform. Descriptive and social network analyses were completed using R (version 4.1.0; R Foundation) and MicrobeTrace (version 0.7.0; CDC), respectively. This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.¶¶

A total of 158 COVID-19 cases were identified among undergraduate students (Figure 1), including 76 (48.1%) in women; the median age of students with COVID-19 was 19.4 years (interquartile range = 18.9–20.3 years) (Table). A total of 114 (72.2%) students with COVID-19 lived in dormitories (Supplementary Table, https://stacks.cdc.gov/view/cdc/109260); the rest lived off-campus but near the university.

Among the 158 students with COVID-19, 140 (88.6%) were interviewed, among whom 127 (90.7%) reported at least one COVID-19 symptom (Table). Two were evaluated in an emergency department after diagnosis; no infected student was hospitalized or died. One student with COVID-19 had a previous laboratory-confirmed diagnosis of COVID-19 >90 days before the infection was identified during the investigation period. Among all interviewed students with COVID-19, 93 (66.4%) were unvaccinated, and 43 (30.7%) were partially vaccinated (i.e., received 1 dose of a 2-dose COVID-19 vaccine

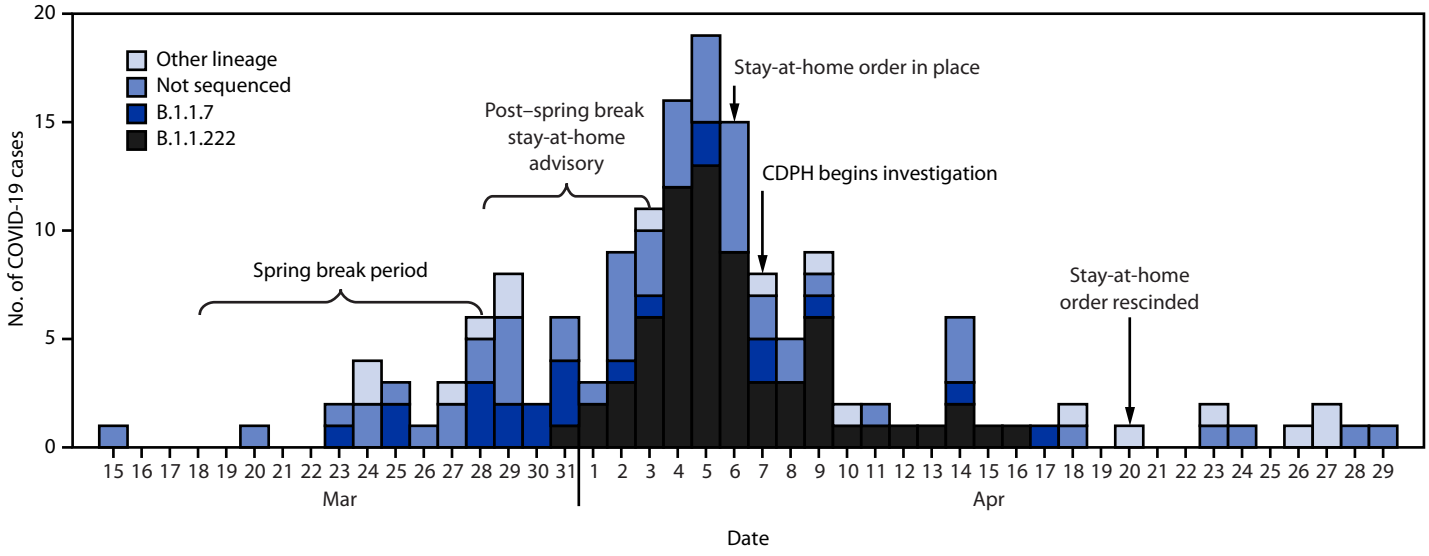
** The investigation period began 2 weeks before the start of spring break and ended 2 weeks after the last positive SARS-CoV-2 test result for an undergraduate student. Any positive test result among undergraduate students who lived on campus or in Chicago was evaluated for inclusion. Graduate students and staff members with COVID-19 were not included in this outbreak case definition. Assessment of cases among these populations indicated very limited or no interaction with undergraduate students who lived on or very near campus.

†† Available SARS-CoV-2 positive specimens were submitted to CDPH's Regional Innovative Public Health Laboratory for whole genome sequencing using the Swift Amplicon SARS-CoV-2 Panel (Swift Biosciences) and deep sequencing on an Illumina instrument. Viral lineages were assigned using the Phylogenetic Assignment of Named Global Outbreak Lineages (PANGOLIN) tool (version v3.0.2; Rambaut Laboratory). Nucleotide differences were assessed with IQ-TREE.

§§ Among the specimens of B.1.1.222 lineage, the majority of sequences were genetically similar (within two nucleotides). Although there is no standard genomic definition of sequences linked by transmission, this level of similarity, together with the lack of detection of similar contemporaneous specimens in Chicago, is likely consistent with one viral introduction.

¶¶ 45 C.F.R. part 46.102(l)(2), 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

FIGURE 1. Date of onset* and viral lineage among undergraduate students with COVID-19 (n = 158) — Chicago, Illinois, March–April 2021



Abbreviation: CDPH = Chicago Department of Public Health.

* Or date of specimen collection for asymptomatic and presymptomatic persons. One specimen was collected and tested in May, but the date of symptom onset for the student was in April.

TABLE. Characteristics of undergraduate students with COVID-19 (n = 158) — Chicago, Illinois, March–May 2021

Characteristic (no. with available information)	No. (%)
Demographics (158)	
Female	76 (48.1)
Median age, yrs (IQR)	19.4 (18.9–20.2)
Residence (158)	
Dormitory A	35 (22.2)
Dormitory B	32 (20.3)
Dormitory C	31 (19.6)
Dormitory D	7 (4.4)
Dormitory E	5 (3.2)
Dormitory F	4 (2.5)
Off-campus	44 (27.8)
Previous COVID-19 diagnosis >90 days before test date*	1 (0.6)
Interviewed (140)	
Symptomatic	127 (90.7)
Provided at least one contact name	88 (62.9)
Reported indoor social exposure	57 (40.7)
Reported party exposure	3 (2.1)
Reported travel	89 (63.6)
Vaccination (140)	
Reported not vaccinated	93 (66.4)
Reported partially vaccinated	43 (30.7)
Reported fully vaccinated†	3 (2.1)
Travel destinations (89)	
Florida	20 (22.5)
California	11 (12.4)
New York	11 (12.4)
Colorado	5 (5.6)
Within Illinois	3 (3.4)
Other U.S. states	32 (36.0)
International	6 (6.7)
Purpose of travel (89)	
Vacation away from home	43 (48.3)
Visiting home	23 (25.8)
Moving to campus	3 (3.4)
Unknown	20 (22.5)
Lineage (104)	
B.1.1.222	66 (63.5)
B.1.1.7	22 (21.2)
P.1	9 (8.7)
B.1.526	3 (2.9)
B.1.526.1	1 (1.0)
B.1.526.2	1 (1.0)
B.1.1	1 (1.0)
B.1.429	1 (1.0)

Abbreviation: IQR = interquartile range.
* Previous diagnosis of COVID-19 was laboratory-confirmed.
† Vaccination information was collected by self-report and verified, when possible, with the state immunization registry. The three persons who reported full vaccination could not be verified because vaccinations were administered out of state (two) and as part of a clinical trial (one).

series or completed a vaccine series <14 days before diagnosis). Three (1.9%) students with COVID-19 reported being fully vaccinated; two of these students experienced symptoms.

The majority (88; 62.9%) of students with COVID-19 provided the name of at least one other student with COVID-19 with whom they had had contact in the 2 weeks preceding symptom onset or test date. Fifty-seven (40.7%) students with COVID-19 described unmasked indoor exposures to other students at small gatherings, meals, or while studying. Although the university was aware of several large gatherings, only three infected students (2.1%) reported having attended a party. A network diagram was constructed to show social connections, residence, travel, and viral lineage (Figure 2). Based on interview data, 25 groups of socially connected students with COVID-19 (clusters) were identified; the median cluster size was two, and the maximum was 45. Several social groups included multiple dormitories.

Overall, 89 (63.6%) interviewed students with COVID-19 reported travel outside Chicago during spring break. Fourteen students traveled with at least one other infected student in five different travel groups. Destinations included seven different countries and 23 U.S. states; the most commonly visited states were California, Colorado, Florida, and New York (Table). The most commonly reported reason for travel was vacation (43; 48.3%).

Residual specimens were available for 120 (75.9%) infected students, 104 (86.7%) of which were successfully sequenced. Sequences were assigned nine different lineages, mostly B.1.1.222 (66; 63.5%), followed by B.1.1.7 (Alpha) (22; 21.2%) (Table) (Supplementary Figure, https://stacks.cdc.gov/view/cdc/109259). All B.1.1.222 sequences differed by fewer than five nucleotides and likely represent a single source introduction. When compared with sequences in GISAID, the B.1.1.222 sequences in this outbreak were most closely related to specimens from California. Eight of the 66 students (12.1%) infected with the SARS-CoV-2 B.1.1.222 lineage had a history of travel to California. In Dormitory A, 25 of 35 (71.4%)

Summary

What is already known about this topic?

SARS-CoV-2 transmission on college and university campuses can occur when unvaccinated students return to campus after travel or attend social gatherings.

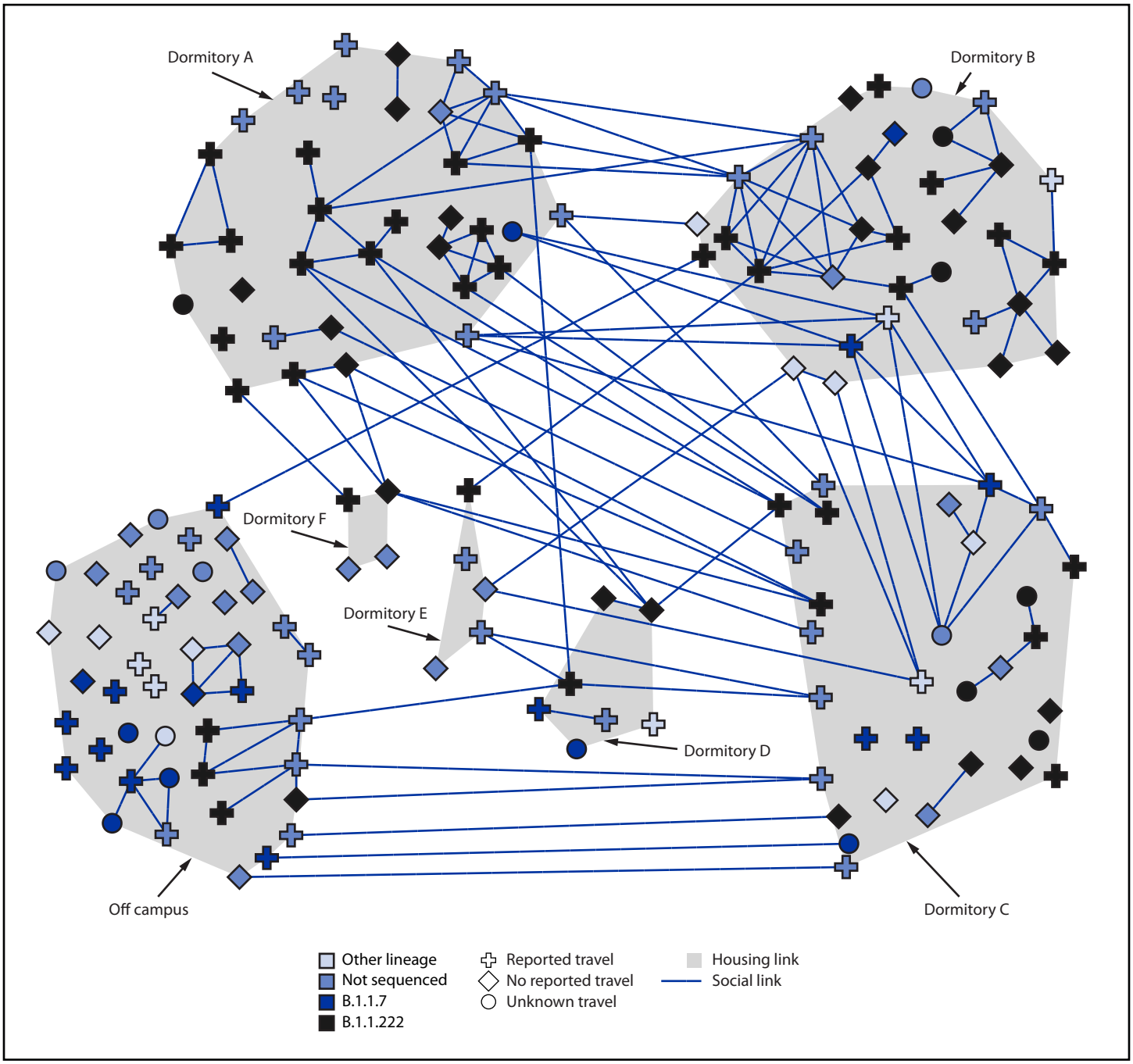
What is added by this report?

After spring break 2021, COVID-19 cases increased rapidly at a Chicago university despite mitigation measures. Interviews indicated that the majority of cases occurred in unvaccinated persons with a history of recent travel. Sequencing corroborated multiple introductions to campus and demonstrated that even a single importation can result in many cases.

What are the implications for public health practice?

To mitigate SARS-CoV-2 transmission, colleges and universities can encourage COVID-19 vaccination; discourage unvaccinated students from traveling, including during university breaks; implement serial screening after university breaks; test based on community transmission; and encourage masking.

FIGURE 2. Social networks among undergraduate students with COVID-19 (n = 158), by residence and viral lineage — Chicago, Illinois, March–May 2021



specimens from infected students were sequenced, and 24 of 25 (96.0%) were confirmed as the B.1.1.222 lineage (Figure 2). Among B.1.1.7 (Alpha) specimens, 10 groups of sequences differed by five or more nucleotides, indicating multiple separate importations; groups ranged in size from one to five students. B.1.1.7 was circulating widely in Chicago and elsewhere in the United States at the time of this outbreak. Among the students who traveled together, some travel groups had the same lineage (though students reported additional close contact on campus), while other groups included several lineages. Specimens from all three fully vaccinated students were available; however, only one (from a symptomatic student) was successfully sequenced as a B.1.1.222 lineage.

Discussion

Previous reports have described outbreaks of COVID-19 among university students with complex social networks and social exposures (*1*–*5*). In this outbreak, 158 cases of COVID-19 were identified after many unvaccinated students traveled during a university break, despite university policies advising against travel. Subsequent on-campus gatherings led to further transmission within and across social networks, including between dormitories. Notably, this outbreak occurred immediately before expansion of eligibility for vaccination in Chicago; undergraduate-aged persons were largely ineligible for vaccination before April 19, 2021.***

WGS identified several lineages and multiple distinct introductions of SARS-CoV-2 that were possibly driven by student travel. Phylogenetic analyses illustrated gaps in the social network; for example, several students with no reported social connections were infected with nearly identical strains of B.1.1.222, a lineage not widely identified in Chicago before or after this outbreak.††† Transmission likely occurred among students without known social connections or through undetected cases associated with the outbreak, although these links cannot be confirmed with available case interview data.

The findings in this report are subject to at least four limitations. First, some students with COVID-19 refused interviews, omitted critical details, or provided false and conflicting information, such as denying travel when other students indicated that they had traveled together. This reticence limited the ability to thoroughly assess social networks and transmission chains. Second, serial screening was mandatory only for students living on-campus; students living off-campus might have had COVID-19 but did not receive testing during the outbreak period. Given potentially undiagnosed infections, the magnitude of the outbreak might have been greater than described. Third, not all SARS-CoV-2 specimens could be sequenced; additional viral introductions or transmission chains might have been missed. Finally, because publicly available sequence data include only a subset of all viruses, the source of viral introductions could not be definitively identified.

These findings support existing CDC recommendations for the control of COVID-19 in colleges and universities; these recommendations are especially important given the rapid spread of the B.1.617.2 (Delta) variant of concern.§§§ Serial testing successfully detected an outbreak among university undergraduates; isolation of students with COVID-19, contact tracing, and university-wide prevention measures contributed to reductions in transmission. Nevertheless, unvaccinated persons traveling during a university break and subsequent socializing among students resulted in multiple clusters of COVID-19 before vaccines were widely offered to undergraduate-aged persons in Chicago. Vaccination is the leading prevention strategy to protect persons from COVID-19, and colleges and universities can benefit from encouraging vaccination for all students, faculty, and staff members. In settings where not everyone is fully vaccinated or where students have contact with community members who are not fully vaccinated, colleges and universities can encourage unvaccinated students to refrain from travel; implement serial screening testing for unvaccinated students, faculty, and staff members after university breaks; test for SARS-CoV-2 based on community transmission levels; encourage masking indoors; and make free, voluntary testing readily available, including for fully vaccinated persons who are experiencing COVID-19 symptoms.¶¶¶

*** https://www.chicago.gov/city/en/sites/covid19-vaccine/home/vaccine-distribution-phases.html

††† Only one other B.1.1.222 sequence from a specimen collected in 2021 in Chicago was available on GISAID (out of 674 Chicago sequences from 2021 not associated with this outbreak). This sequence, from a specimen collected 3 months before this outbreak, differed by more than five nucleotides from the largely homogenous sequences observed in this outbreak.

§§§ https://www.cdc.gov/coronavirus/2019-ncov/community/colleges-universities/considerations.html

¶¶¶ https://www.cdc.gov/coronavirus/2019-ncov/community/colleges-universities/considerations.html#section3

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Screening Programs for SARS-CoV-2 Infections on a University Campus — Austin, Texas, September 30–November 30, 2020

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Colleges and universities in the United States have relied on various measures during the COVID-19 pandemic to prevent transmission of SARS-CoV-2, the virus that causes COVID-19, including implementing testing programs (*1*–*3*). These programs have permitted a safer return to campus for students by identifying infected persons and temporarily isolating them from the campus population (*2*,*3*). The University of Texas at Austin (UT Austin) implemented COVID-19 prevention measures in Fall 2020* including the following testing programs: clinic-based diagnostic testing, voluntary community screening, and targeted screening (testing of specific student populations in situations of increased transmission risk). During September 30–November 30, 2020, UT Austin students participated in tests for SARS-CoV-2, which resulted in the detection of 401 unique student cases of COVID-19 from among 32,401 tests conducted.† Among students who participated in one targeted screening program for students attending campus events, 18 (37.5%) of 48 infected students were asymptomatic at the time of their positive test result compared with 45 (23%) of 195 students identified through community testing and nine (5.8%) of 158 students identified through clinic-based testing. Targeted screening also identified a different population of students than did clinic-based and community testing programs. Infected students tested through targeted screening were more likely to be non-Hispanic White persons (chi square = 20.42; p<0.03), less likely to engage in public health measures, and more likely to have had interactions in settings where the risk for SARS-CoV-2 transmission is higher, such as restaurants, gyms, and residence halls. In addition to clinic-based SARS-CoV-2 testing at colleges and universities, complementary testing programs such as community and targeted screening might enhance efforts to identify and control SARS-CoV-2 transmission, especially among asymptomatic persons and disproportionately affected populations that might not otherwise be reached.

During September 30–November 30, 2020, UT Austin employed the following SARS-CoV-2 testing programs: 1) clinic-based diagnostic testing administered by University Health Services for persons who were symptomatic or reported exposure to SARS-CoV-2 (clinic-based testing); 2) Proactive Community Testing, which involved voluntary screening of asymptomatic persons offered at several fixed or rotating sites on-and-off campus (community testing); and 3) targeted screening of specific student populations in situations of increased transmission risk. One targeted screening program focused on Big Ticket holders, students with season tickets to athletic events. These events are large gatherings that might involve several SARS-CoV-2 infection risk factors such as several hours of possible exposure, the potential for crowding, and behaviors such as singing and shouting.§ Students were tested up to 3 days before each event. Either a negative test result or proof of previous SARS-CoV-2 infection 14–90 days before the event was required for entry. Community testing and targeted screening programs were provided to students at no cost; clinic-based tests were billed to students' insurance. Cases were identified through clinic-based testing using SARS-CoV-2 nucleic acid amplification tests (NAATs), including reverse transcription–polymerase chain reaction (RT-PCR) or isothermal NAAT (ID NOW [Abbott] or Aptima SARS-CoV-2 Assay [Hologic]). Community testing used a Clinical Laboratory Improvement Amendments (CLIA)-certified RT-PCR test performed at a UT laboratory, and testing for Big Ticket holders used an antigen test (Sofia SARS Antigen Fluorescent Immunoassay [Quidel Corporation])¶ or UT's CLIA-certified RT-PCR test. Test results were reported to Dell Medical School at UT Austin, which was delegated by Austin Public Health to conduct contact tracing. Contact tracers interviewed infected persons to identify close contacts** during their infectious period,†† and collected exposure details, including dates, proximity, location, duration of exposure, and mask use.

* https://protect.utexas.edu/

† A COVID-19 case was defined as a positive SARS-CoV-2 nucleic acid amplification test or antigen test result.

