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Changes in Suicide Rates — United States, 2018–2019

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Suicide is the 10th leading cause of death in the United States overall, and the second and fourth leading cause among persons aged 10–34 and 35–44 years, respectively (*1*). In just over 2 decades (1999–2019), approximately 800,000 deaths were attributed to suicide, with a 33% increase in the suicide rate over the period (*1*). In 2019, a total of 12 million adults reported serious thoughts of suicide during the past year, 3.5 million planned a suicide, and 1.4 million attempted suicide (*2*). Suicides and suicide attempts in 2019 led to a lifetime combined medical and work-loss cost (i.e., the costs that accrue from the time of the injury through the course of a person's expected lifetime) of approximately $70 billion (https://wisqars.cdc.gov:8443/costT/). From 2018 to 2019, the overall suicide rate declined for the first time in over a decade (*1*). To understand how the decline varied among different subpopulations by demographic and other characteristics, CDC analyzed changes in counts and age-adjusted suicide rates from 2018 to 2019 by demographic characteristics, county urbanicity, mechanism of injury, and state. Z-tests and 95% confidence intervals were used to assess statistical significance. Suicide rates declined by 2.1% overall, by 3.2% among females, and by 1.8% among males. Significant declines occurred, overall, in five states. Other significant declines were noted among subgroups defined by race/ethnicity, age, urbanicity, and suicide mechanism. These declines, although encouraging, were not uniform, and several states experienced significant rate increases. A comprehensive approach to prevention that uses data to drive decision-making, implements prevention strategies from CDC's Preventing Suicide: A Technical Package of Policy, Programs, and Practices with the best available evidence, and targets the multiple risk factors associated with suicide, especially in populations disproportionately affected, is needed to build on initial progress from 2018 to 2019 (*3*).

Data from the 2018–2019 National Vital Statistics System multiple cause-of-death mortality files were analyzed. Suicide deaths were identified by using *International Classification of Diseases, Tenth Revision* underlying cause-of-death codes U03, X60–X84, and Y87.0. Two-digit age-adjusted death rates (per 100,000 population) and confidence intervals were calculated by using the direct method and the 2000 U.S. standard population, rounded to one digit. Data for persons aged <10 years are not shown in results by age group because determining suicidal intent in younger children is difficult and case counts were <20, indicating unstable rates (*4*). Urbanization level of the decedent's county of residence was categorized by using the 2013 National Center for Health Statistics Urban–Rural

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Classification Scheme for Counties (https://www.cdc.gov/nchs/data_access/urban_rural.htm). The classification levels for counties are as follows: 1) large central metropolitan: part of a metropolitan statistical area with ≥1 million population and covers a principal city; 2) large fringe metropolitan: part of a metropolitan statistical area with ≥1 million population but does not cover a principal city; 3) medium metropolitan: part of a metropolitan statistical area with ≥250,000 but <1 million population; 4) small metropolitan: part of a metropolitan statistical area with <250,000 population; 5) micropolitan (nonmetropolitan): part of a micropolitan statistical area (has an urban cluster of ≥10,000 but <50,000 population); and 6) noncore (nonmetropolitan): not part of a metropolitan or micropolitan statistical area.

Changes in suicide rates from 2018 to 2019 were examined overall and by age, sex, race/ethnicity, county urbanization level, mechanism of injury, and state. Single-race estimates are presented and might not be comparable to earlier years produced by bridging multiple race to a single race choice (https://wonder.cdc.gov/wonder/help/mcd-expanded.html). Hispanic and unknown ethnicity include persons of any race. Racial groups exclude persons of Hispanic or unknown ethnicity. Differences in rates between 2018 and 2019 were assessed by using z-tests when deaths were ≥100 and by using nonoverlapping confidence intervals based on a gamma distribution when deaths were <100; p-values <0.05 were considered statistically significant (*5*). Relative and absolute changes in rates were calculated; however, only relative changes are presented in the text.

In 2019, a total of 47,511 deaths were attributable to suicide. From 2018 to 2019, the overall suicide rate declined significantly by 2.1% (14.2 per 100,000 population to 13.9) (Table); among females, the rate declined by 3.2% (6.2 to 6.0) and among males by 1.8% (22.8 to 22.4). Among racial/ethnic groups, rates of suicide were highest in 2019 among American Indian/Alaskan Native (AI/AN) persons (22.5 per 100,000) overall, and among AI/AN females and males. Counts of suicide were highest among White persons (37,428). White persons were the only race for whom rates significantly declined from 2018 to 2019, declining 2.2% (18.1 to 17.7) overall, and declining significantly among females and males. Suicide rates did not significantly change from 2018 to 2019 for any other racial/ethnic group examined.