§ https://www.cdc.gov/coronavirus/2019-ncov/community/large-events/considerations-for-events-gatherings.html

¶ https://www.fda.gov/media/137884/download

** Close contact was defined as being within 6 ft of a person with laboratory-confirmed or probable COVID-19 infection for a cumulative total of ≥15 minutes during a 24-hour period; or having physical contact with; or sharing living spaces such as bedrooms, bathrooms, or kitchens. https://www.cdc.gov/coronavirus/2019-ncov/php/contact-tracing/contact-tracing-plan/appendix.html

†† The infectious period was estimated to begin 2 days before symptom onset and end ≥10 days after symptom onset or positive test result, as long as other symptoms (except loss of taste or smell) were improving and the patient had been fever-free for 24 hours without fever-reducing medication, according to CDC guidance. https://www.cdc.gov/coronavirus/2019-ncov/php/contact-tracing/contact-tracing-plan/investigating-covid-19-case.html

Characteristics, symptom status, isolation practices, and case investigation outcomes among students with COVID-19 were assessed; statistical comparisons among cases identified by the different testing programs were performed using chi square tests or one-way ANOVA in Python (version 3.7.9; Python Software Foundation) using the SciPy statistical package (version 1.5.4; Python Software Foundation); p values <0.05 were considered statistically significant. This study was reviewed by a UT Institutional Review Board and deemed to not be human subjects research. This activity was reviewed by CDC and conducted consistent with applicable federal law and CDC policy.[§§]

Among 32,401 tests of UT Austin students, 401 unique COVID-19 cases were identified (Table 1); 3,044 tests were done through clinic-based testing, 25,042 through community testing, and 4,314 through testing of Big Ticket holders. Among one targeted screening program for Big Ticket holders, 75% of infected students self-identified as non-Hispanic White persons, compared with 48.7% of infected students detected by community testing and 58.9% of infected students detected by clinic-based testing (chi square = 20.42; p<0.03). The proportion of non-Hispanic White students identified by each of the three testing programs was higher than that reported for the overall UT Austin student population[¶¶] (38.9%; chi square = 177; p<0.001). UT contact tracers interviewed 85.5% of all infected persons. Among Big Ticket holders, 75% of infected persons were interviewed, 20.8% were unreachable by phone, and 4.2% stated they were unwilling to

[§§] 45 C.F.R. part 46, 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

[¶¶] https://www.utexas.edu/about/facts-and-figures

TABLE 1. Demographic characteristics, symptom status, isolation practices, and case investigation outcomes among students with COVID-19, by testing program — University of Texas at Austin, September 30–November 30, 2020

Characteristic (no. with available information)	No. (%)			
		Testing program		
	Total	Big Ticket holder*	Community	Clinic-based
Students in testing programs	**401 (100)**	48 (12.0)	195 (48.6)	158 (39.4)
Age, yrs, median (range)	**20 (18–29)**	19.5 (18–22)	20 (18–28)	21 (18–29)
Sex (401)				
Male	**187 (46.6)**	19 (39.6)	86 (44.1)	82 (51.9)
Female	**213 (53.1)**	29 (60.4)	108 (55.4)	76 (48.1)
Unknown	**1 (0.2)**	0 (—)	1 (0.5)	0 (—)
Race/Ethnicity (401)				
White, non-Hispanic	**224 (55.9)**	36 (75.0)	95 (48.7)	93 (58.9)
Black, non-Hispanic	**14 (3.5)**	0 (—)	7 (3.6)	7 (4.4)
Asian, non-Hispanic	**37 (9.2)**	2 (4.2)	21 (10.8)	14 (8.9)
White, Hispanic	**89 (22.2)**	5 (10.4)	56 (28.7)	28 (17.7)
Multiracial	**8 (2.0)**	0 (—)	3 (1.5)	5 (3.2)
Unknown	**29 (7.2)**	5 (10.4)	13 (6.7)	11 (6.9)
Outcomes of COVID-19 case investigations (401)				
Interviewed	**343 (85.5)**	36 (75.0)	171 (87.7)	136 (86.1)
Unable to interview	**53 (13.2)**	10 (20.8)	22 (11.3)	21 (13.3)
Unwilling to participate	**5 (1.2)**	2 (4.2)	2 (1.0)	1 (0.6)
Symptom status				
Symptomatic	**284 (70.8)**	22 (45.8)	129 (66.2)	133 (84.2)
Asymptomatic	**72 (18.0)**	18 (37.5)	45 (23.1)	9 (5.7)
Unknown	**45 (11.2)**	8 (16.7)	21 (10.7)	16 (10.1)
Patient isolation (343)[†]				
Yes	**317 (92.4)**	29 (80.6)	156 (91.2)	132 (97.1)
No	**23 (6.7)**	5 (13.9)	14 (8.2)	4 (2.9)
Unknown	**3 (0.9)**	2 (5.6)	1 (0.6)	0 (—)
Specimen collection relative to symptom onset[§] (274)				
Before symptom onset	**28 (10.2)**	3 (15.0)	18 (14.2)	7 (5.5)
On or after symptom onset	**246 (89.8)**	17 (85.0)	109 (85.8)	120 (94.5)
Start of isolation relative to symptom onset[§] (274)				
Before symptom onset	**42 (15.3)**	0 (—)	15 (11.8)	27 (21.3)
On or after symptom onset	**203 (74.1)**	13 (65.0)	98 (77.2)	92 (72.4)
Unknown	**29 (10.6)**	7 (35.0)	14 (11.0)	8 (6.3)

* Screening targeted to students who held season tickets to athletic events.
† Population limited to persons who were interviewed.
§ Population limited to persons who were interviewed and symptomatic.

participate in the interview, a larger proportion of refusals than for community testing (1.0%) and clinic-based testing (0.6%).

Approximately 38% of cases among Big Ticket holders occurred in persons who were asymptomatic at the time of their positive test results, compared with 23% identified through community testing and 6% through clinic-based testing (chi square = 35; p<0.001). Higher proportions of infected students from the Big Ticket and community testing programs were tested before symptom onset (15.0% and 14.2%, respectively) compared with clinic-based testing (5.5%); however, these differences were not statistically significant. Infected persons detected through testing of Big Ticket holders were less likely to have isolated after receiving a positive result (80%) than were those identified through community (91.2%) and clinic-based testing (97.1%).

Among 195 cases detected through community testing and 48 through testing of Big Ticket holders, 120 (61.5%) and 35 (72.9%) persons, respectively had no previous engagement with community testing (Table 2). Among 40 asymptomatic infected persons who had no previous community testing history, the testing program for Big Ticket holders identified a higher proportion of asymptomatic cases than did community testing (31.4% versus 24.2%; chi square = 7.53; p = 0.02).

A similar average number of close contacts was reported by infected persons identified from testing of Big Ticket holders (2.6 per person), community testing (3.1), and clinic-based testing (2.7) (p = 0.5). The most frequently reported exposure location among all testing programs was household (44%), defined as a shared living space (including a shared room or suite in a residence hall) (Table 3). The second most common exposure location identified through community and clinic-based testing was private residence or apartment visits (24% and 29%, respectively). In contrast, restaurants (22%) and residence halls (16%) were the next most common exposure locations among infected persons identified through testing for Big Ticket holders. These persons also reported a higher proportion of exposures in fitness or recreational facilities (6%) than did persons identified through community testing (3%) and clinic-based testing (1%), and a lower proportion of exposures outdoors (2% versus 13% and 6%, respectively; chi square = 145; p<0.001). Across all programs, most exposures were characterized by one or both students not wearing

TABLE 2. Symptom status* of student COVID-19 cases detected by community testing and testing for Big Ticket holders,† stratified by previous history with community testing — University of Texas at Austin, September 30–November 30, 2020

	No. (%)				
		History of community testing			
		No n = 155		Yes§ n = 88	
Symptom status	Total N = 243	Community n = 120	Big Ticket holder¶ n = 35	Community n = 75	Big Ticket holder n = 13
Asymptomatic	**63 (25.9)**	29 (24.2)	11 (31.4)	16 (21.3)	7 (53.8)
Symptomatic	**151 (62.1)**	76 (63.3)	17 (48.6)	53 (70.7)	5 (38.5)
Unknown	**29 (11.9)**	15 (12.5)	7 (20.0)	6 (8.0)	1 (7.7)

* Symptom status reported at time of case investigation.
† Excluding cases detected by the University Health Services clinic-based testing.
§ Infected persons had at least one COVID-19 test via community testing at any time before their positive result and during the study period.
¶ Students who held season tickets to athletic events.

TABLE 3. Location of exposure* among persons with COVID-19† and their contacts, by testing program — University of Texas at Austin, September 30–November 30, 2020

		Testing program, no. (%)		
Location	Total N = 1,147	Big Ticket holder§ n = 123	Community n = 603	Clinic-based n = 421
Household	**502 (44)**	42 (34)	250 (41)	210 (50)
Restaurant	**74 (6)**	27 (22)	34 (6)	13 (3)
Residence hall visit	**53 (5)**	20 (16)	25 (4)	8 (2)
Private residence visit	**292 (25)**	17 (14)	145 (24)	130 (31)
Fitness or recreational facility	**32 (3)**	7 (6)	20 (3)	5 (1)
Outdoor	**105 (9)**	2 (2)	77 (13)	26 (6)
Other	**89 (8)**	8 (7)	52 (9)	29 (7)

* If an infected person and a close contact interacted in multiple locations, contact tracers chose the most likely transmission site based on duration, proximity, ventilation, and mask use.
† Population limited to persons who were interviewed and named close contacts.
§ Students who held season tickets to athletic events.

a mask (91.4% of Big Ticket holders and 87.9% of those who received community and clinic-based testing) (chi square = 1.1; p = 0.3). Contact tracers provided counseling to both infected persons and close contacts on appropriate mask use to prevent future exposures or reinfection.

Discussion

Clinic-based diagnostic testing is a valuable tool to detect SARS-CoV-2 infection, particularly among symptomatic persons; however, complementary testing programs might enhance case detection (*4*). At UT Austin, one targeted screening program (conducted before vaccine availability) that tested Big Ticket holders identified a significantly higher proportion of asymptomatic persons than did clinic-based diagnostic testing at University Health Services (as expected), and voluntary screening through Proactive Community Testing. This targeted testing program resulted in the identification of potential asymptomatic spreaders, who might not have been detected through clinic-based or community testing (*5*).

Targeted screening of Big Ticket holders identified a different population from those identified by community and clinic-based testing: students who were predominantly non-Hispanic White and less likely to participate in voluntary public health prevention strategies including community testing, early isolation, and contact tracing. These Big Ticket holders also had more exposures in restaurants, a documented risk factor for SARS-CoV-2 infection (*6*), and in fitness or recreational facilities, locations of several large outbreaks (*7*). They also interacted more within residence halls, which include shared facilities and social areas; risks for transmission in these settings might be similar to those experienced in long-term care facilities (*1*,*8*,*9*).

The findings of this study are subject to at least six limitations. First, this study analyzed only one targeted testing program among students aged 18–29 years. Assessment of other targeted programs to include a broader age range might alter these findings. Second, both antigen tests and NAATs were used in testing of Big Ticket holders with different turnaround times for results (<2 hours for antigen tests and 24–48 hours for NAATs), which might have affected infected persons' isolation timing and number of close contacts during their infectious period. Differences in NAAT and antigen test sensitivity might have also affected case ascertainment, with antigen tests potentially missing contagious persons and NAAT potentially detecting persons no longer infectious (*10*). Antigen tests were not confirmed with NAATs, because rapid results were required to exclude potentially infectious persons from next-day events. Third, symptom status was self-reported and recorded at the time of the interview; therefore, the number of asymptomatic cases could have been overestimated. However, targeted screening would have still succeeded in identifying presymptomatic cases. Fourth, symptoms caused by allergies, stress, or other infectious diseases might have been incorrectly attributed to COVID-19, inflating the number of symptomatic cases, particularly among those from clinic-based testing. Fifth, whether symptoms that started the day of the test began before or after the test is not known, which might underestimate the proportion of students who were tested before symptom onset. Finally, the higher proportion of infected Big Ticket holders who were unavailable or unwilling to participate in contact tracing compared with the other testing program groups, might have affected comparisons of symptom status, isolation, and exposures to close contacts.

Screening tests are an important part of risk-reduction strategies on college and university campuses and in other congregate settings. Targeted testing in this university effort facilitated reaching and identifying infected persons who might not have been detected through other testing measures. Therefore, targeted testing might be used as a complement to diagnostic and voluntary community screening measures on college and university campuses, particularly in high-risk or large gatherings such as university athletic events or graduation ceremonies. However, if antigen tests are used for asymptomatic screening, confirmatory NAATs of positive results should be considered if the likelihood of SARS-CoV-2 infection is low, such as if the person has no known exposure (*10*). Further research on targeted testing in other potential high-risk settings such as residence halls is warranted, especially if a large proportion of these persons are unvaccinated, or as variants of SARS-CoV-2 emerge.

Summary

What is already known about this topic?

University testing programs have permitted a safer return of students to campus by identifying persons with COVID-19 and temporarily isolating them from the campus population.

What is added by this report?

Targeted screening identified 48 cases of COVID-19 during September–November 2020, 18 (38%) of which were in asymptomatic persons. This population of infected students was demographically different from those identified through other testing programs, more risk-tolerant, and less willing to participate in public health prevention activities.

What are the implications for public health practice?

In addition to clinic-based diagnostic SARS-CoV-2 testing at colleges and universities, a complementary strategy of community and targeted screening programs might enhance efforts to identify and control transmission of COVID-19.

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COVID-19 Vaccination Coverage Among Adolescents Aged 12–17 Years — United States, December 14, 2020–July 31, 2021

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Although severe COVID-19 illness and hospitalization are more common among adults, these outcomes can occur in adolescents (*1*). Nearly one third of adolescents aged 12–17 years hospitalized with COVID-19 during March 2020–April 2021 required intensive care, and 5% of those hospitalized required endotracheal intubation and mechanical ventilation (*2*). On December 11, 2020, the Food and Drug Administration (FDA) issued Emergency Use Authorization (EUA) of the Pfizer-BioNTech COVID-19 vaccine for adolescents aged 16–17 years; on May 10, 2021, the EUA was expanded to include adolescents aged 12–15 years; and on August 23, 2021, FDA granted approval of the vaccine for persons aged ≥16 years. To assess progress in adolescent COVID-19 vaccination in the United States, CDC assessed coverage with ≥1 dose* and completion of the 2-dose vaccination series† among adolescents aged 12–17 years using vaccine administration data for 49 U.S. states (all except Idaho) and the District of Columbia (DC) during December 14, 2020–July 31, 2021. As of July 31, 2021, COVID-19 vaccination coverage among U.S. adolescents aged 12–17 years was 42.4% for ≥1 dose and 31.9% for series completion. Vaccination coverage with ≥1 dose varied by state (range = 20.2% [Mississippi] to 70.1% [Vermont]) and for series completion (range = 10.7% [Mississippi] to 60.3% [Vermont]). By age group, 36.0%, 40.9%, and 50.6% of adolescents aged 12–13, 14–15, and 16–17 years, respectively, received ≥1 dose; 25.4%, 30.5%, and 40.3%, respectively, completed the vaccine series. Improving vaccination coverage and implementing COVID-19 prevention strategies are crucial to reduce COVID-19–associated morbidity and mortality among adolescents and to facilitate safer reopening of schools for in-person learning.

Data on COVID-19 vaccine administration in the United States are reported to CDC by jurisdictions, pharmacies, and federal entities through immunization information systems (IISs),§ the Vaccine Administration Management System (VAMS),¶ or direct data submission.** Adolescents aged 12–17 years with valid residence in one of 49 states or DC who received ≥1 dose of a COVID-19 vaccine during December 14, 2020–July 31, 2021, and whose data were reported to CDC by August 11, 2021, were included in this analysis.†† COVID-19 vaccine doses administered to persons residing in Idaho were excluded because the state has data-sharing restrictions on information reported to CDC.

Receipt of ≥1 COVID-19 vaccine dose and series completion among adolescents aged 12–17 years was calculated overall and stratified by age (12–13, 14–15, and 16–17 years), sex, and jurisdiction (49 states and DC). As of August 17, 2021, only the Pfizer-BioNTech vaccine had been authorized for use among adolescents aged 12–17 years in the United States. Moderna and Janssen (Johnson & Johnson) COVID-19 vaccines were not authorized under emergency use for this age group during the analysis period; however, for reasons that are

* Receipt of ≥1 COVID-19 vaccine dose is defined as having received either ≥1 of the 2 Pfizer-BioNTech or Moderna vaccine doses, or a single dose of the Janssen (Johnson & Johnson) vaccine. As of August 17, 2021, only the Pfizer-BioNTech vaccine had been authorized for use among adolescents aged 12–17 years. Moderna and Janssen COVID-19 vaccines were not authorized under emergency use for this age group during December 14, 2020–July 31, 2021. However, doses of these vaccines administered to persons aged 12–17 years were included in this analysis. During February 27, 2021–July 31, 2021, a total of 21,919 adolescents aged 12–17 years were reported to have received 1 dose of the Janssen COVID-19 vaccine. During December 14, 2021–July 31, 2021, a total of 27,226 adolescents aged 12–17 years were reported to have received only the first dose of the Moderna COVID-19 vaccine; 66,032 adolescents aged 12–17 years were reported to have received both doses of the Moderna COVID-19 vaccine; 2,190 were reported to have received Pfizer-BioNTech for the first dose but Moderna for the second dose; and 5,726 were reported to receive Moderna for the first dose but Pfizer-BioNTech for the second dose.

† Series completion was defined as receipt of either both doses of the Pfizer-BioNTech or Moderna vaccines, including those that might have received mismatched products between the first and second dose (i.e., Pfizer-BioNTech for the first dose and Moderna for the second dose or vice versa) or a single dose of the Janssen vaccine.

§ IISs are confidential, computerized, population-based systems that collect and consolidate vaccination data from providers in 64 public health jurisdictions and can be used to track administered vaccines and measure vaccination coverage. The 64 IIS jurisdictions comprise the 50 U.S. states, eight U.S. territories and freely associated states (Puerto Rico, U.S. Virgin Islands, American Samoa, Commonwealth of the Northern Mariana Islands, Guam, Marshall Islands, Palau, and the Federated States of Micronesia), and six local jurisdictions (Chicago, IL; Houston, TX; San Antonio, TX; Philadelphia, PA; New York City, NY; and Washington, DC).

¶ https://www.cdc.gov/vaccines/covid-19/reporting/vams/program-information.html

** https://www.cdc.gov/vaccines/covid-19/reporting/overview/IT-systems.html

†† Providers are required to document vaccination in their medical records within 24 hours of administration and submit these data to their jurisdiction's IIS within 72 hours of administration.

not known, many adolescents were reported to have received these vaccines, and doses administered to adolescents were included in this analysis. Vaccination coverage by race and ethnicity was not calculated because of high rates of missing data. Population size by age group and sex was obtained from the U.S. Census Bureau's 2019 Population Estimates Program (*3*). Second dose completion was calculated among adolescents who received ≥1 dose of a 2-dose COVID-19 vaccination series and for whom sufficient time to receive a second dose during the analysis period had elapsed.[§§] Among adolescents who received the first dose of a 2-dose COVID-19 vaccination series, the proportions of adolescents who had already received the second dose, of those who had not received the second dose but were still within the recommended time interval to receive the second dose, and of those who had not received and were overdue for the second dose were calculated. Tests for statistical significance were not conducted because these data are reflective of the U.S. population (excluding Idaho) and were not based on population samples. All analyses were conducted using SAS software (version 9.4; SAS Institute). This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.[¶¶]

As of July 31, 2021, 42.4% of adolescents aged 12–17 years had received ≥1 dose of a COVID-19 vaccine (Table 1), and 31.9% had completed the vaccination series (Table 2). Adolescent COVID-19 vaccination coverage with ≥1 dose varied by state (range = 20.2% [Mississippi] to 70.1% [Vermont]), as it did for series completion (range = 10.7% [Mississippi] to 60.3% [Vermont]), with higher vaccination coverage in the Northeast and on the West Coast and lower vaccination coverage in the South (Figure). Coverage was higher among adolescents aged 16–17 years (50.6% for ≥1 dose; 40.3% for series completion) than among those aged 12–13 years (36.0% for ≥1 dose; 25.4% for series completion) and 14–15 years (40.9% for ≥1 dose; 30.5% for series completion). Vaccination coverage was similar among males and females across all age groups.

Overall, 86.8% of adolescents aged 12–17 years who received the first dose of a 2-dose COVID-19 vaccination series[***] received the second dose within the recommended interval. A total of 2.4% had not received the second dose but were within the allowable interval, and 10.8% were overdue for the second dose (i.e., >42 days since receipt of the first dose) (Supplementary Table, https://stacks.cdc.gov/view/cdc/109000).

Discussion

Among all U.S. adolescents aged 12–17 years who received the first dose of a 2-dose COVID-19 vaccine series, the vast majority received the second dose, indicating high adherence to completing the COVID-19 vaccine series. However, as of July 31, 2021, only 42.4% of adolescents had received ≥1 dose of a COVID-19 vaccine, and fewer than one third (31.9%) had completed the vaccination series. Further, vaccination coverage varied widely by state, with those in the Northeast and on the West Coast reporting the highest COVID-19 vaccination coverage among adolescents. Vaccination coverage also varied widely by age group, with reported coverage higher among those aged 16–17 years compared with those aged 12–15 years. This is likely because the older age group has been vaccine-eligible for a longer period (i.e., since December 2020).

After the start of the COVID-19 pandemic, many schools shifted to virtual or hybrid learning. Because in-person learning fosters social and emotional development,[†††] safely returning to schools for in-person learning remains a goal. However, given the rapid emergence and spread of the highly transmissible B.1.617.2 (Delta) variant of SARS-CoV-2, the virus that causes COVID-19, and the increase in cases and hospitalizations among children and adolescents (*1*), ensuring high adolescent vaccination coverage is crucial to a safer return to the classroom. Unvaccinated or undervaccinated adolescents can become ill with COVID-19 and spread the SARS-CoV-2 virus in schools, and by extension, in local communities, placing other populations at risk. School systems can consider implementing layered prevention strategies consistent with CDC's guidance for COVID-19 prevention in schools, including universal indoor masking regardless of vaccination status, improving ventilation, screening testing, physical distancing where feasible, and contact tracing in combination with quarantine and isolation. As the 2021–22 school year begins, concerted public health efforts are needed to increase

[§§] Although the recommended interval between doses is 21 days for the Pfizer-BioNTech vaccine, adolescents whose second doses were administered as early as 17 days after the first dose or >21 days after the first dose were considered to have completed the vaccination series. As of August 17, 2021, the Moderna COVID-19 vaccine had not been authorized for use among adolescents. However, the interval between the 2 Moderna COVID-19 vaccine doses was assessed in the analysis. Although the recommended interval between doses is 28 days for the Moderna vaccine, second doses received as early as 24 days after the first dose or >28 days after the first dose were considered to complete the vaccine series.

[¶¶] 45 C.F.R. part 46.102(l)(2); 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

[***] Among persons who received their first dose on or before July 6, 2021, for Pfizer-BioNTech (i.e., >25 days between the first dose and July 31, 2021) or June 29, 2021, for Moderna (i.e., >32 days between the first dose and July 31, 2021). Percentages might not sum to 100% because persons who were not yet due for the second dose were excluded from this analysis.

[†††] https://www.cdc.gov/coronavirus/2019-ncov/community/schools-childcare/k-12-guidance.html#anchor_1625661937509

TABLE 1. Receipt of ≥1 COVID-19 vaccine dose by adolescents aged 12–17 years,* by age group and sex† — United States,§ December 14, 2020–July 31, 2021

	Age group and sex, no. (%)											
	12–17 yrs			12–13 yrs			14–15 yrs			16–17 yrs		
Jurisdiction	Total	Female	Male	Total	Female	Male	Total	Female	Male	Total	Female	Male
United States	**10,677,934 (42.4)**	**5,425,265 (44.1)**	**5,216,450 (40.5)**	**3,094,245 (36.0)**	**1,543,152 (36.8)**	**1,541,710 (35.0)**	**3,454,771 (40.9)**	**1,750,329 (42.2)**	**1,693,216 (39.5)**	**4,128,918 (50.6)**	**2,131,784 (53.9)**	**1,981,524 (47.1)**
Alabama	**77,773 (20.6)**	40,050 (22.4)	37,692 (19.0)	**127,065 (17.5)**	11,189 (18.7)	11,094 (16.5)	**25,257 (19.6)**	12,996 (20.3)	12,256 (18.9)	**30,221 (24.8)**	15,865 (28.7)	14,342 (21.6)
Alaska	**23,706 (46.4)**	11,621 (50.6)	11,788 (41.9)	**14,859 (46.0)**	3,279 (38.2)	3,480 (55.5)	**7,627 (37.0)**	3,755 (42.5)	3,789 (32.1)	**9,241 (59.2)**	4,587 (82.9)	4,519 (44.8)
Arizona	**224,638 (38.9)**	114,136 (40.9)	109,744 (36.8)	**201,971 (32.3)**	32,501 (32.7)	32,543 (31.7)	**72,338 (37.3)**	36,750 (38.9)	35,297 (35.5)	**87,023 (48.1)**	44,885 (52.7)	41,904 (43.7)
Arkansas	**73,861 (30.3)**	37,256 (31.6)	35,813 (28.6)	**80,882 (25.0)**	9,905 (24.7)	10,097 (24.8)	**24,873 (31.2)**	12,407 (30.4)	12,209 (31.5)	**28,754 (34.7)**	14,944 (40.3)	13,507 (29.5)
California	**1,642,427 (53.2)**	836,970 (55.5)	801,906 (50.8)	**1,054,889 (44.3)**	233,673 (45.3)	232,862 (43.2)	**541,389 (52.3)**	275,356 (54.7)	264,914 (49.9)	**633,560 (63.6)**	327,941 (67.2)	304,130 (59.8)
Colorado	**222,780 (50.3)**	113,015 (53.3)	109,520 (47.6)	**147,908 (45.0)**	33,118 (48.3)	33,343 (42.0)	**73,879 (48.7)**	37,316 (51.5)	36,481 (46.1)	**82,383 (57.6)**	42,581 (59.8)	39,696 (55.3)
Connecticut	**166,941 (62.3)**	84,333 (64.6)	82,242 (59.9)	**87,364 (55.1)**	23,935 (55.1)	24,047 (54.7)	**53,242 (58.7)**	27,015 (62.4)	26,116 (55.1)	**65,592 (72.9)**	33,383 (76.0)	32,079 (69.7)
Delaware	**32,169 (45.2)**	16,559 (49.0)	15,560 (41.6)	**21,190 (44.0)**	4,614 (50.5)	4,698 (39.0)	**10,526 (37.8)**	5,428 (34.9)	5,080 (41.2)	**12,319 (55.7)**	6,517 (71.3)	5,782 (44.6)
District of Columbia	**17,256 (52.3)**	8,872 (53.3)	8,325 (50.9)	**11,514 (49.8)**	2,965 (56.6)	2,741 (43.7)	**5,356 (46.0)**	2,700 (38.3)	2,637 (57.5)	**6,168 (62.6)**	3,207 (73.4)	2,947 (53.7)
Florida	**558,957 (37.6)**	286,050 (39.4)	272,548 (35.9)	**514,351 (31.0)**	80,517 (32.9)	78,894 (29.3)	**183,765 (37.2)**	93,750 (37.6)	89,911 (36.8)	**215,683 (45.3)**	111,783 (48.4)	103,743 (42.3)
Georgia	**271,600 (30.7)**	138,608 (32.6)	132,222 (28.8)	**307,972 (25.5)**	39,194 (26.1)	39,086 (24.8)	**87,107 (29.1)**	44,308 (30.9)	42,597 (27.3)	**105,965 (38.3)**	55,106 (41.8)	50,539 (34.9)
Hawaii	**60,457 (63.7)**	30,251 (67.7)	30,035 (59.8)	**33,044 (52.3)**	8,501 (54.1)	8,725 (50.4)	**19,774 (64.0)**	9,869 (74.0)	9,857 (56.0)	**23,409 (75.7)**	11,881 (76.0)	11,453 (74.8)
Illinois	**527,953 (53.2)**	268,107 (54.1)	257,707 (52.0)	**331,413 (45.4)**	75,084 (44.8)	74,889 (45.7)	**175,184 (52.1)**	88,684 (52.1)	85,790 (51.7)	**202,272 (62.4)**	104,339 (65.9)	97,028 (58.5)
Indiana	**164,717 (29.8)**	84,039 (31.5)	79,638 (28.0)	**194,055 (24.6)**	23,834 (25.1)	23,786 (24.0)	**52,778 (29.8)**	26,775 (31.6)	25,704 (27.9)	**64,144 (35.4)**	33,430 (38.2)	30,148 (32.2)
Iowa	**88,317 (36.7)**	45,436 (38.6)	42,643 (34.8)	**83,053 (31.8)**	13,341 (32.8)	13,058 (30.8)	**28,451 (36.9)**	14,440 (36.2)	13,970 (37.5)	**33,421 (41.6)**	17,655 (47.3)	15,615 (36.4)
Kansas	**88,601 (36.4)**	45,509 (38.0)	42,995 (34.9)	**84,150 (31.6)**	13,211 (30.7)	13,352 (32.5)	**27,907 (34.8)**	14,328 (40.8)	13,557 (30.1)	**34,100 (43.3)**	17,970 (43.1)	16,086 (43.3)
Kentucky	**115,204 (32.7)**	59,363 (34.5)	55,723 (31.0)	**122,071 (27.8)**	17,009 (27.7)	16,927 (27.9)	**37,571 (33.0)**	19,163 (35.5)	18,375 (30.6)	**43,680 (37.6)**	23,191 (40.7)	20,421 (34.4)
Louisiana	**81,272 (21.9)**	41,478 (23.4)	39,560 (20.3)	**131,531 (17.7)**	11,736 (19.3)	11,536 (16.3)	**26,369 (21.6)**	13,273 (22.2)	13,019 (20.9)	**31,616 (26.7)**	16,469 (29.1)	15,005 (24.4)
Maine	**48,729 (55.1)**	24,474 (59.0)	23,874 (50.9)	**27,699 (53.3)**	7,247 (64.3)	7,370 (44.9)	**16,031 (52.4)**	8,004 (54.5)	7,858 (49.4)	**17,937 (59.6)**	9,223 (59.6)	8,646 (59.2)
Maryland	**263,433 (56.3)**	132,880 (57.8)	130,206 (54.7)	**163,386 (49.1)**	39,948 (51.2)	40,174 (47.1)	**84,806 (53.6)**	42,484 (52.7)	42,206 (54.4)	**98,420 (67.4)**	50,448 (70.9)	47,826 (63.8)
Massachusetts	**319,741 (65.7)**	161,726 (68.5)	157,494 (62.9)	**158,110 (59.9)**	47,185 (62.7)	47,336 (57.1)	**105,067 (65.2)**	53,176 (64.4)	51,711 (65.7)	**120,042 (71.7)**	61,365 (78.3)	58,447 (65.7)
Michigan	**273,071 (36.0)**	139,194 (38.1)	133,776 (34.1)	**254,314 (30.6)**	39,045 (31.8)	38,746 (29.5)	**86,078 (34.7)**	43,910 (36.8)	42,132 (32.7)	**109,164 (42.7)**	56,239 (45.5)	52,898 (40.0)
Minnesota	**198,287 (44.3)**	101,571 (45.8)	95,698 (42.4)	**149,301 (40.8)**	30,696 (39.3)	30,025 (42.1)	**60,068 (38.7)**	30,610 (40.9)	29,257 (36.4)	**77,289 (54.1)**	40,265 (58.4)	36,416 (49.3)
Mississippi	**49,940 (20.2)**	25,444 (21.0)	24,454 (19.3)	**86,695 (16.7)**	7,162 (17.7)	7,272 (15.7)	**16,559 (21.4)**	8,298 (20.3)	8,245 (22.7)	**18,931 (22.6)**	9,984 (25.0)	8,937 (20.4)
Missouri	**152,486 (32.4)**	77,515 (33.0)	74,807 (31.7)	**158,781 (28.9)**	22,844 (29.3)	23,025 (28.5)	**49,384 (31.0)**	25,006 (31.7)	24,325 (30.2)	**57,185 (37.5)**	29,665 (38.0)	27,457 (37.0)
Montana	**23,962 (30.3)**	12,105 (31.5)	11,683 (28.8)	**25,348 (28.9)**	3,579 (28.1)	3,669 (29.1)	**7,428 (28.9)**	3,730 (28.5)	3,638 (28.9)	**9,209 (32.9)**	4,796 (38.0)	4,376 (28.5)
Nebraska	**62,131 (39.2)**	31,723 (39.8)	30,292 (38.5)	**56,881 (33.1)**	9,447 (31.5)	9,343 (34.7)	**19,599 (37.1)**	9,928 (40.0)	9,649 (34.5)	**23,719 (48.7)**	12,348 (49.6)	11,300 (47.5)
Nevada	**89,835 (37.2)**	46,021 (37.7)	43,775 (36.6)	**85,434 (29.8)**	12,717 (30.8)	12,723 (28.8)	**29,148 (36.3)**	14,933 (34.9)	14,202 (37.8)	**35,241 (46.5)**	18,371 (48.4)	16,850 (44.6)
New Hampshire	**48,188 (49.5)**	24,264 (49.9)	23,250 (47.7)	**34,943 (38.1)**	6,575 (38.3)	6,609 (37.2)	**15,129 (51.1)**	7,567 (47.1)	7,332 (54.2)	**19,747 (60.1)**	10,122 (65.7)	9,309 (53.3)
New Jersey	**357,267 (52.5)**	180,504 (54.7)	175,521 (50.0)	**232,003 (43.8)**	50,304 (42.3)	51,137 (45.2)	**113,832 (50.9)**	57,509 (54.3)	55,960 (47.5)	**141,702 (62.9)**	72,691 (69.2)	68,424 (56.9)
New Mexico	**92,891 (55.1)**	46,824 (55.5)	44,864 (53.1)	**57,115 (49.5)**	13,992 (49.8)	13,800 (47.6)	**29,505 (50.9)**	14,745 (49.8)	14,367 (50.7)	**35,137 (65.5)**	18,087 (68.0)	16,697 (61.6)
New York	**651,562 (46.6)**	328,743 (48.5)	319,985 (44.5)	**471,237 (39.3)**	91,375 (39.4)	93,069 (38.9)	**205,664 (44.3)**	103,529 (46.5)	101,489 (42.0)	**260,904 (56.6)**	133,839 (60.1)	125,427 (52.6)
North Carolina	**288,722 (35.4)**	147,723 (35.7)	139,514 (34.8)	**280,592 (29.4)**	41,310 (28.5)	40,939 (30.1)	**95,543 (35.3)**	48,666 (35.0)	46,473 (35.3)	**110,577 (42.0)**	57,747 (44.3)	52,102 (39.1)

See table footnotes on the next page.

TABLE 1. (*Continued*) Receipt of ≥1 COVID-19 vaccine dose by adolescents aged 12–17 years,* by age group and sex† — United States,§ December 14, 2020–July 31, 2021

	Age group and sex, no. (%)											
	12–17 yrs			12–13 yrs			14–15 yrs			16–17 yrs		
Jurisdiction	Total	Female	Male	Total	Female	Male	Total	Female	Male	Total	Female	Male
North Dakota	**13,910 (26.3)**	7,084 (25.4)	6,613 (26.5)	**18,993 (20.2)**	1,888 (20.4)	1,894 (19.5)	**4,533 (27.4)**	2,290 (24.1)	2,175 (30.8)	**5,535 (32.0)**	2,906 (31.8)	2,544 (31.3)
Ohio	**284,374 (31.9)**	145,410 (33.8)	138,167 (29.9)	**300,214 (27.1)**	40,975 (28.2)	40,302 (26.0)	**89,895 (29.9)**	45,960 (31.6)	43,719 (28.2)	**113,035 (38.8)**	58,475 (42.1)	54,146 (35.5)
Oklahoma	**92,409 (29.1)**	47,313 (31.4)	44,973 (27.1)	**113,915 (23.4)**	13,242 (25.7)	13,346 (21.4)	**29,283 (29.1)**	15,020 (30.0)	14,228 (28.2)	**36,505 (35.5)**	19,051 (38.7)	17,399 (32.5)
Oregon	**147,476 (49.3)**	74,896 (49.7)	72,231 (48.8)	**100,819 (43.5)**	21,971 (44.0)	21,828 (42.9)	**48,739 (48.1)**	24,714 (47.6)	23,927 (48.3)	**54,859 (56.8)**	28,211 (57.6)	26,476 (55.5)
Pennsylvania	**437,303 (47.7)**	219,211 (48.7)	209,686 (44.8)	**308,332 (41.3)**	62,448 (41.8)	62,623 (39.4)	**140,842 (45.2)**	70,283 (46.6)	67,547 (42.1)	**168,972 (56.7)**	86,480 (57.7)	79,516 (53.7)
Rhode Island	**42,660 (55.4)**	21,683 (60.8)	20,919 (50.6)	**25,863 (48.2)**	6,167 (45.7)	6,290 (50.9)	**13,645 (51.2)**	7,024 (61.9)	6,595 (43.1)	**16,544 (67.4)**	8,492 (78.4)	8,034 (58.6)
South Carolina	**100,830 (25.8)**	51,820 (26.7)	48,946 (24.9)	**135,830 (19.9)**	13,591 (20.5)	13,384 (19.2)	**33,001 (24.6)**	17,005 (25.3)	15,977 (23.9)	**40,842 (33.7)**	21,224 (34.9)	19,585 (32.5)
South Dakota	**24,848 (34.4)**	12,468 (34.6)	11,989 (33.1)	**24,483 (30.1)**	3,612 (32.6)	3,661 (27.3)	**8,051 (30.9)**	4,073 (29.1)	3,850 (31.9)	**9,439 (43.5)**	4,783 (43.5)	4,478 (41.8)
Tennessee	**126,159 (24.3)**	65,267 (26.1)	60,591 (22.6)	**185,246 (19.6)**	18,164 (20.1)	18,156 (19.2)	**40,295 (24.0)**	20,848 (24.2)	19,407 (23.8)	**49,495 (29.9)**	26,255 (35.8)	23,028 (24.9)
Texas	**1,028,789 (40.6)**	521,461 (42.2)	506,643 (39.0)	**854,580 (34.6)**	147,957 (35.6)	147,505 (33.6)	**330,444 (38.5)**	167,302 (39.9)	162,971 (37.1)	**402,745 (49.1)**	206,202 (51.6)	196,167 (46.6)
Utah	**129,559 (41.9)**	65,495 (43.8)	63,818 (40.0)	**106,783 (34.6)**	18,393 (34.5)	18,549 (34.7)	**39,977 (38.8)**	20,029 (41.4)	19,925 (36.5)	**52,615 (53.1)**	27,073 (56.6)	25,344 (49.3)
Vermont	**28,904 (70.1)**	14,332 (74.4)	14,474 (65.9)	**11,732 (75.0)**	4,306 (83.5)	4,464 (67.9)	**9,454 (70.3)**	4,790 (91.7)	4,627 (56.3)	**10,649 (66.3)**	5,236 (58.9)	5,383 (75.1)
Virginia	**342,958 (53.7)**	173,904 (56.1)	168,793 (51.3)	**222,929 (45.3)**	50,509 (46.5)	50,461 (44.1)	**113,259 (53.0)**	57,040 (54.8)	56,153 (51.2)	**128,655 (63.6)**	66,355 (68.2)	62,179 (59.2)
Washington	**296,782 (53.1)**	149,501 (53.6)	145,592 (52.0)	**192,800 (48.7)**	46,631 (49.0)	46,691 (47.8)	**95,740 (50.0)**	47,895 (48.3)	47,255 (51.2)	**107,187 (61.3)**	54,975 (64.9)	51,646 (57.3)
West Virginia	**38,159 (30.2)**	19,127 (31.5)	18,459 (28.2)	**44,298 (23.8)**	5,126 (24.7)	5,263 (22.3)	**12,061 (30.2)**	6,090 (32.4)	5,782 (27.3)	**15,564 (37.1)**	7,911 (37.2)	7,414 (35.8)
Wisconsin	**174,211 (39.9)**	88,947 (41.5)	84,996 (38.2)	**142,836 (35.8)**	25,720 (38.3)	25,427 (33.6)	**55,260 (36.8)**	28,010 (37.0)	27,178 (36.4)	**67,750 (47.1)**	35,217 (49.2)	32,391 (44.9)
Wyoming	**9,729 (20.4)**	4,982 (21.7)	4,706 (19.0)	**18,337 (15.8)**	1,420 (16.5)	1,471 (15.2)	**3,058 (20.9)**	1,548 (19.9)	1,497 (21.8)	**3,772 (25.7)**	2,014 (30.8)	1,738 (21.4)

* Receipt of ≥1 COVID-19 vaccine dose is defined either as receiving at least one of the 2 doses of the Pfizer-BioNTech or Moderna vaccines or a single dose of the Janssen (Johnson & Johnson) vaccine. As of August 17, 2021, only the Pfizer-BioNTech vaccine had been authorized for use among adolescents aged 12–17 years. Moderna and Janssen COVID-19 vaccines were not authorized under emergency use for this age group during the analysis period; however, these vaccinations were included in this analysis.
† Fewer than 0.5% of the records were missing information on sex.
§ COVID-19 vaccine doses administered to adolescents residing in Idaho were excluded because the state has data-sharing restrictions on information reported to CDC.

COVID-19 vaccination coverage among adolescents in addition to implementing COVID-19 prevention strategies based on community transmission.

Public health practitioners can use various measures to increase adolescent COVID-19 vaccination coverage. Building on lessons from the public-private partnership between CDC and retail pharmacies in the Federal Retail Pharmacy Partnership§§§ regarding vaccination clinics offered for selected population groups at different times throughout the response (*4*), local public health agencies and pharmacies could partner with school districts and school systems to provide COVID-19 vaccinations to students at schools. Vaccine administration on site at schools is an effective, evidence-based intervention that improves childhood and adolescent vaccination rates for routinely recommended vaccines (*5*). State and local governments, school administrators, community leaders, health care professionals, and public health practitioners can facilitate safer return to schools and improve equity among sociodemographic groups by prioritizing COVID-19 vaccination among adolescents and incorporating on-site school vaccinations for eligible students (*6*,*7*). In addition, on-site vaccination clinics might also be planned in coordination with other school-based vaccination programs, such as those for seasonal influenza and routine adolescent vaccination.

Concerted outreach can help inform adolescents and their parents about the importance of COVID-19 vaccination. Effective outreach with tailored communication could help improve vaccine confidence, acceptance, and coverage among adolescents and their parents. In a recent report, only 56% of parents of unvaccinated adolescents aged 12–17 years expressed intent for their adolescent to receive a COVID-19 vaccine (*8*). Given that parental vaccination status is a marker

§§§ https://www.cdc.gov/vaccines/covid-19/retail-pharmacy-program/index.html

TABLE 2. COVID-19 vaccination coverage among adolescents aged 12–17 years who completed the vaccine series,* by age group and sex† — United States,§ December 14, 2020–July 31, 2021

	Age group and sex, no. (%)											
	12–17 yrs			12–13 yrs			14–15 yrs			16–17 yrs		
Jurisdiction	Total	Female	Male	Total	Female	Male	Total	Female	Male	Total	Female	Male
United States	**8,045,685 (31.9)**	**4,117,404 (33.5)**	**3,905,344 (30.3)**	**2,183,597 (25.4)**	**1,093,057 (26.0)**	**1,085,039 (24.7)**	**2,570,498 (30.5)**	**1,311,724 (31.6)**	**1,251,765 (29.2)**	**3,291,590 (40.3)**	**1,712,623 (43.3)**	**1,568,540 (37.3)**
Alabama	**40,925 (10.8)**	21,303 (11.9)	19,606 (9.9)	**10,360 (8.2)**	5,234 (8.7)	5,118 (7.6)	**12,421 (9.6)**	6,452 (10.1)	5,969 (9.2)	**18,144 (14.9)**	9,617 (17.4)	8,519 (12.8)
Alaska	**18,394 (36.0)**	9,066 (39.5)	9,148 (32.5)	**4,947 (33.3)**	2,384 (27.7)	2,522 (40.2)	**5,678 (27.5)**	2,778 (31.4)	2,847 (24.1)	**7,769 (49.7)**	3,904 (70.6)	3,779 (37.4)
Arizona	**167,297 (29.0)**	85,471 (30.6)	81,203 (27.3)	**44,661 (22.1)**	22,273 (22.4)	22,209 (21.7)	**52,639 (27.1)**	26,854 (28.4)	25,546 (25.7)	**69,997 (38.7)**	36,344 (42.6)	33,448 (34.9)
Arkansas	**41,891 (17.2)**	21,742 (18.4)	19,956 (15.9)	**10,494 (13.0)**	5,259 (13.1)	5,194 (12.7)	**13,552 (17.0)**	6,945 (17.0)	6,551 (16.9)	**17,845 (21.5)**	9,538 (25.7)	8,211 (17.9)
California	**1,271,593 (41.2)**	652,802 (43.3)	616,318 (39.0)	**344,509 (32.7)**	172,803 (33.5)	171,083 (31.7)	**416,508 (40.3)**	213,322 (42.4)	202,396 (38.1)	**510,576 (51.2)**	266,677 (54.6)	242,839 (47.7)
Colorado	**185,447 (41.9)**	94,420 (44.5)	90,901 (39.5)	**52,056 (35.2)**	25,885 (37.8)	26,150 (32.9)	**61,301 (40.4)**	31,074 (42.9)	30,191 (38.2)	**72,090 (50.4)**	37,461 (52.6)	34,560 (48.1)
Connecticut	**136,730 (51.0)**	69,481 (53.2)	66,983 (48.8)	**36,973 (42.3)**	18,513 (42.6)	18,368 (41.8)	**43,625 (48.1)**	22,287 (51.5)	21,253 (44.8)	**56,132 (62.4)**	28,681 (65.3)	27,362 (59.5)
Delaware	**25,675 (36.1)**	13,313 (39.4)	12,334 (33.0)	**7,027 (33.2)**	3,496 (38.2)	3,524 (29.3)	**8,378 (30.1)**	4,378 (28.2)	3,990 (32.3)	**10,270 (46.4)**	5,439 (59.5)	4,820 (37.2)
District of Columbia	**11,239 (34.1)**	5,818 (34.9)	5,393 (33.0)	**3,574 (31.0)**	1,847 (35.2)	1,716 (27.4)	**3,607 (31.0)**	1,849 (26.2)	1,748 (38.1)	**4,058 (41.2)**	2,122 (48.6)	1,929 (35.1)
Florida	**377,443 (25.4)**	194,735 (26.8)	182,570 (24.0)	**98,344 (19.1)**	49,892 (20.4)	48,418 (18.0)	**120,847 (24.5)**	62,121 (24.9)	58,694 (24.0)	**158,252 (33.2)**	82,722 (35.8)	75,458 (30.7)
Georgia	**166,329 (18.8)**	85,830 (20.2)	80,219 (17.5)	**41,215 (13.4)**	20,691 (13.8)	20,437 (13.0)	**48,426 (16.2)**	24,922 (17.4)	23,455 (15.0)	**76,688 (27.7)**	40,217 (30.5)	36,327 (25.1)
Hawaii	**35,203 (37.1)**	17,549 (39.3)	17,546 (34.9)	**9,931 (30.1)**	4,831 (30.7)	5,072 (29.3)	**11,450 (37.0)**	5,705 (42.8)	5,715 (32.5)	**13,822 (44.7)**	7,013 (44.9)	6,759 (44.2)
Illinois	**348,478 (35.1)**	179,085 (36.1)	168,328 (33.9)	**95,818 (28.9)**	48,301 (28.8)	47,255 (28.8)	**113,863 (33.9)**	58,356 (34.3)	55,143 (33.2)	**138,797 (42.8)**	72,428 (45.8)	65,930 (39.7)
Indiana	**131,406 (23.8)**	67,329 (25.2)	63,257 (22.2)	**35,025 (18.0)**	17,450 (18.4)	17,450 (17.6)	**41,394 (23.4)**	21,124 (24.9)	20,030 (21.7)	**54,987 (30.4)**	28,755 (32.8)	25,777 (27.6)
Iowa	**70,809 (29.4)**	36,654 (31.1)	34,002 (27.7)	**19,670 (23.7)**	9,953 (24.5)	9,692 (22.8)	**22,623 (29.3)**	11,540 (28.9)	11,059 (29.7)	**28,516 (35.5)**	15,161 (40.6)	13,251 (30.9)
Kansas	**61,300 (25.2)**	31,698 (26.4)	29,559 (24.0)	**16,594 (19.7)**	8,240 (19.2)	8,339 (20.3)	**18,868 (23.5)**	9,778 (27.8)	9,082 (20.2)	**25,838 (32.8)**	13,680 (32.8)	12,138 (32.7)
Kentucky	**81,664 (23.2)**	42,709 (24.8)	38,895 (21.6)	**22,107 (18.1)**	11,199 (18.2)	10,903 (18.0)	**26,034 (22.8)**	13,521 (25.1)	12,500 (20.8)	**33,523 (28.8)**	17,989 (31.6)	15,492 (26.1)
Louisiana	**46,411 (12.5)**	24,126 (13.6)	22,181 (11.4)	**11,607 (8.8)**	5,905 (9.7)	5,695 (8.0)	**13,932 (11.4)**	7,128 (11.9)	6,772 (10.9)	**20,872 (17.6)**	11,093 (19.6)	9,714 (15.8)
Maine	**42,857 (48.5)**	21,496 (51.9)	21,044 (44.8)	**12,259 (44.3)**	5,993 (53.1)	6,149 (37.4)	**14,157 (46.2)**	7,069 (48.1)	6,953 (43.7)	**16,441 (54.7)**	8,434 (54.5)	7,942 (54.4)
Maryland	**218,233 (46.7)**	110,698 (48.2)	107,376 (45.1)	**62,420 (38.2)**	31,169 (39.9)	31,214 (36.6)	**70,372 (44.5)**	35,469 (44.0)	34,851 (44.9)	**85,441 (58.5)**	44,060 (61.9)	41,311 (55.1)
Massachusetts	**263,919 (54.2)**	134,332 (56.9)	129,099 (51.5)	**74,471 (47.1)**	37,267 (49.5)	37,081 (44.7)	**86,063 (53.4)**	43,839 (53.1)	42,066 (53.5)	**103,385 (61.8)**	53,226 (67.9)	49,952 (56.2)
Michigan	**229,551 (30.3)**	117,541 (32.1)	111,939 (28.5)	**61,506 (24.2)**	30,932 (25.2)	30,548 (23.3)	**72,163 (29.1)**	36,968 (31.0)	35,175 (27.3)	**95,882 (37.5)**	49,641 (40.2)	46,216 (34.9)
Minnesota	**174,700 (39.0)**	89,821 (40.5)	84,347 (37.4)	**50,776 (34.0)**	25,668 (32.9)	25,006 (35.1)	**56,104 (36.1)**	28,844 (38.5)	27,156 (33.8)	**67,820 (47.4)**	35,309 (51.2)	32,185 (43.5)
Mississippi	**26,576 (10.7)**	13,709 (11.3)	12,846 (10.2)	**6,393 (7.4)**	3,182 (7.9)	3,204 (6.9)	**8,134 (10.5)**	4,094 (10.0)	4,033 (11.1)	**12,049 (14.4)**	6,433 (16.1)	5,609 (12.8)
Missouri	**104,029 (22.1)**	53,410 (22.7)	50,568 (21.4)	**28,825 (18.2)**	14,385 (18.5)	14,432 (17.8)	**32,843 (20.6)**	16,854 (21.4)	15,979 (19.8)	**42,361 (27.8)**	22,171 (28.4)	20,157 (27.1)
Montana	**18,046 (22.8)**	9,197 (23.9)	8,794 (21.7)	**5,167 (20.4)**	2,551 (20.0)	2,598 (20.6)	**5,430 (21.2)**	2,784 (21.3)	2,626 (20.9)	**7,449 (26.6)**	3,862 (30.6)	3,570 (23.2)
Nebraska	**48,472 (30.6)**	25,035 (31.4)	23,394 (29.8)	**13,509 (23.7)**	6,854 (22.9)	6,647 (24.7)	**15,152 (28.7)**	7,759 (31.3)	7,384 (26.4)	**19,811 (40.7)**	10,422 (41.9)	9,363 (39.4)
Nevada	**55,558 (23.0)**	28,686 (23.5)	26,854 (22.5)	**14,043 (16.4)**	7,011 (17.0)	7,030 (15.9)	**17,412 (21.7)**	8,995 (21.0)	8,411 (22.4)	**24,103 (31.8)**	12,680 (33.4)	11,413 (30.2)
New Hampshire	**39,480 (40.5)**	19,952 (41.0)	18,996 (38.9)	**10,267 (29.4)**	5,083 (29.6)	5,094 (28.7)	**12,290 (41.5)**	6,173 (38.4)	5,945 (43.9)	**16,923 (51.5)**	8,696 (56.4)	7,957 (45.5)
New Jersey	**289,682 (42.5)**	146,961 (44.6)	141,715 (40.3)	**77,253 (33.3)**	38,290 (32.2)	38,734 (34.3)	**92,001 (41.1)**	46,666 (44.1)	45,052 (38.2)	**120,428 (53.4)**	62,005 (59.0)	57,929 (48.2)
New Mexico	**72,669 (43.1)**	37,085 (44.0)	35,178 (41.7)	**20,417 (35.7)**	10,265 (36.5)	10,012 (34.5)	**22,917 (39.6)**	11,613 (39.2)	11,184 (39.5)	**29,335 (54.6)**	15,207 (57.2)	13,982 (51.6)
New York	**537,956 (38.5)**	272,326 (40.2)	263,665 (36.6)	**143,966 (30.6)**	71,259 (30.7)	72,385 (30.2)	**169,430 (36.5)**	85,566 (38.4)	83,440 (34.5)	**224,560 (48.7)**	115,501 (51.9)	107,840 (45.2)

See table footnotes on the next page.

TABLE 2. (*Continued*) COVID-19 vaccination coverage among adolescents aged 12–17 years who completed the vaccine series,* by age group and sex† — United States,§ December 14, 2020–July 31, 2021

	Age group and sex, no. (%)											
	12–17 yrs			12–13 yrs			14–15 yrs			16–17 yrs		
Jurisdiction	Total	Female	Male	Total	Female	Male	Total	Female	Male	Total	Female	Male
North Carolina	**210,162 (25.8)**	108,311 (26.2)	100,839 (25.2)	**55,824 (19.9)**	28,001 (19.3)	27,612 (20.3)	**68,736 (25.4)**	35,229 (25.3)	33,228 (25.2)	**85,602 (32.5)**	45,081 (34.6)	39,999 (30.0)
North Dakota	**10,254 (19.4)**	5,257 (18.9)	4,842 (19.4)	**2,516 (13.2)**	1,259 (13.6)	1,219 (12.5)	**3,234 (19.5)**	1,628 (17.2)	1,556 (22.1)	**4,504 (26.1)**	2,370 (26.0)	2,067 (25.4)
Ohio	**239,023 (26.8)**	122,890 (28.6)	115,636 (25.0)	**63,374 (21.1)**	32,046 (22.0)	31,238 (20.2)	**74,684 (24.8)**	38,484 (26.4)	36,083 (23.3)	**100,965 (34.7)**	52,360 (37.7)	48,315 (31.7)
Oklahoma	**61,250 (19.3)**	31,546 (20.9)	29,633 (17.8)	**15,691 (13.8)**	7,764 (15.0)	7,913 (12.7)	**18,709 (18.6)**	9,633 (19.2)	9,056 (18.0)	**26,850 (26.1)**	14,149 (28.8)	12,664 (23.7)
Oregon	**126,346 (42.3)**	64,593 (42.8)	61,618 (41.6)	**36,145 (35.9)**	18,188 (36.4)	17,937 (35.3)	**41,459 (40.9)**	21,114 (40.7)	20,319 (41.0)	**48,742 (50.4)**	25,291 (51.7)	23,362 (49.0)
Pennsylvania	**303,836 (33.1)**	153,011 (34.0)	145,168 (31.0)	**84,516 (27.4)**	41,529 (27.8)	41,414 (26.0)	**98,297 (31.6)**	49,226 (32.6)	47,005 (29.3)	**121,023 (40.6)**	62,256 (41.5)	56,749 (38.3)
Rhode Island	**35,520 (46.1)**	18,100 (50.7)	17,380 (42.0)	**9,733 (37.6)**	4,786 (35.4)	4,938 (40.0)	**11,386 (42.7)**	5,862 (51.6)	5,508 (36.0)	**14,401 (58.7)**	7,452 (68.8)	6,934 (50.6)
South Carolina	**72,130 (18.4)**	37,476 (19.3)	34,621 (17.6)	**17,802 (13.1)**	8,967 (13.5)	8,831 (12.7)	**22,947 (17.1)**	11,939 (17.7)	10,996 (16.4)	**31,381 (25.9)**	16,570 (27.3)	14,794 (24.5)
South Dakota	**16,383 (22.7)**	8,318 (23.1)	7,813 (21.6)	**4,264 (17.4)**	2,113 (19.1)	2,108 (15.7)	**5,037 (19.3)**	2,585 (18.5)	2,374 (19.7)	**7,082 (32.6)**	3,620 (32.9)	3,331 (31.1)
Tennessee	**87,019 (16.8)**	45,491 (18.2)	41,307 (15.4)	**22,260 (12.0)**	11,200 (12.4)	11,035 (11.6)	**26,342 (15.7)**	13,724 (15.9)	12,597 (15.4)	**38,417 (23.2)**	20,567 (28.0)	17,675 (19.1)
Texas	**718,918 (28.4)**	369,600 (29.9)	348,945 (26.9)	**193,523 (22.6)**	97,354 (23.4)	96,096 (21.9)	**225,520 (26.2)**	115,724 (27.6)	109,695 (24.9)	**299,875 (36.5)**	156,522 (39.1)	143,154 (34.0)
Utah	**96,759 (31.3)**	49,212 (32.9)	47,466 (29.8)	**25,119 (23.5)**	12,578 (23.6)	12,530 (23.4)	**29,095 (28.3)**	14,641 (30.3)	14,449 (26.4)	**42,545 (42.9)**	21,993 (46.0)	20,487 (39.9)
Vermont	**24,881 (60.3)**	12,395 (64.3)	12,437 (56.6)	**7,388 (63.0)**	3,657 (70.9)	3,720 (56.6)	**8,118 (60.4)**	4,095 (78.4)	4,006 (48.8)	**9,375 (58.4)**	4,643 (52.2)	4,711 (65.7)
Virginia	**283,385 (44.3)**	144,360 (46.6)	138,878 (42.2)	**79,268 (35.6)**	39,685 (36.5)	39,546 (34.6)	**93,389 (43.7)**	47,282 (45.5)	46,077 (42.0)	**110,728 (54.7)**	57,393 (59.0)	53,255 (50.7)
Washington	**245,243 (43.9)**	124,122 (44.5)	119,901 (42.8)	**73,427 (38.1)**	36,514 (38.4)	36,573 (37.4)	**79,630 (41.6)**	40,075 (40.4)	39,149 (42.5)	**92,186 (52.7)**	47,533 (56.1)	44,179 (49.0)
West Virginia	**27,203 (21.6)**	13,567 (22.3)	13,174 (20.1)	**6,953 (15.7)**	3,372 (16.3)	3,453 (14.6)	**8,505 (21.3)**	4,299 (22.9)	4,066 (19.2)	**11,745 (28.0)**	5,896 (27.7)	5,655 (27.3)
Wisconsin	**140,545 (32.2)**	72,235 (33.7)	68,167 (30.6)	**37,736 (26.4)**	19,067 (28.4)	18,641 (24.6)	**43,634 (29.0)**	22,269 (29.4)	21,335 (28.6)	**59,175 (41.2)**	30,899 (43.1)	28,191 (39.1)
Wyoming	**6,866 (14.4)**	3,540 (15.4)	3,305 (13.4)	**1,874 (10.2)**	912 (10.6)	956 (9.8)	**2,162 (14.8)**	1,088 (14.0)	1,070 (15.6)	**2,830 (19.3)**	1,540 (23.6)	1,279 (15.7)

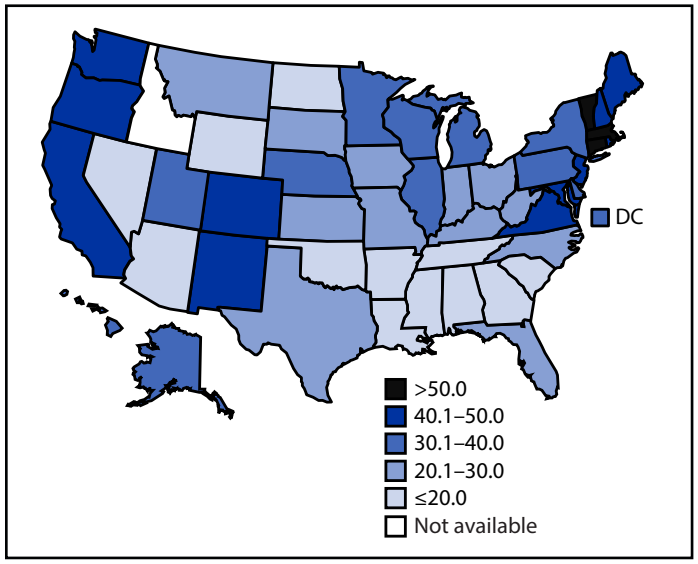
* Vaccine series completion was defined as receiving either both doses of the Pfizer-BioNTech or Moderna vaccines, including mismatched products between the first and second dose (i.e., Pfizer-BioNTech for the first dose and Moderna for the second dose or vice versa) or a single dose for the Janssen (Johnson & Johnson) vaccine. As of August 17, 2021, only the Pfizer-BioNTech vaccine had been authorized for use among adolescents aged 12–17 years. Moderna and Janssen COVID-19 vaccines were not authorized under emergency use for this age group during the analysis period; however, these vaccinations were included in this analysis.
† Fewer than 0.5% of the records were missing information on sex.
§ COVID-19 vaccine doses administered to adolescents residing in Idaho were excluded because the state has data-sharing restrictions on information reported to CDC.

for adolescent vaccination status,¶¶¶ vaccine hesitancy or anti-vaccination sentiments among parents might directly lead to missed opportunities to vaccinate adolescents (*9*). Among adolescents and their parents who were surveyed about their intent to receive a COVID-19 vaccine, many reported that having more information about the safety and efficacy of COVID-19 vaccines would increase their likelihood of receiving a vaccine (*8*). Public health practitioners can use multimodal outreach efforts involving a variety of traditional and social media platforms to engage adolescents and their parents to improve vaccination acceptance and coverage. Further, state and local governments can consider strategies that encourage receipt by adolescents of all vaccines recommended by the Advisory Committee on Immunization Practices, especially given the declines in routine childhood and adolescent vaccinations during the pandemic (*10*).

The findings in this report are subject to at least five limitations. First, vaccination coverage rates were aggregated and analyzed only at the state level. Calculating coverage at more specific levels (e.g., by county or urban-rural classification) could potentially identify geographic areas with low vaccination coverage rates. Second, because Idaho was excluded from the analysis, the findings are not representative of the entire United States. Third, adolescents who received COVID-19 vaccines from different entities that used different methods for submitting data (e.g., if the first dose was administered at a pharmacy and the second dose was given at a mass vaccination site) might not have their first and second doses linked,

¶¶¶ https://www.kff.org/coronavirus-covid-19/poll-finding/kff-covid-19-vaccine-monitor-parents-and-the-pandemic

FIGURE. Percentage of adolescents aged 12–17 years who completed the COVID-19 vaccination series*,† — United States,§ December 14, 2020–July 31, 2021



Abbreviation: DC = District of Columbia.

* As of August 17, 2021, only the Pfizer-BioNTech vaccine had been authorized for use among adolescents aged 12–17 years. Moderna and Janssen (Johnson & Johnson) COVID-19 vaccines were not authorized under emergency use for this age group during the analysis period; however, many adolescents had documentation of receipt of these vaccines. Thus, these vaccine doses were included in this analysis if they were administered to adolescents aged 12–17 years.

† Series completion was defined as receipt of either both doses of the Pfizer-BioNTech or Moderna vaccines, including those who might have received mismatched products between the first and second dose (i.e., Pfizer-BioNTech for the first dose and Moderna for the second dose or vice versa) or a single dose of the Janssen vaccine.

§ COVID-19 vaccine doses administered to adolescents residing in Idaho were excluded because the state has data-sharing restrictions on information reported to CDC.

which could have led to underestimation of the percentage of adolescents who completed the vaccination series. Fourth, if an adolescent had inadvertently received a different recipient ID when receiving their second dose, first and second doses could not be linked. Finally, vaccination coverage could not be calculated on the basis of race and ethnicity because of incomplete reporting.

An estimated 2 million COVID-19 cases and approximately 300 associated deaths have been reported among children aged 5–17 years since the start of the COVID-19 pandemic (*1*). As persons in younger age groups become eligible for COVID-19 vaccination, public health practitioners, health care professionals, school administrators, and state and local governments can use evidence-based practices to decrease barriers to vaccination and increase confidence in COVID-19 vaccines, which can help facilitate the safer return to in-person learning at schools and ultimately reduce COVID-19–associated morbidity and mortality.

Summary

What is already known about this topic?

Although more common among adults, severe COVID-19 illness and hospitalization occur among adolescents.

What is added by this report?

As of July 31, 2021, coverage with ≥1 dose of COVID-19 vaccine among adolescents aged 12–17 years was 42%, and 32% had completed the series. Series completion rates varied widely by state, ranging from 11% to 60%, and was 25% for adolescents aged 12–13 years, 30% for those aged 14–15 years, and 40% for those aged 16–17 years.

What are the implications for public health practice?

Improving adolescent COVID-19 vaccination coverage is crucial to reduce COVID-19–associated morbidity and mortality among adolescents and can help facilitate safer reopening of schools for in-person learning.

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Morbidity and Mortality Weekly Report

Outbreak Associated with SARS-CoV-2 B.1.617.2 (Delta) Variant in an Elementary School — Marin County, California, May–June 2021

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On August 27, 2021, this report was posted as an MMWR *Early Release on the* MMWR *website (https://www.cdc.gov/mmwr).*

On May 25, 2021, the Marin County Department of Public Health (MCPH) was notified by an elementary school that on May 23, an unvaccinated teacher had reported receiving a positive test result for SARS-CoV-2, the virus that causes COVID-19. The teacher reported becoming symptomatic on May 19, but continued to work for 2 days before receiving a test on May 21. On occasion during this time, the teacher read aloud unmasked to the class despite school requirements to mask while indoors. Beginning May 23, additional cases of COVID-19 were reported among other staff members, students, parents, and siblings connected to the school. To characterize the outbreak, on May 26, MCPH initiated case investigation and contact tracing that included whole genome sequencing (WGS) of available specimens. A total of 27 cases were identified, including that of the teacher. During May 23–26, among the teacher's 24 students, 22 students, all ineligible for vaccination because of age, received testing for SARS-CoV-2; 12 received positive test results. The attack rate in the two rows seated closest to the teacher's desk was 80% (eight of 10) and was 28% (four of 14) in the three back rows (Fisher's exact test; p = 0.036). During May 24–June 1, six of 18 students in a separate grade at the school, all also too young for vaccination, received positive SARS-CoV-2 test results. Eight additional cases were also identified, all in parents and siblings of students in these two grades. Among these additional cases, three were in persons fully vaccinated in accordance with CDC recommendations (*1*). Among the 27 total cases, 22 (81%) persons reported symptoms; the most frequently reported symptoms were fever (41%), cough (33%), headache (26%), and sore throat (26%). WGS of all 18 available specimens identified the B.1.617.2 (Delta) variant. Vaccines are effective against the Delta variant (*2*), but risk of transmission remains elevated among unvaccinated persons in schools without strict adherence to prevention strategies. In addition to vaccination for eligible persons, strict adherence to nonpharmaceutical prevention strategies, including masking, routine testing, facility ventilation, and staying home when symptomatic, are important to ensure safe in-person learning in schools (*3*).

Investigation and Findings

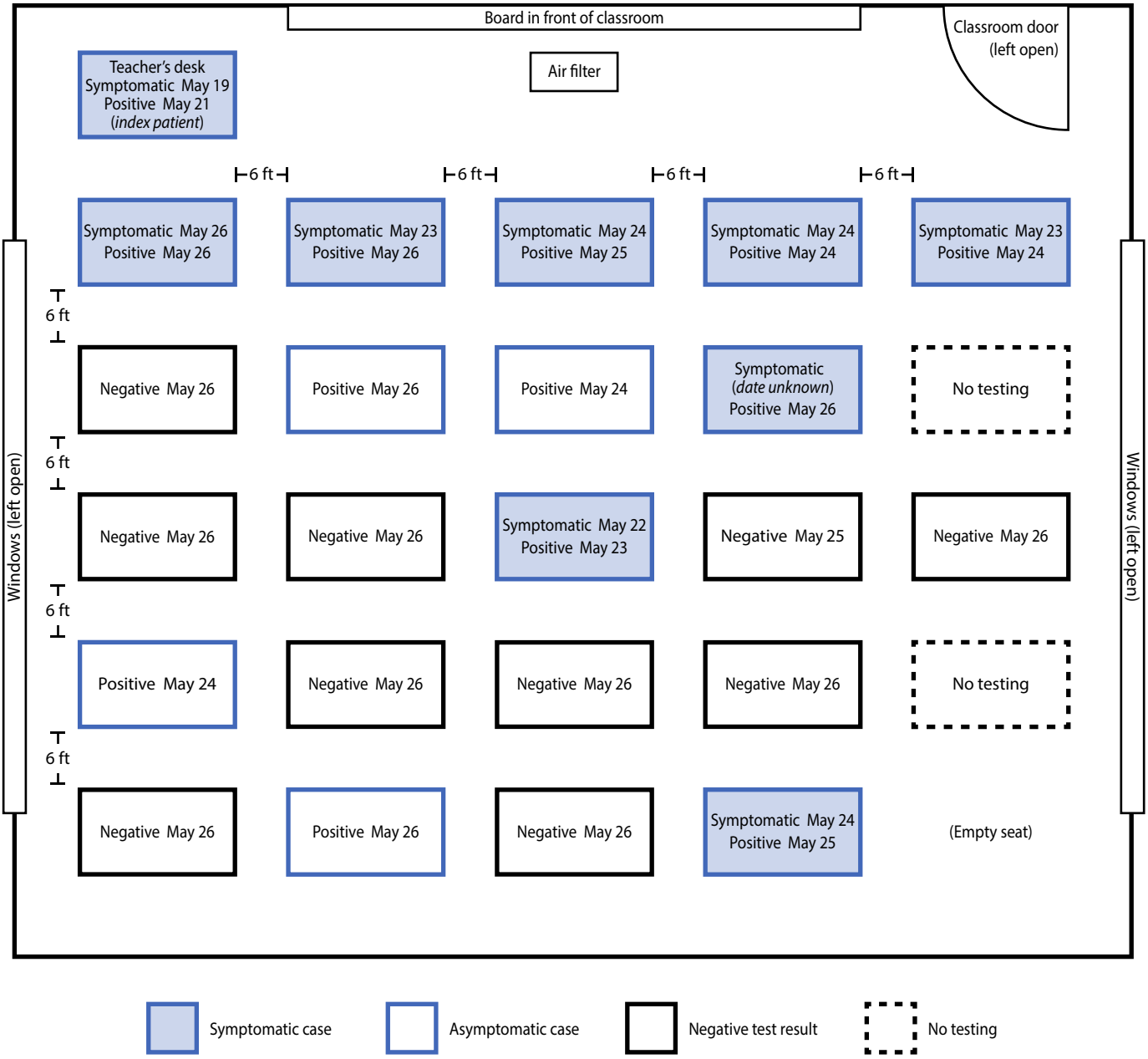
The outbreak location was an elementary school in Marin County, California, which serves 205 students in prekindergarten through eighth grade and has 24 staff members. Each grade includes 20 to 25 students in single classrooms. Other than two teachers, one of whom was the index patient, all school staff members were vaccinated (verified in California's Immunization Registry). The index patient became symptomatic on May 19 with nasal congestion and fatigue. This teacher reported attending social events during May 13–16 but did not report any known COVID-19 exposures and attributed symptoms to allergies. The teacher continued working during May 17–21, subsequently experiencing cough, subjective fever, and headache. The school required teachers and students to mask while indoors; interviews with parents of infected students suggested that students' adherence to masking and distancing guidelines in line with CDC recommendations (*3*) was high in class. However, the teacher was reportedly unmasked on occasions when reading aloud in class. On May 23, the teacher notified the school that they received a positive result for a SARS-CoV-2 test performed on May 21 and self-isolated until May 30. The teacher did not receive a second COVID-19 test, but reported fully recovering during isolation.

The index patient's students began experiencing symptoms on May 22. During May 23–26, among 24 students in this grade, 22 were tested. A COVID-19 case was defined as a positive SARS-CoV-2 reverse transcription–polymerase chain reaction (RT-PCR) or antigen test result.* Twelve (55%) of the 22 students received a positive test result, including eight who experienced symptom onset during May 22–26. Throughout this period, all desks were separated by 6 ft. Students were seated in five rows; the attack rate in the two rows seated closest to the teacher's desk was 80% (eight of 10) and was 28% (four of 14) in the three back rows (Fisher's exact test; p = 0.036) (Figure 1).

On May 22, students in a another classroom, who differed in age by 3 years from the students in the class with the index case and who were also ineligible for vaccination began to experience symptoms. The two classrooms were separated by a large outdoor courtyard with lunch tables that were blocked off from use with yellow tape. All classrooms had portable

*https://cdn.ymaws.com/www.cste.org/resource/resmgr/ps/positionstatement2020/Interim-20-ID-02_COVID-19.pdf

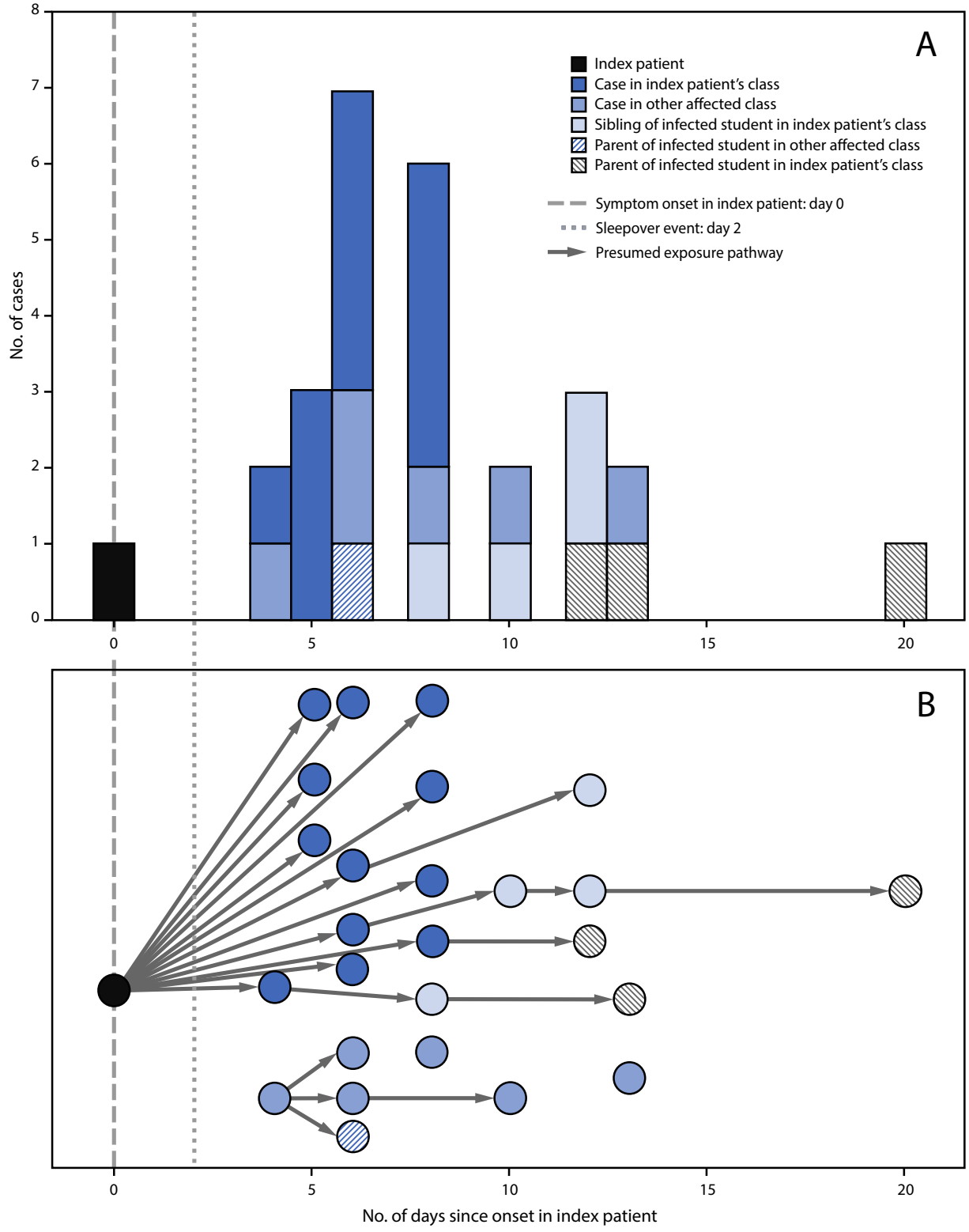
FIGURE 1. Classroom layout and seating chart for 24 students in index patient's class, by SARS-CoV-2 testing date, result or status, and symptoms — Marin County, California, May–June 2021



high-efficiency particulate air filters and doors and windows were left open. Fourteen of 18 students in this separate grade received testing; six tests had positive results. Investigation revealed that one student in this grade hosted a sleepover on May 21 with two classmates from the same grade. All three of these students experienced symptoms after the sleepover and received positive SARS-CoV-2 test results. Among infected students in this class, test dates ranged from May 24 to June 1; symptom onset occurred during May 22–31.

In addition to the documented infections in the two initial grades, cases were identified in one student each from four other grades. Three patients were symptomatic; dates for testing were May 30 or June 2. These four students were siblings of three students with cases in the index patient's class, and exposure was assumed to have occurred in their respective homes. In addition to the teacher and 22 infected students, four parents of students with cases were also infected, for a total of 27 cases (23 confirmed by RT-PCR and four by antigen testing) (Figure 2). Among the five infected adults, one

FIGURE 2. Timeline of SARS-CoV-2 illness onset* after onset in the index patient (A) and presumed transmission† pathway (B) among students, siblings, and parents, relative to onset in the index patient — Marin County, California, May 2021



* Symptom onset date or specimen collection date, if asymptomatic.
† Presumed transmission based on phylogenetic and epidemiologic analyses.

parent and the teacher were unvaccinated; the others were fully vaccinated. The vaccinated adults and one unvaccinated adult were symptomatic with fever, chills, cough, headache, and loss of smell. No other school staff members reported becoming ill. No persons infected in this outbreak were hospitalized. This activity was reviewed by Marin County and was conducted consistent with applicable law.

Public Health Response

On May 26 and June 2, MCPH held testing events at the school as part of outbreak control. During these 2 days, 231 persons were tested, including 194 of 205 students, 21 of 24 staff members and teachers, and 16 parents and siblings of students. The California Department of Public Health assisted with guidance, application of additional prevention strategies, and on-site testing. Community contacts and all students and staff members were encouraged to participate. Specimens for WGS were collected during May 26–June 12; all 18 positive specimens with detectable virus (cycle threshold value <32) were sequenced using ClearDx instruments (Clear Laboratories), Oxford Nanopore MinION sequencing technology, and SARS-CoV-2 ARTIC V3 protocol for amplicon sequencing.[†] Consensus genome assembly was performed in Terra using Titan Clear Laboratories workflow.[§] All sequences generated were classified as the Delta variant. A phylogenetic tree was constructed using the UShER pipeline and visualized using Auspice.us[¶] (*4*) (Figure 3). Eleven sequences were genetically indistinguishable from one another; seven sequences contained additional single nucleotide variations. Among the indistinguishable specimens, six were from students of the index patient, four were from students in the separate grade, and one was from a sibling of a student in the index patient's class, suggesting that infections occurring in the two grades likely were part of the same outbreak. The epidemiologic link between the two grades remains unknown but is thought to be interaction at the school. Five additional related sequences from community cases (in two adults and three children) were later identified, including three more genetically indistinguishable sequences. One was from an adult with specimen collection 1 day before symptom onset in the index patient. Case investigation records did not establish an epidemiologic link between these five community cases and the school outbreak.

Following the outbreak, infected persons were isolated for 10 days after onset of symptoms (or positive test date for asymptomatic cases). All students with known exposure to an infected person quarantined at home for 10 days following their last known contact. Unvaccinated household and community contacts were directed to quarantine for 10 days following their last known exposure to an infected person, with the option to leave quarantine after 7 days if they remained asymptomatic and received a negative test result from a specimen collected on day 5 of quarantine or later. The two affected classrooms were closed and sanitized during May 21–30 and May 24–June 2, respectively.

Discussion

This outbreak of COVID-19 that originated with an unvaccinated teacher highlights the importance of vaccinating school staff members who are in close indoor contact with children ineligible for vaccination as schools reopen. The outbreak's attack rate highlights the Delta variant's increased transmissibility[**]and potential for rapid spread, especially in unvaccinated populations such as schoolchildren too young for vaccination. However, transmission to community contacts appeared lower than that of some previously reported Delta variant outbreaks (*5*). Further transmission might have been prevented by high levels of community vaccination; at the time of this outbreak, approximately 72% of eligible persons in the city where the school is located were fully vaccinated.[††] These findings support evidence that the current COVID-19 vaccines with Food and Drug Administration approval or Emergency Use Authorization are effective against the Delta variant; however, transmission risk remains elevated among unvaccinated persons in schools. In addition to vaccination of eligible persons, implementation of and strict adherence to multipronged nonpharmaceutical prevention strategies including proper masking, routine testing, ventilation, and staying home while symptomatic are important to ensure safe school instruction.

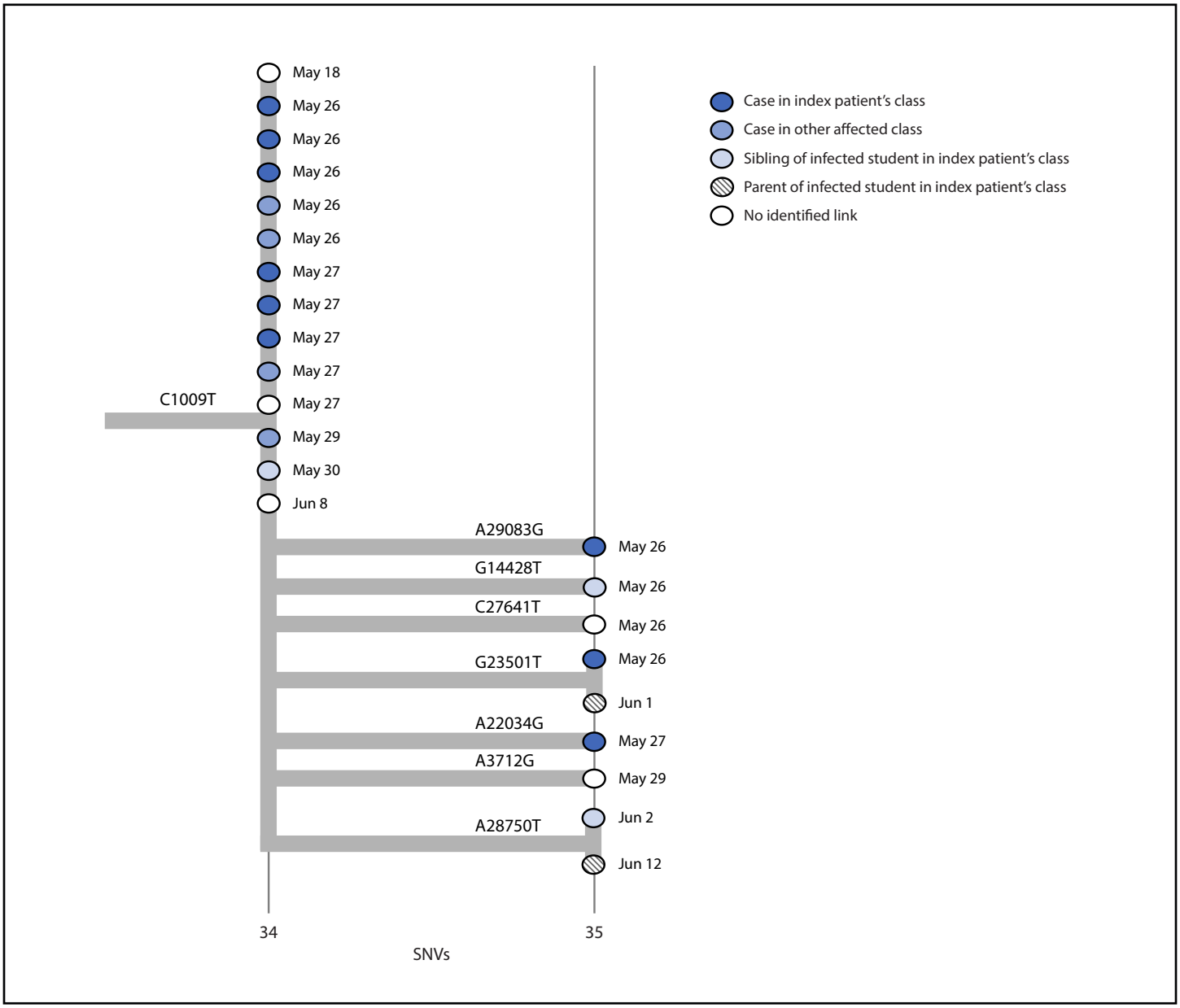
The findings in this study are subject to at least three limitations. First, the teacher's specimen was unavailable for WGS, which prevented phylogenetic identification of the outbreak's index patient. Second, testing for parents and siblings was self-directed and took place mostly outside the school setting, which could have led to underascertainment of cases. Finally, challenges in testing acceptance among possible contacts from outside the school led to difficulty in characterizing the outbreak's actual spread into the community, as is evidenced by later discovery of additional community cases with sequences indistinguishable from those in the school outbreak.

Ineligibility because of age and lack of vaccination contribute to persistent elevated risk for outbreaks in schools, especially as new SARS-CoV-2 variants emerge. However, implementation

[†] https://www.protocols.io/view/ncov-2019-sequencing-protocol-bbmuik6w
[§] https://public-health-viral-genomics-theiagen.readthedocs.io/en/latest/titan_workflows.html
[¶] https://auspice.us

[**] https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html (accessed August 10, 2021)
[††] https://coronavirus.marinhhs.org/ (accessed August 10, 2021)

FIGURE 3. Phylogenetic tree*,† of SARS-CoV-2 whole genome sequences and specimen collection dates§ from a COVID-19 outbreak in an elementary school¶ — Marin County, California, May–June 2021



Abbreviations: SNV = single nucleotide variant; WGS = whole genome sequencing.

* Phylogenetic tree was created with UShER, which uses the Fitch–Sankoff algorithm (a maximum parsimony-based phylogenetic placement approach). https://doi.org/10.1038/s41588-021-00862-7

† Specimen for the index patient was not available for WGS and is not included on the phylogenetic tree.

§ Dates in this diagram reflect the collection date for specimens that underwent WGS; thus dates might differ from those reported in the text for persons whose initial specimens were discarded.

¶ Branches are labeled with SNVs; cases (circles) are color-coded to indicate social relationship within the outbreak and labeled with the collection date for the specimen that was sequenced. Vertical lines represent genetically identical viruses; horizontal lines represent genetic descendants with additional SNVs. All sequenced specimens are classified as the SARS-CoV-2 B.1.617.2 (Delta) variant.

Summary

What is already known about this topic?

The SARS-CoV-2 B.1.617.2 (Delta) variant is highly transmissible. Prevention guidance in schools varies by jurisdiction.

What is added by this report?

During May 23–June 12, 2021, 26 laboratory-confirmed COVID-19 cases occurred among Marin County, California, elementary school students and their contacts following exposure to an unvaccinated infected teacher. The attack rate in one affected classroom was 50%; risk correlated with seating proximity to the teacher.

What are the implications for public health practice?

Vaccines are effective against the Delta variant, but transmission risk remains elevated among unvaccinated persons in schools. In addition to vaccination, strict adherence to multiple nonpharmaceutical prevention strategies, including masking, are important to ensure safe school instruction.

of multiple prevention strategies within schools can mitigate this risk. The rapid transmission and vaccine breakthrough infections in this outbreak might have resulted from the schoolchildren's vulnerability because of ineligibility for vaccination, coupled with the high transmissibility of the Delta variant. New evidence of the Delta variant's high transmissibility, even among fully vaccinated persons (*6*,*7*), supports recommendations for universal masking in schools[§§] (*1*). Further application of nonpharmaceutical prevention strategies, including routine testing, ventilation, and staying home while symptomatic, are also important for protecting the health of schoolchildren ineligible for vaccination because of their age (*3*). In addition, phylogenetic analysis can help to clarify transmission patterns and characterize outbreak progression. Capacity-building efforts offered by regional and state laboratories enabled more sophisticated analysis at the local level; such efforts might be useful as vaccination rates increase, new variants emerge, and outbreaks become more localized.

[§§] https://www.cdph.ca.gov/Programs/CID/DCDC/Pages/COVID-19/K-12-Guidance-2021-22-School-Year.aspx (accessed August 2, 2021)

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COVID-19 Case Rates in Transitional Kindergarten Through Grade 12 Schools and in the Community — Los Angeles County, California, September 2020–March 2021

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In-person instruction during the COVID-19 pandemic concerns educators, unions, parents, students, and public health officials as they plan to create a safe and supportive learning environment for children and adolescents (*1*). Los Angeles County (LAC), the nation's largest county, has an estimated population of 10 million, including 1.7 million children and adolescents aged 5–17 years (*2*). LAC school districts moved to remote learning for some or all students in transitional kindergarten* through grade 12 (TK–12) schools during the 2020–21 school year (*3*). Schools that provided in-person instruction were required by LAC Health Officer orders to implement prevention measures such as symptom screening, masking, physical distancing, cohorting, and contact tracing (*4*). This analysis compares COVID-19 case rates in TK–12 schools among students and staff members who attended school in person with LAC case rates during September 2020–March 2021.

LAC schools are required to report all laboratory-confirmed COVID-19 cases in persons who were on campus during their incubation or infectious period to the LAC Department of Public Health (DPH).† School-associated cases were defined as cases among students and staff members who were on campus for any length of time from 14 days before symptom onset or testing (whichever was earlier) until isolation. Cases among students and staff members who participated exclusively in online learning or worked remotely were not considered school-associated cases. DPH and the LAC Office of Education also collected information from the county's 80 public school districts on the estimated number of students and staff members routinely on campus each month during September 2020–March 2021. Monthly attendance was prorated based on when schools opened and ranged from 2,738 to 62,369 students and 36,862 to 45,757 staff members. Student and staff member case rates were calculated using the number of school-associated cases reported to DPH, assigned to a month by episode date, and divided by monthly attendance. Community case rates among children and adolescents aged 5–17 years and adults aged 18–79 years were calculated using the number of reported cases in LAC divided by the 2019 county population.§ Standard errors were calculated for school-associated rates. Analyses were conducted using SAS (version 9.4; SAS Institute). This public health surveillance activity was approved by DPH.

During September 1, 2020–March 31, 2021, a total of 463 school-associated cases were reported among students attending public TK–12 schools in person and 3,927 among staff members working on-site. During the same period, 105,577 cases among children and adolescents aged 5–17 years and 771,409 cases among adults aged 18–79 years were reported in LAC. School-associated case rates remained low among students, ranging from 110 per 100,000 in September to 859 in December 2020 (Figure). Case rates among all children and adolescents aged 5–17 years in the county were higher during most of the period, ranging from 167 per 100,000 in September to 2,938 in December 2020. School-associated case rates among staff members were lowest in September 2020 (125 per 100,000), peaked in December 2020 (4,109), and fell sharply through March 2021 (188). These rates reflected the trend among all adults aged 18–79 years in the county (319 per 100,000 in September 2020; 4,624 in December 2020; and 181 in March 2021) but were lower for most of the period. As total cases fell sharply in February, rates across the four groups declined to similar levels by March 2021.

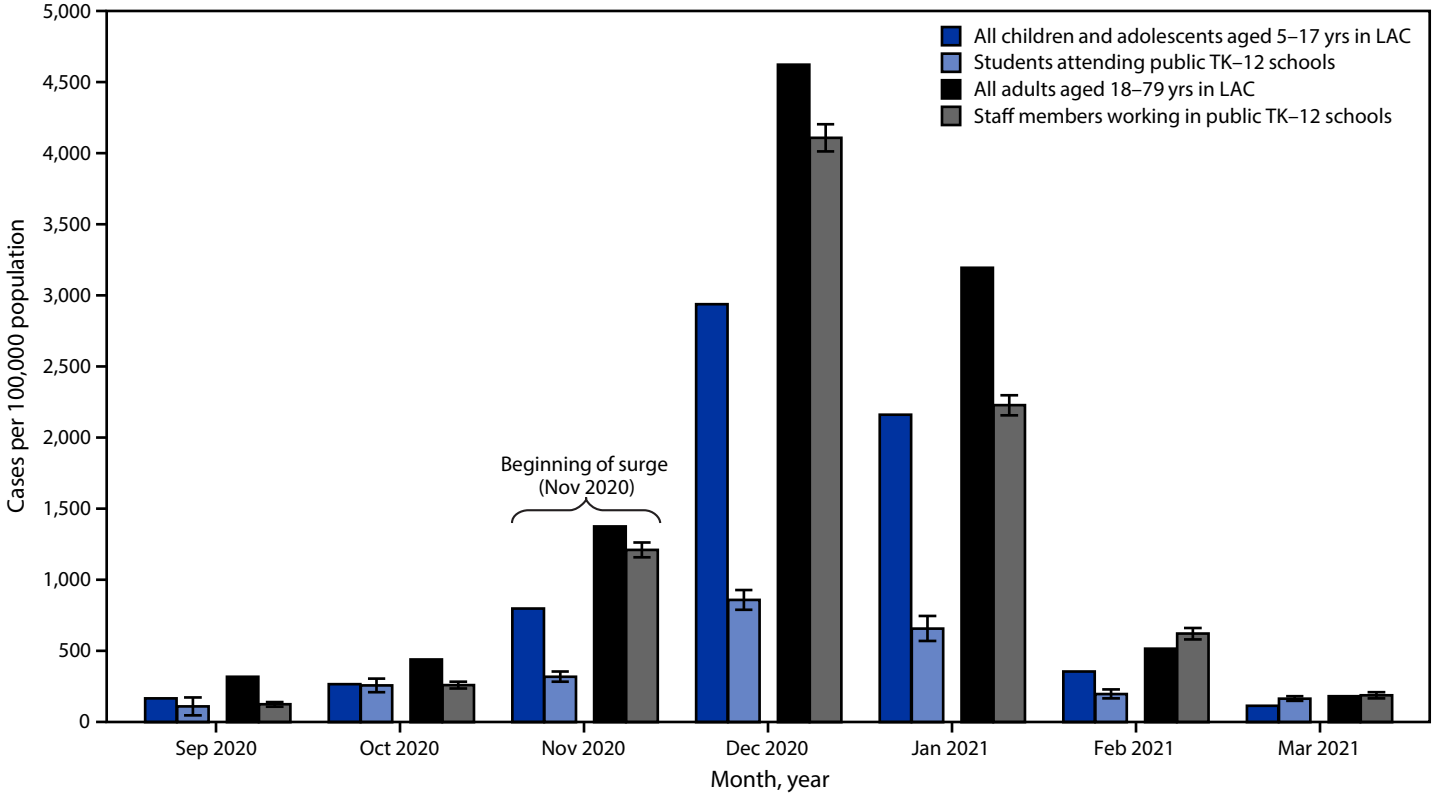
The findings in this report are subject to at least three limitations. First, these findings from one county should be interpreted with caution and are not necessarily generalizable to other areas. Second, the analysis did not include the entire school year because estimates of students and staff members on campus were collected only through March 2021. Finally, because of limited available information about the population on campus, rates were unadjusted and did not examine potential differences in demographic and socioeconomic characteristics by in-person status. However, sensitivity analysis showed similar trends across LAC's eight Service Planning Areas.

* Transitional kindergarten is a public school program serving to bridge preschool and kindergarten.

† During the observation period, school districts recommended diagnostic testing for students and staff members to identify persons with active infection based on symptoms and exposure. In addition to mandatory laboratory or provider reporting of positive COVID-19 nucleic acid amplification test (NAAT) and antigen test results, schools also notified DPH of cases occurring on campus. Schools relied on staff members, students, parents and guardians, and testing programs where available to inform them of cases and worked with DPH to identify and provide testing for close contacts on campus. The Los Angeles Unified School District (largest of the 80 school districts in the county) implemented a screening testing program using NAATs for staff members and students on campus beginning September 2020 and reported all positive results to DPH.

§ Cities of Long Beach and Pasadena were not included because they have their own health departments separate from LAC DPH. The adult age range reflects the age range of staff members working at TK–12 schools in LAC during the analysis period.

FIGURE. COVID-19 case rates* among children, adolescents, and adults† in transitional kindergarten through grade 12 schools and in the community, by month — Los Angeles County, California, September 2020–March 2021



Abbreviations: LAC = Los Angeles County; TK–12 = transitional kindergarten through grade 12.
* New cases per month per 100,000 persons; standard error bars shown for school case rates.
† Adult staff members comprise all school employees and associated workers on campus, including teachers, nurses, public safety officers, administrative staff members, campus aides, food service workers, custodians, and transportation staff members.

The findings suggest that implementing recommended prevention measures might protect children, adolescents, and adults from COVID-19 in TK–12 schools. The level of protection appears to be higher in children and adolescents than in adults, which is promising for children aged <12 years because no COVID-19 vaccine is currently authorized for this age group. In schools with safety protocols in place for prevention and containment, case rates in children and adolescents were 3.4 times lower during the winter peak compared with rates in the community. This analysis reflects transmission patterns before the more transmissible SARS-CoV-2 B.1.617.2 (Delta) variant became predominant in the United States. A multipronged prevention strategy, including masking, physical distancing, testing, and most recently vaccination of children and adolescents aged ≥12 years, will remain critical to reducing transmission as more students return to the classroom (5). These findings from a large and diverse county present preliminary evidence that schools provided a relatively safe environment during the 2020–21 school year.

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Epidemiologically Linked COVID-19 Outbreaks at a Youth Camp and Men's Conference — Illinois, June–July 2021

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On June 30, 2021, the Illinois Department of Public Health (IDPH) contacted CDC concerning COVID-19 outbreaks at two events sponsored by the same organization: a 5-day overnight church camp for persons aged 14–18 years and a 2-day men's conference. Neither COVID-19 vaccination nor COVID-19 testing was required before either event. As of August 13, a total of 180 confirmed and probable cases had been identified among attendees at the two events and their close contacts. Among the 122 cases associated with the camp or the conference (primary cases), 18 were in persons who were fully vaccinated, with 38 close contacts. Eight of these 38 close contacts subsequently became infected with SARS-CoV-2, the virus that causes COVID-19 (secondary cases); among the eight close contacts with secondary cases, one half (four) were fully vaccinated. Among the 180 total persons with outbreak-associated cases, five (2.8%) were hospitalized; no deaths occurred. None of the vaccinated persons with cases were hospitalized. Approximately 1,000 persons across at least four states were exposed to SARS-CoV-2 through attendance at these events or through close contact with a person who had a primary case. This investigation underscores the impact of secondary SARS-CoV-2 transmission during large events, such as camps and conferences, when COVID-19 prevention strategies are not implemented. In Los Angeles County, California, during July 2021, when the SARS-CoV-2 B.1.617.2 (Delta) variant was predominant, unvaccinated residents were five times more likely to be infected and 29 times more likely to be hospitalized from infection than were vaccinated residents (*1*). Implementation of multiple prevention strategies, including vaccination and nonpharmaceutical interventions such as masking, physical distancing, and screening testing, are critical to preventing SARS-CoV-2 transmission and serious complications from COVID-19.

Investigation and Findings

The camp was held during June 13–17, 2021, and included persons aged 14–18 years from a church organization with multiple locations across western Illinois, Iowa, and Missouri. A total of 294 campers arrived on buses or large passenger vans and were met by 41 staff members. No proof of COVID-19 vaccination or SARS-CoV-2 pretesting or testing on arrival was required, and the list of suggested items to bring to camp did not include masks. Campers were housed in large, shared boarding facilities of approximately 100 campers each, dined in a cafeteria together, participated in indoor and outdoor small group activities in which campers were with the same persons during program events, and participated in activities with all campers during all 5 days.

On June 16, the second to last camp day, one camper departed after becoming ill with a fever and respiratory symptoms and subsequently received a laboratory-confirmed diagnosis of COVID-19. Campers and staff members were notified, encouraged to receive SARS-CoV-2 testing, and instructed to quarantine per CDC guidance and isolate if they received a positive test result.*

Six camp staff members who received positive SARS-CoV-2 test results also attended the conference during June 18–19 but did not receive their results until after the conference ended; all six staff members had symptom onset during June 17–29.† The conference was held at a different location from the camp and included 500 attendees and 30 staff members, and, as with the camp, no COVID-19 vaccination, SARS-CoV-2 testing, or masking was required. The first case in a conference attendee was diagnosed on June 21, 2 days after the conference. After conference-associated COVID-19 cases were identified, conference attendees and staff members were notified, encouraged to receiving SARS-CoV-2 testing, and instructed to quarantine per CDC guidance and isolate if they received a positive test result.

A confirmed case was defined as receipt of a positive SARS-CoV-2 nucleic acid amplification test result in a camp or conference attendee, and a probable case was defined as receipt of a positive SARS-CoV-2 antigen test result.§ Cases were identified through case investigation after laboratory notification of a positive test result. Information on symptom onset or specimen collection dates (available for 174 [97%] of

* Persons with positive SARS-CoV-2 test results were instructed to isolate in accordance with CDC guidance at the time (https://www.cdc.gov/coronavirus/2019-ncov/hcp/duration-isolation.html), and close contacts were instructed to quarantine in accordance with CDC guidance at the time (https://www.cdc.gov/coronavirus/2019-ncov/if-you-are-sick/quarantine.html).

† Six staff members (three at the camp and three at the conference) were identified as having cases on the basis of their symptom onset date. Because the complete rosters had not been provided to IDPH, persons might have been counted as attendees at both events.

§ https://ndc.services.cdc.gov/case-definitions/coronavirus-disease-2019-2020-08-05/

180 persons), COVID-19 vaccination status (from the state immunization registry), county of residence, test results, and viral sequencing data (available for 31 [17%] persons) was collected for persons with camp- and conference-associated cases (primary cases). IDPH's contact tracing system identified close contacts of persons with primary cases; close contacts were defined as unmasked persons who were within 6 ft of a person with a primary case for >15 minutes during a 24-hour period while that person was infectious, which was 2 days before through 10 days after symptom onset (for symptomatic persons) or after specimen collection date (for asymptomatic persons). Secondary cases were defined as COVID-19 cases that occurred in close contacts of persons with a primary case of confirmed or probable COVID-19.

Persons who had received 2 doses of Pfizer BioNTech or Moderna COVID-19 mRNA vaccine or 1 dose of Janssen (Johnson & Johnson) COVID-19 vaccine ≥14 days before exposure were considered fully vaccinated. IDPH laboratories performed whole genome sequencing on 25 of 31 available specimens.[¶] Descriptive analyses were conducted to determine the distribution of cases by vaccination status, the proportion of SARS-CoV-2 variants, and the secondary transmission rate. This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.[**]

As of August 13, a total of 180 outbreak-associated cases had been identified, including 122 primary cases, 87 (48%) of which were in camp attendees (among 335 total campers and staff members; attack rate = 26%) and 35 (19%) in conference attendees (among 530 total conference participants and staff members; attack rate = 7%). Among 262 close contacts of camp or conference attendees, 58 (22%) secondary cases were identified, representing 32% of the 180 identified cases (Figure) (Table). Among the 87 persons with camp-associated cases, none reported symptom onset before the camp started on June 13. Among the 35 persons with conference-associated cases, three reported being symptomatic during the conference (not including one camp-associated staff member who attended the conference while symptomatic).

Among the 180 total persons with outbreak-associated cases, 13 (7.2%) required medical care in an emergency department, and five (2.8%) were hospitalized; no deaths occurred (Table). None of the vaccinated persons with cases were hospitalized; three sought care at an emergency department. Overall, 29 (16.1%) cases occurred in fully vaccinated persons (camp cases: 9%; conference cases: 29%). Among the 262 close contacts of persons with a primary case, 52 (20%) were fully vaccinated; 11 of these fully vaccinated persons received a positive SARS-CoV-2 test result, representing 19% of the 58 secondary cases among close contacts of camp or conference attendees with primary cases.

Among the 122 cases in camp or conference attendees, 18 were in fully vaccinated persons (eight in camp attendees and 10 in conference attendees). These 18 fully vaccinated persons reported a total of 38 close contacts; eight (21%) of these close contacts received positive SARS-CoV-2 test results, four (50%) of whom were fully vaccinated. Among the 224 reported close contacts of unvaccinated and partially vaccinated persons with primary cases, 50 (22%) received positive SARS-CoV-2 test results, including seven fully vaccinated persons. Among 58 persons with secondary cases, 48 (83%) were infected by household members, four by nonhousehold family members, three by friends, and one each by a neighbor, at work, or during a Bible study group.

Overall, 1,127 persons from at least four states and 18 counties were exposed to SARS-CoV-2 through attendance at the camp or conference or through close contact with a person who had a camp- or conference-associated case. In the 7 days before the camp (June 6–12), Adams County, Illinois,[††] reported 31 COVID-19 cases, with an average of 4.4 cases per day. In the 7 days after the last identified secondary case (July 16–22), the county reported 232 cases, with an average of 33.1 per day, a 648% increase from the number reported during the week before the camp (*2*).

Among samples sequenced from specimens from 31 infected persons (15 from camp-associated cases, eight from conference-associated cases, and eight from secondary cases), the B.1.617.2 (Delta) variant was identified in 27 (87%), including two AY.3 (Delta) sequences; the B.1.1.7 (Alpha) variant was identified in three (10%); and the P.1 (Gamma) variant was identified in one (3%) (Table). Among eight sequenced samples from specimens from vaccinated persons, the Delta variant was identified in seven samples, and Alpha in one.[§§]

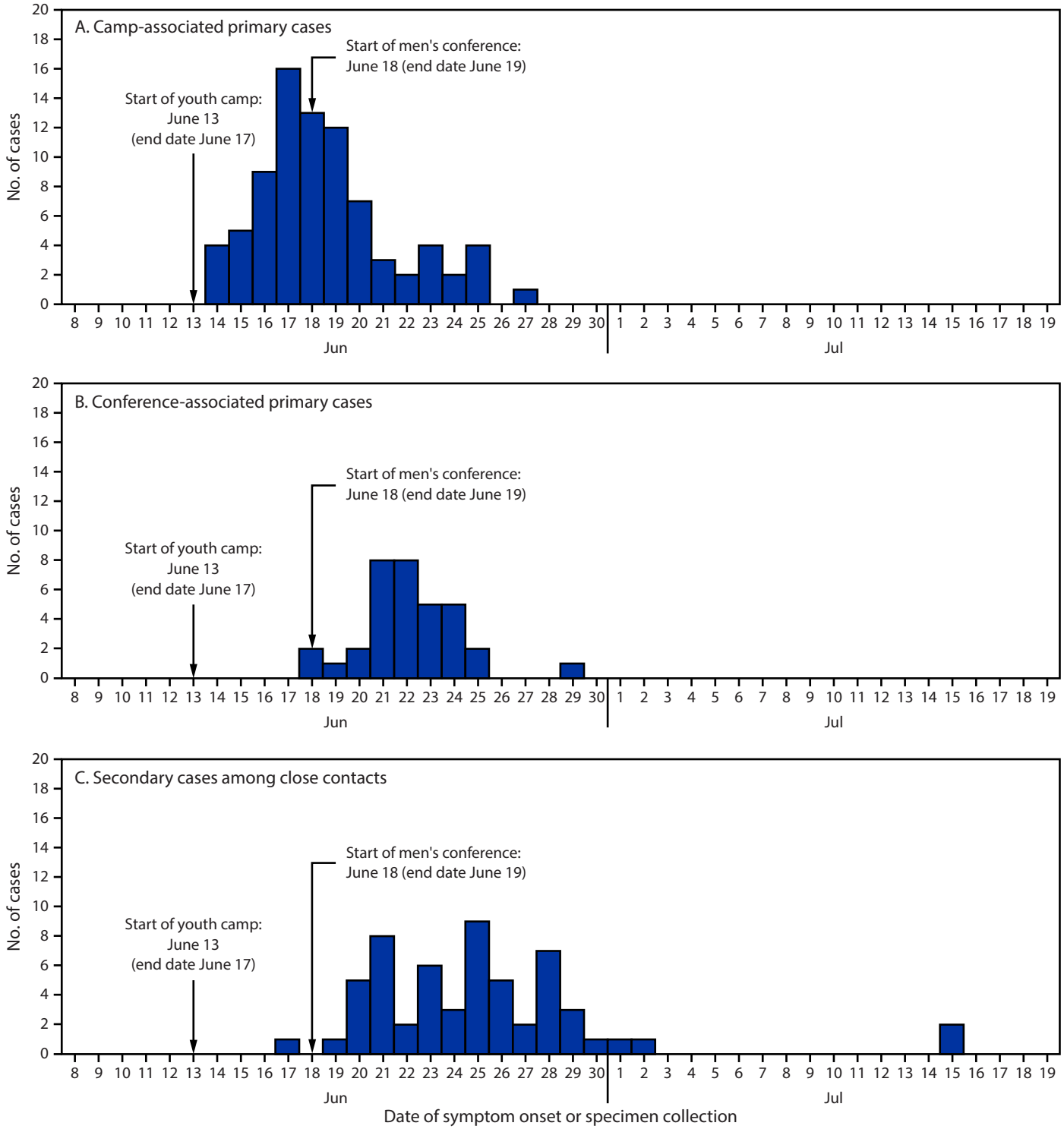
[¶] Whole genome sequencing was performed on Illumina's NextSeq 550 instrument using the COVID-Seq workflow. Consensus genome assembly was performed in Illumina's DRAGEN analytical pipeline, and variants were assigned using the most recent Pangolin version.

[**] 45 C.F.R. part 46.102(l)(2), 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

[††] Adams County is used as the reference county because it was the county of residence for 49% (43) of persons with camp-associated cases, 40% (14) of persons with conference-associated cases, and 59% (34) of persons with secondary cases.

[§§] Six of these eight vaccinated persons who were infected with SARS-CoV-2 variants of concern were from households with two persons with sequenced samples; two pairs of the Delta variant and one discordant pair of Delta and Alpha variants were identified in samples from these households.

FIGURE. Number of primary COVID-19 cases among attendees of a youth camp (A) and men's conference (B) and secondary cases among close contacts* (C), by date of symptom onset or specimen collection† — Illinois, June–July 2021



* Close contacts were defined as unmasked persons who were within 6 ft of a person with a camp-or conference-associated (primary) case for >15 minutes during a 24-hour period while that person was infectious (i.e., 2 days before through 10 days after symptom onset or specimen collection date). Secondary cases were defined as COVID-19 cases in close contacts of persons with a primary case of confirmed or probable COVID-19 (confirmed: receipt of a positive SARS-CoV-2 nucleic acid amplification test result in an attendee; probable: receipt of a positive SARS-CoV-2 antigen test result).

† Symptom onset date or specimen collection date was missing for six out-of-state persons. Among the remaining 174, onset date was available for 158 (91%), and specimen collection date was available for 16 (9%).

Public Health Response

IDPH sent three Epi-X notifications[¶¶] about these outbreaks to state and local health departments and received case data from the state health departments in Iowa, Michigan, and Missouri. On June 30, IDPH requested CDC's assistance with investigating these outbreaks. On July 19, a CDC field team arrived in Illinois to assist with active case finding in several jurisdictions, collection and analysis of samples, and ascertainment of secondary transmission. As of August 13, complete rosters of attendees and staff members at both events were not available.

Discussion

COVID-19 vaccines currently authorized by the Food and Drug Administration are safe and highly effective for preventing COVID-19–related serious illness, hospitalization, and death.[***] In this investigation, most reported COVID-19 cases were identified among unvaccinated persons. However, transmission of SARS-CoV-2 from vaccinated persons both to unvaccinated and vaccinated persons likely occurred. These breakthrough cases among vaccinated persons were identified among attendees of the camp and the conference and in persons exposed to the attendees. Consistent with previous studies, much of the identified secondary transmission occurred within households, where most prolonged contact occurs (*3*).

Approximately 1,000 persons in at least four states were exposed to SARS-CoV-2 through attendance at the camp or conference or through close contact with a person infected at the event. The high rate of transmission was likely driven by the number of persons infected with the SARS-CoV-2 Delta variant. However, because multiple SARS-CoV-2 variants of concern were identified from the specimens of camp attendees, this suggests multiple introductions of SARS-CoV-2 into the camp, rather than a single introduction event. As of August 7, COVID-19 outbreaks in at least 21 overnight camps had been reported in Illinois, reinforcing the importance of COVID-19 prevention measures at these camps, including identifying infected persons through prearrival and screening testing programs and consistent implementation of other prevention efforts, including vaccination, masking, and physical distancing (*4*–*6*). Several camp staff members who were infected with SARS-CoV-2 (including at least one symptomatic person) or who had been exposed to the virus attended another large group event during their infectious period. Therefore, timely notification of all close contacts and compliance with isolation and quarantine guidance are also critical.

The findings in this report are subject to at least two limitations. First, the investigation likely underestimates the number of SARS-CoV-2 primary infections, secondary exposures, and secondary cases because the case definition required laboratory confirmation; therefore, infected persons who did not receive testing or who used at-home SARS-CoV-2 antigen tests (i.e., self-collection kits) were not included in the case count. In addition, not all persons with cases participated in contact tracing; the close contacts of persons who did participate were

TABLE. Characteristics of persons with primary COVID-19 cases after attendance at a youth camp or men's conference and of close contacts with secondary COVID-19 cases — Illinois, June–July 2021

Characteristic	No. (%)			
	Camp cases	Conference cases	Secondary cases	Total
Minimum no. of persons exposed	**335**	**530**	**262**	**1,127**
Reported cases*	87 (26)	35 (7)	58 (22)	**180 (16)**
Median age, yrs (range)[†]	17 (13–54)	44 (15–68)	38 (3–72)	**26 (3–72)**
Sex[†]				
Male	28 (34)	35 (100)	20 (34)	**83 (47)**
Female	55 (66)	0 (—)	38 (66)	**93 (53)**
Persons who required emergency department care	3 (3)	5 (14)	5 (9)	**13 (7)**
Persons hospitalized	1 (1)	3 (9)	1 (2)	**5 (3)**
Fully vaccinated persons[§]	8 (9)	10 (29)	11 (19)	**29 (16)**
Vaccine product received by fully vaccinated persons				
Pfizer-BioNTech	3 (38)	5 (50)	3 (27)	**11 (41)**
Moderna	2 (25)	3 (30)	2 (18)	**7 (24)**
Janssen (Johnson & Johnson)	3 (38)	2 (20)	6 (55)	**11 (38)**
Unknown vaccine product received or partially vaccinated	79 (91)	25 (71)	47 (81)	**151 (84)**
No. of viruses sequenced[¶]	15	8	8	**31**
B.1.617.2 (Delta)	13 (87)	7 (88)	7 (88)	**27 (87)**
B.1.1.7 (Alpha)	1 (7)	1 (13)	1 (13)	**3 (10)**
P.1 (Gamma)	1 (7)	0 (—)	0 (—)	**1 (3)**
Minimum no. of affected counties**	16	7	8	**18**

* Percentages might not sum to 100% because of rounding.
† For 174 of 180 cases in persons with a reported onset or specimen collection date, sex (176), and date of birth.
§ Fully vaccinated persons were defined as persons who had received 2 doses of Pfizer BioNTech or Moderna COVID-19 mRNA vaccine or 1 dose of Janssen (Johnson & Johnson) COVID-19 vaccine ≥14 days before exposure.
¶ Illinois Department of Public Health laboratories performed whole genome sequencing on 25 of 31 specimens using Illumina's NextSeq 550 instrument with the COVID-Seq workflow. Consensus genome assembly was performed in Illumina's DRAGEN analytical pipeline, and variants were assigned using the most recent Pangolin version.
** Because seven of 16 counties of residence identified among camp and conference attendees were outside of Illinois, contact tracing data were extremely limited.

¶¶ Epi-X is a secure, web-based notification system, with approximately 6,000 users from public health agencies, that guides and coordinates public health professionals during public health threats and investigations. https://emergency.cdc.gov/epix/index.asp
*** https://www.cdc.gov/coronavirus/2019-ncov/vaccines/vaccine-benefits.html

Summary

What is already known about this topic?

The Illinois Department of Public Health investigated COVID-19 outbreaks at two events sponsored by the same organization: a 5-day overnight church camp for persons aged 14–18 years and a 2-day men's conference.

What is added by this report?

Neither COVID-19 vaccination nor COVID-19 testing was required before either event. Among 122 primary cases, 104 (85%) were in persons who were not fully vaccinated, and 18 (15%) were in fully vaccinated persons. Eight of 38 (21%) close contacts of the 18 fully vaccinated persons subsequently became infected with SARS-CoV-2. No vaccinated persons with COVID-19 were hospitalized.

What are the implications for public health practice?

This investigation underscores the impact of secondary SARS-CoV-2 transmission during large events such as camps and conferences when COVID-19 prevention strategies, including vaccination, masking, physical distancing, and screening testing, are not implemented.

likely underreported and were biased toward household contacts (*7*). Second, investigators did not have access to complete rosters for the camp or conference, which limited case finding efforts and analyses involving persons who were not infected (particularly findings related to vaccination status).

These findings underscore the risk for COVID-19 outbreaks at camps and large events where prevention strategies are not implemented and highlight the importance of implementing such strategies to reduce transmission of SARS-CoV-2 in these settings (*8*). Promoting vaccination, implementing and encouraging compliance with prompt quarantine and isolation measures for exposed and infected persons, staying home when sick, and using nonpharmaceutical interventions including masking, physical distancing, and screening testing in large group settings can help reduce secondary infections in homes and the community and serious complications from COVID-19 (*9*).

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Association Between COVID-19 and Myocarditis Using Hospital-Based Administrative Data — United States, March 2020–January 2021

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Viral infections are a common cause of myocarditis, an inflammation of the heart muscle (myocardium) that can result in hospitalization, heart failure, and sudden death (*1*). Emerging data suggest an association between COVID-19 and myocarditis (*2*–*5*). CDC assessed this association using a large, U.S. hospital-based administrative database of health care encounters from >900 hospitals. Myocarditis inpatient encounters were 42.3% higher in 2020 than in 2019. During March 2020–January 2021, the period that coincided with the COVID-19 pandemic, the risk for myocarditis was 0.146% among patients diagnosed with COVID-19 during an inpatient or hospital-based outpatient encounter and 0.009% among patients who were not diagnosed with COVID-19. After adjusting for patient and hospital characteristics, patients with COVID-19 during March 2020–January 2021 had, on average, 15.7 times the risk for myocarditis compared with those without COVID-19 (95% confidence interval [CI] = 14.1–17.2); by age, risk ratios ranged from approximately 7.0 for patients aged 16–39 years to >30.0 for patients aged <16 years or ≥75 years. Overall, myocarditis was uncommon among persons with and without COVID-19; however, COVID-19 was significantly associated with an increased risk for myocarditis, with risk varying by age group. These findings underscore the importance of implementing evidence-based COVID-19 prevention strategies, including vaccination, to reduce the public health impact of COVID-19 and its associated complications.

Data for this study were obtained from the Premier Healthcare Database Special COVID-19 Release (PHD-SR), a large hospital-based administrative database.† The monthly number of myocarditis§ and COVID-19¶ inpatient encounters was assessed before and during the COVID-19 pandemic, from January 2019 through May 2021.

A patient-level cohort was created to assess the association between COVID-19 and myocarditis. The cohort included all patients with at least one inpatient or hospital-based outpatient encounter with discharge during March 2020–January 2021. To minimize potential bias from vaccine-associated myocarditis (*6*), 277,892 patients with a COVID-19 vaccination record in PHD-SR during December 2020–February 2021 were excluded. In addition, 37,896 patients for whom information on sex was missing were excluded. Patients with COVID-19 were defined as those who had their first inpatient or outpatient encounter with a COVID-19 *International Classification of Diseases, Tenth Revision, Clinical Modification* (ICD-10-CM) code during March 2020–January 2021. Patients with myocarditis were defined as those who had their first of at least one inpatient encounter, at least two outpatient encounters, or at least one outpatient encounter with a relevant specialist** with a myocarditis ICD-10-CM code during March 2020–February 2021.†† Among patients with COVID-19, the first myocarditis encounter could have occurred during or after the first COVID-19 health care encounter.

The risk for myocarditis was defined as the percentage of patients with myocarditis and was calculated among patients with and without COVID-19, overall and by sex (male or

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† PHD-SR, formerly known as the PHD COVID-19 Database, is a large U.S. hospital-based all-payer database that includes inpatient and hospital-based outpatient (e.g., emergency department or clinic) health care encounters from >900 geographically diverse, nonprofit, nongovernmental, community, and teaching hospitals and health systems from rural and urban areas. PHD-SR represents approximately 20% of inpatient admissions in the United States. Updated PHD-SR data are released every 2 weeks; release date August 4, 2021, access date August 4, 2021. http://offers.premierinc.com/rs/381-NBB-525/images/PHD_COVID-19_White_Paper.pdf

§ Myocarditis was identified by the following *International Classification of Diseases, Tenth Revision, Clinical Modification* (ICD-10-CM) codes: B33.20, B33.22, B33.24, I40.0, I40.1, I40.8, I40.9, or I51.4.

¶ COVID-19 was identified by ICD-10-CM code B97.29 (other coronavirus as the cause of diseases classified elsewhere) during March–April 2020 or ICD-10-CM code U07.1 (COVID-19, virus identified [laboratory-confirmed]) during or after April 2020. ICD-10-CM code B97.29 was recommended before the April 1, 2020, release of ICD-10-CM code U07.1. https://www.cdc.gov/nchs/data/icd/Announcement-New-ICD-code-for-coronavirus-3-18-2020.pdf

** Attending physician with one of the following specializations: cardiac electrophysiology, cardiovascular diseases, cardiovascular surgery, infectious diseases, or rheumatology.

†† Myocarditis was assessed using all encounters for each patient from January 2019 to February 2021. Patients were defined as having new myocarditis during the study period if their first myocarditis encounter in PHD-SR occurred during or after March 2020. Myocarditis was assessed through February 2021 to allow for myocarditis diagnoses to occur after COVID-19 diagnoses in January 2021.

female) and age group (<16, 16–24, 25–39, 40–49, 50–64, 65–74, and ≥75 years). The percentage of myocarditis patients with a history of COVID-19 was calculated for each age group.

Associations between COVID-19 and myocarditis were estimated using a multiple logit model with the following covariates: three-way interaction between COVID-19, sex, and age group, including lower-order interactions and main effects; race/ethnicity; payer type; hospital U.S. Census region; and hospital urbanicity. Adjusted risk differences (aRDs, measure of absolute risk) were calculated as the difference between 1) the adjusted predicted risk for myocarditis (outcome) among patients with COVID-19 (exposed group) and 2) adjusted predicted risk for myocarditis among patients without COVID-19 (unexposed group); adjusted risk ratios (aRRs, measure of relative risk) were calculated as the ratio of the adjusted predicted risk among exposed to the adjusted predicted risk among unexposed[§§] (*7,8*). All models used standard errors clustered on a unique hospital identifier. R (version 4.0.2; R Foundation) and Stata (version 15.1; StataCorp) were used to conduct all analyses. This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.[¶¶]

During 2020, the number of myocarditis inpatient encounters (4,560) was 42.3% higher than that during 2019 (3,205). Peaks in myocarditis inpatient encounters during April–May 2020 and November 2020–January 2021 generally aligned with peaks in COVID-19 inpatient encounters (Figure 1).

Within the cohort of 36,005,294 patients, 1,452,773 (4.0%) received a diagnosis of COVID-19 during March 2020–January 2021, and 5,069 (0.01%) received a diagnosis of myocarditis during March 2020–February 2021. Overall, 4,339 (85.6%) patients with myocarditis were identified by an inpatient encounter. Patients with myocarditis were slightly older than patients without myocarditis (median age = 54 years versus 50 years) and were more commonly male (59.3% versus 41.7%) (Supplementary Table, https://stacks.cdc.gov/view/cdc/109261).

[§§] First, a multiple logit model was performed with the following covariates: three-way interaction between COVID-19, sex, and age group, including lower-order interactions and main effects; race/ethnicity; payer type; hospital U.S. Census region; and hospital urbanicity. Then the following average predicted probabilities (predictive margins) were estimated: 1) P1: the average predicted probability of myocarditis with COVID-19 set to be present and all other covariates set to their original values, and 2) P0: the average predicted probability of myocarditis with COVID-19 set to be absent and all other covariates set to their original values. aRD represents the difference in predicted probabilities (P1 minus P0); aRR represents the ratio of the predicted probabilities (P1 divided by P0). aRRs and aRDs were obtained for the full sample (where all covariates were set at their original values), for each age group (where age was set at the specific category of interest and other covariates were set at their original values), and for each sex (where sex was set at the specific category of interest and other covariates were set at their original values).

[¶¶] 45 C.F.R. part 46, 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. Sect. 3501 et seq.

Among patients with myocarditis, 2,116 (41.7%) had a history of COVID-19; this percentage was similar among males (42.4%) and females (40.9%) and differed by age group, with the lowest percentages among persons aged 16–24 years (23.7%) and 25–39 years (24.1%) and the highest among adults aged ≥75 years (64.6%) (Table). Among the 2,116 patients with COVID-19 and myocarditis, 1,895 (89.6%) received a diagnosis of COVID-19 and myocarditis during the same month; the remaining patients received a myocarditis diagnosis 1 month (139; 6.6%) or ≥2 months (82; 3.9%) after their COVID-19 diagnosis.

During March 2020–January 2021, the risk for myocarditis was 0.146% among patients with COVID-19 and 0.009% among patients without COVID-19. Among patients with COVID-19, the risk for myocarditis was higher among males (0.187%) than among females (0.109%) and was highest among adults aged ≥75 years (0.238%), 65–74 years (0.186%), and 50–64 years (0.155%) and among children aged <16 years (0.133%).

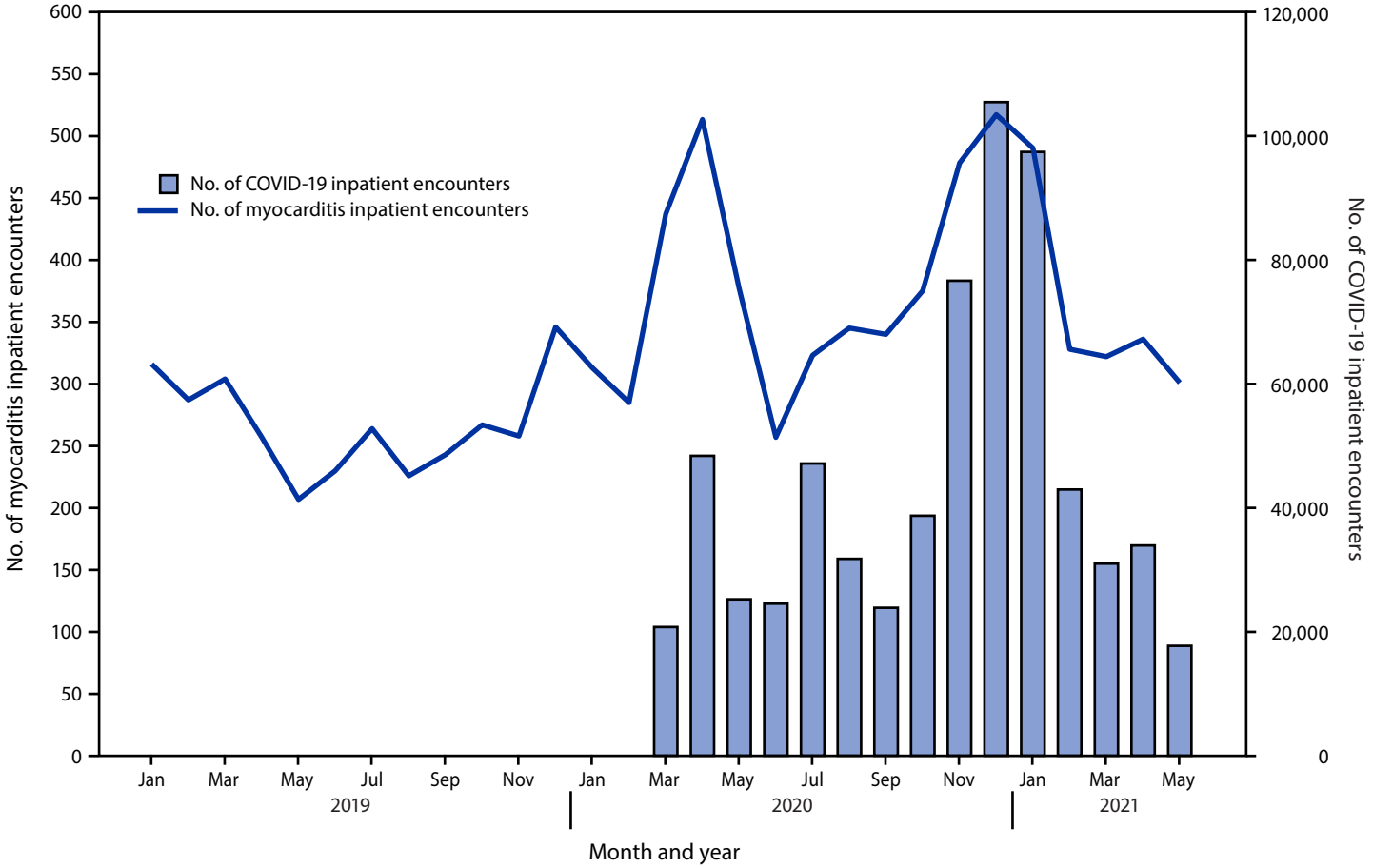
In adjusted analyses, patients with COVID-19 had, on average, 15.7 (95% CI = 14.1–17.2) times the risk for myocarditis compared with patients without COVID-19; however, because of the low risk for myocarditis in both groups, the aRD between patients with and without COVID-19 was small (aRD = 0.126%; 95% CI = 0.112%–0.140%) (Table) (Figure 2). The aRR of myocarditis was higher among females (17.8; 95% CI = 15.6–20.0) than among males (13.8; 95% CI = 12.3–15.3), whereas the aRD was higher among males (0.165%; 95% CI = 0.146%–0.183%) than among females (0.100%; 95% CI = 0.087%–0.113%). The aRR and aRD were lowest for patients aged 25–39 years and were higher among younger and older age groups. The aRRs ranged from approximately 7.0 for patients aged 16–24 and 25–39 years to >30.0 for patients aged <16 years and ≥75 years.

Discussion

In this study, the occurrence of myocarditis inpatient encounters was 42% higher in 2020 than in 2019. The risk for myocarditis among patients with COVID-19 during March 2020–January 2021 was nearly 16 times as high as the risk among patients without COVID-19, with the association between COVID-19 and myocarditis being most pronounced among children and older adults. Further, in this cohort, approximately 40% of patients with myocarditis had a history of COVID-19.

These findings suggest an association between COVID-19 and myocarditis, although causality cannot be inferred from observational data, and are consistent with those from previous studies (*2–5*). Before this report, the two largest known studies, in the United States and in Israel, also found that

FIGURE 1. Number of myocarditis and COVID-19 inpatient encounters, by month* — Premier Healthcare Database Special COVID-19 Release, United States, January 2019–May 2021



* Data from recent months might be incomplete.

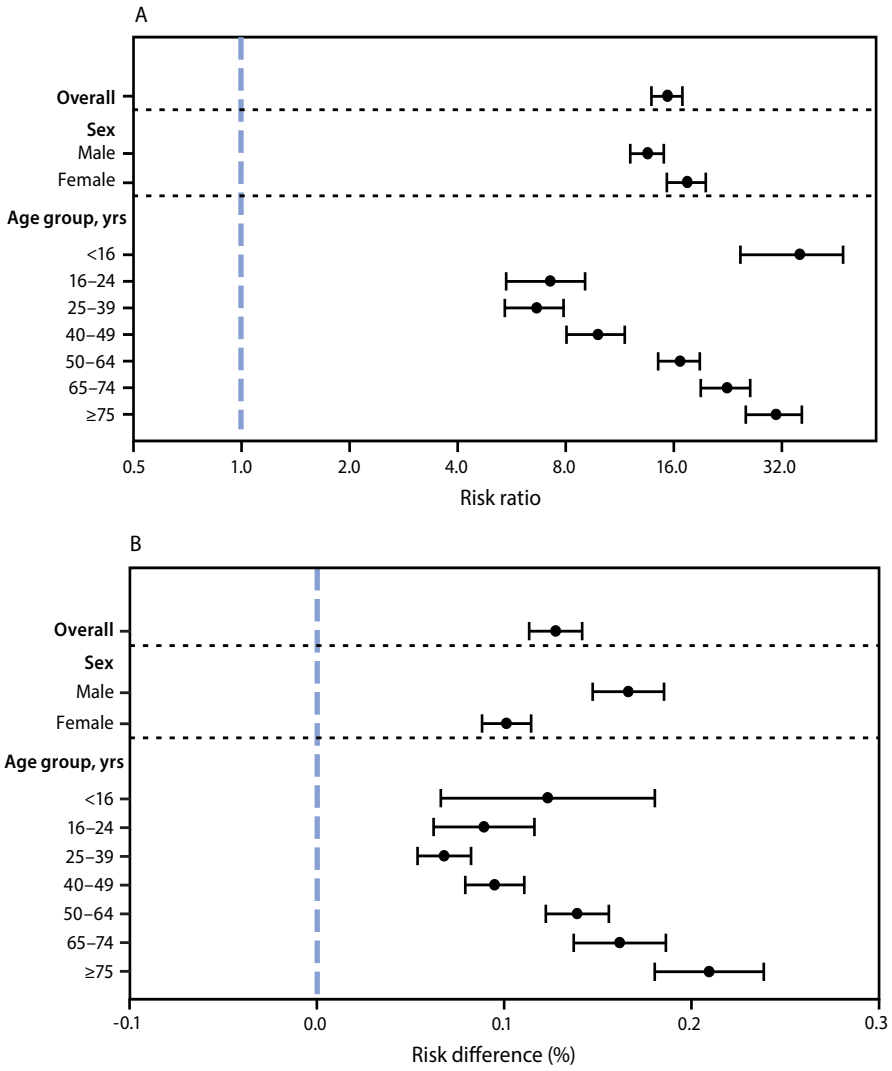
TABLE. Frequency of and risk for myocarditis among patients with and without COVID-19 and adjusted* myocarditis risk differences and risk ratios comparing patients with and without COVID-19 — Premier Healthcare Database Special COVID-19 Release, United States, March 2020–January 2021

Characteristic	No. of patients with COVID-19	No. of patients without COVID-19	No. of patients with myocarditis	Myocarditis among patients with COVID-19		Myocarditis among patients without COVID-19		Adjusted myocarditis risk difference (95% CI)	Adjusted myocarditis risk ratio (95% CI)
				No. (% of patients with myocarditis)	Risk, %	No. (% of patients with myocarditis)	Risk, %		
Overall	**1,452,773**	**34,552,521**	**5,069**	**2,116 (41.7)**	**0.146**	**2,953 (58.3)**	**0.009**	**0.126 (0.112–0.140)**	**15.7 (14.1–17.2)**
Sex									
Male	680,722	14,339,356	3,008	1,274 (42.4)	0.187	1,734 (57.6)	0.012	0.165 (0.146–0.183)	13.8 (12.3–15.3)
Female	772,051	20,213,165	2,061	842 (40.9)	0.109	1,219 (59.1)	0.006	0.100 (0.087–0.113)	17.8 (15.6–20.0)
Age group, yrs									
<16	64,898	3,670,762	218	86 (39.4)	0.133	132 (60.6)	0.004	0.122 (0.065–0.179)	36.8 (25.0–48.6)
16–24	123,865	3,067,575	511	121 (23.7)	0.098	390 (76.3)	0.013	0.088 (0.061–0.115)	7.4 (5.5–9.2)
25–39	268,549	6,246,568	862	208 (24.1)	0.077	654 (75.9)	0.010	0.067 (0.052–0.081)	6.7 (5.5–8.0)
40–49	198,561	4,147,909	620	213 (34.4)	0.107	407 (65.6)	0.010	0.093 (0.078–0.109)	10.0 (8.1–11.9)
50–64	356,697	7,965,264	1,226	553 (45.1)	0.155	673 (54.9)	0.008	0.137 (0.121–0.154)	17.0 (14.7–19.3)
65–74	214,331	5,318,474	801	398 (49.7)	0.186	403 (50.3)	0.008	0.160 (0.135–0.184)	23.0 (19.4–26.7)
≥75	225,872	4,135,969	831	537 (64.6)	0.238	294 (35.4)	0.007	0.208 (0.179–0.237)	31.6 (25.9–37.2)

Abbreviation: CI = confidence interval.

* Adjusted risk differences and risk ratios for myocarditis during or after COVID-19 (reference group: no COVID-19), obtained from a single logit model with the following covariates: a three-way interaction between presence of COVID-19, sex, and age group, including lower-order interactions and main effects; race/ethnicity; payer type; hospital U.S. Census region; and hospital urbanicity.

FIGURE 2. Adjusted risk ratio (A) and adjusted risk difference (B) of myocarditis comparing patients with and without COVID-19,* overall and by sex and age group — Premier Healthcare Database Special COVID-19 Release, United States, March 2020–January 2021



* The panels show adjusted risk ratios (A) and adjusted risk differences (B) of myocarditis comparing patients with COVID-19 to patients without COVID-19 (reference), obtained from a single logit model with the following covariates: a three-way interaction between presence of COVID-19, sex, and age group, including lower-order interactions and main effects; race/ethnicity; payer type; hospital U.S. Census region; and hospital urbanicity. 95% confidence intervals indicated by error bars.

COVID-19 was strongly associated with myocarditis (U.S. study: odds ratio = 8.17, 95% CI = 3.58–18.62; Israel study: risk ratio = 18.28, 95% CI = 3.95–25.12) (*3*,*4*).

In this study, the association between COVID-19 and myocarditis was lowest for persons aged 25–39 years and higher among younger (<16 years) and older (≥50 years) age groups, a pattern that has not been previously described in age-stratified analyses and that warrants further investigation. This finding might be partially explained by age-related differences in COVID-19 case ascertainment, because younger adults with less severe disease might be less likely than older adults to have a health care encounter with a COVID-19 diagnosis captured within PHD-SR. This age-related differential misclassification (underascertainment) of COVID-19 status might bias risk differences and risk ratios toward the null more for younger adults and could partially explain the observed age-related association.

The risk difference for myocarditis between persons with and without COVID-19 was higher among males than among females, consistent with some earlier studies (*2*,*5*). The finding of a higher risk ratio among females than among males is novel. However, it likely reflects the low risk for myocarditis among female patients without COVID-19 (*5*).

Although the exact mechanism of SARS-CoV-2 infection possibly leading to myocarditis is unknown, the pathophysiology is likely similar to that of other viruses (*1*). Among persons with COVID-19 and myocarditis, some myocarditis diagnoses might represent cases of multisystem inflammatory syndrome (MIS), particularly among children aged <16 years (*9*). Further study is warranted to understand how the clinical course of myocarditis among patients with COVID-19 might differ by presence or absence of MIS (*10*).

Since the introduction of mRNA COVID-19 vaccines in the United States in December 2020, an elevated risk for myocarditis among mRNA COVID-19 vaccine recipients has been observed, particularly among males aged 12–29 years, with 39–47 expected cases of myocarditis, pericarditis, and myopericarditis per million second mRNA COVID-19 vaccine doses administered (*6*). A recent study from Israel reported that mRNA COVID-19 vaccination was associated with an elevated risk for myocarditis (risk ratio = 3.24; 95% CI = 1.55–12.44); in the same study, a separate analysis showed that SARS-CoV-2 infection was a strong risk factor for myocarditis (risk ratio = 18.28, 95% CI = 3.95–25.12) (*4*). On June 23, 2021, the Advisory Committee on Immunization Practices concluded that the benefits of COVID-19 vaccination clearly outweighed the risks for myocarditis after vaccination (*6*). The present study supports this recommendation by providing evidence of an elevated risk for myocarditis among persons of all ages with diagnosed COVID-19.

The findings in this study are subject to at least six limitations. First, the risk estimates from this study reflect the risk for myocarditis among persons who received a diagnosis of COVID-19 during an outpatient or inpatient health care encounter and do not reflect the risk among all persons who had COVID-19. Second, misclassification of COVID-19 and myocarditis is possible because conditions were determined by ICD-10-CM codes, which were not confirmed by clinical data (e.g., laboratory tests or cardiac imaging) and could be improperly coded or coded with a related condition (e.g., pericarditis). Third, encounters for COVID-19, myocarditis, and COVID-19 vaccination occurring outside of hospital systems that contribute to PHD-SR are not included within this data set. Fourth, underlying medical conditions and alternative etiologies for myocarditis (e.g., autoimmune disease) were not ascertained or excluded. Fifth, the obtained measures of association could be biased because of the choice of the comparison group (all patients without COVID-19) and if physicians were more likely to suspect or diagnose myocarditis among patients with COVID-19. Finally, the findings represent a convenience sample of patients from hospitals reporting to PHD-SR and might not be generalizable to the U.S. population.

Myocarditis is uncommon among patients with and without COVID-19; however, COVID-19 is a strong and significant risk factor for myocarditis, with risk varying by age group. The findings in this report underscore the importance of implementing evidence-based COVID-19 prevention strategies, including vaccination, to reduce the public health impact of COVID-19 and its associated complications.

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Summary

What is already known about this topic?

Viral infections are a common cause of myocarditis. Some studies have indicated an association between COVID-19 and myocarditis.

What is added by this report?

During March 2020–January 2021, patients with COVID-19 had nearly 16 times the risk for myocarditis compared with patients who did not have COVID-19, and risk varied by sex and age.

What are the implications for public health practice?

These findings underscore the importance of implementing evidence-based COVID-19 prevention strategies, including vaccination, to reduce the public health impact of COVID-19 and its associated complications.

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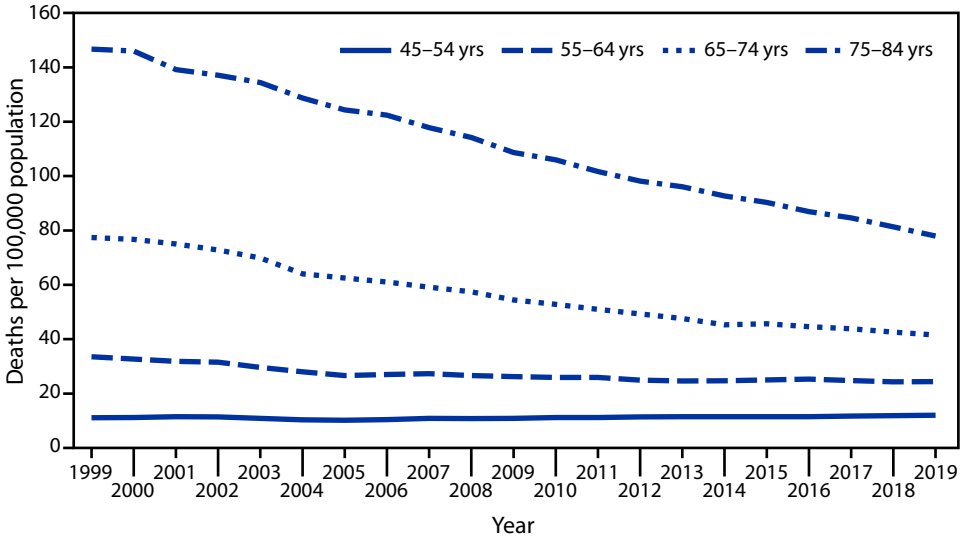
QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Death Rates* from Colorectal Cancer,† by Age Group — United States, 1999–2019



* Deaths per 100,000 population in each age group.
† Deaths from colorectal cancer were identified using *International Classification of Diseases, Tenth Revision* underlying cause-of-death codes C18–21.

During 1999–2019, deaths per 100,000 persons from colorectal cancer decreased among persons aged 55–64 years (from 33.5 to 24.4), persons aged 65–74 years (from 77.4 to 41.5), and persons aged 75–84 years (from 146.7 to 77.9). The death rate from colorectal cancer among persons aged 45–54 years generally increased from 1999 (11.1) to 2019 (12.0). In each year during 1999–2019, the death rate was highest among persons aged 75–84 years and lowest among persons aged 45–54 years.

Source: National Center for Health Statistics, National Vital Statistics System, Mortality Data, 1999–2019. https://www.cdc.gov/nchs/nvss/deaths.htm

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