Rates in 2019 were highest among persons aged ≥85 years (20.1 per 100,000), with counts highest among persons aged 55–64 years (8,238) (Table). The number of suicides among males was highest for those aged 25–34 years, a change from 2018, when counts were highest among males aged 55–64 years. Among females, the largest counts and highest rate of suicide were among those aged 45–54 years. Rates declined significantly among persons aged 15–24 years (3.4%; 14.5 to 14.0), 55–64 years (4.0%; 20.2 to 19.4), and 65–74 years (4.9%; 16.3 to 15.5). Significant declines also occurred among males aged 10–14 years (16.2%; 3.7 to 3.1), females aged 25–34-years

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TABLE. Annual number and age-adjusted* rate of suicide† per 100,000 population, by selected characteristics — National Vital Statistics System, United States, 2018 and 2019

Characteristic	2018 No. (rate) [95% CI]	2019 No. (rate) [95% CI]	Absolute change§	Relative change¶
Overall				
Total	**48,344 (14.2) [14.1–14.4]**	**47,511 (13.9) [13.8–14.1]**	**–0.3****	**–2.1****
Race/Ethnicity††				
American Indian/Alaska Native	545 (22.3) [20.4–24.2]	546 (22.5) [20.5–24.4]	0.2	0.9
Asian	1,315 (6.7) [6.4–7.1]	1,342 (6.7) [6.3–7.1]	0	0
Black or African American	3,022 (7.3) [7.0–7.5]	3,115 (7.5) [7.2–7.8]	0.2	2.7
Native Hawaiian/Other Pacific Islander	73 (11.9) [9.3–15.0]	90 (14.4) [11.5–17.7]	2.5	21.0
White	38,415 (18.1) [17.9–18.3]	37,428 (17.7) [17.5–17.9]	–0.4**	–2.2**
Multiracial	514 (9.0) [8.1–9.8]	527 (8.8) [8.0–9.6]	–0.2	–2.2
Hispanic	4,313 (7.4) [7.2–7.7]	4,331 (7.3) [7.0–7.5]	–0.1	–1.4
Unknown	147 (—)	132 (—)	—	—
Age group, yrs§§				
10–14	596 (2.9) [2.6–3.1]	534 (2.6) [2.4–2.8]	–0.3	–10.3
15–24	6,211 (14.5) [14.1–14.8]	5,954 (14.0) [13.6–14.3]	–0.5**	–3.4**
25–34	8,020 (17.6) [17.2–17.9]	8,059 (17.5) [17.2–17.9]	0.1	–0.6
35–44	7,521 (18.2) [17.8–18.6]	7,525 (18.1) [17.7–18.5]	–0.1	–0.5
45–54	8,345 (20.0) [19.6–20.5]	8,012 (19.6) [19.2–20.0]	–0.4	–2.0
55–64	8,540 (20.2) [19.8–20.6]	8,238 (19.4) [19.0–19.8]	–0.8**	–4.0**
65–74	4,974 (16.3) [15.9–16.8]	4,867 (15.5) [15.0–15.9]	–0.8**	–4.9**
75–84	2,880 (18.7) [18.0–19.4]	2,977 (18.6) [18.0–19.3]	–0.1	–0.5
≥85	1,248 (19.1) [18.0–20.1]	1,329 (20.1) [19.0–21.2]	1.0	5.2
Urbanization¶¶				
Large central metropolitan	11,978 (11.4) [11.2–11.6]	11,762 (11.2) [11.0–11.4]	–0.2	–1.8
Large fringe metropolitan	11,028 (13.0) [12.7–13.2]	10,840 (12.6) [12.4–12.8]	–0.4**	–3.1**
Medium metropolitan	10,862 (15.4) [15.1–15.7]	10,789 (15.2) [14.9–15.5]	–0.2	–1.3
Small metropolitan	5,373 (17.6) [17.1–18.0]	5,327 (17.4) [16.9–17.9]	–0.2	–1.1
Micropolitan (nonmetropolitan)	5,337 (19.2) [18.6–19.7]	5,009 (18.1) [17.6–18.6]	–1.1**	–5.7**
Noncore (nonmetropolitan)	3,766 (19.7) [19.0–20.4]	3,784 (20.1) [19.5–20.8]	0.4	2.0
Mechanism of injury				
Cut/Pierce	897 (0.3) [0.3–.03]	921 (0.3) [0.2–0.3]	0	0
Drowning	522 (0.1) [0.1–0.2]	506 (0.2) [0.1–0.2]	0.1	100***
Fall	1,149 (0.4) [0.3–0.4]	1,183 (0.4) [0.3–0.4]	0	0
Fire/Flame	214 (0.1) [0.1–0.1]	187 (0.1) [0–0.1]	0	0
Firearm	24,432 (7.0) [7.0–7.1]	23,941 (6.8) [6.8–6.9]	–0.2**	–2.9**
Poisoning	6,237 (1.8) [1.7–1.8]	6,125 (1.8) [1.7–1.8]	0	0
Suffocation	13,840 (4.3) [4.2–4.4]	13,563 (4.2) [4.1–4.3]	–0.1	–2.3
Other†††	1,053 (0.3) [0.3–.03]	1,085 (0.3) [0.3–0.3]	0	0

See table footnotes on page 265.

(8.1%; 7.4 to 6.8), males aged 45–54 years (4.0%; 30.2 to 29.0), females aged 55–64 years (6.3%; 9.5 to 8.9), and males aged 65–74 years (5.0%; 27.8 to 26.4).

Suicide rates in 2019 were lowest in large central metropolitan areas (11.2 per 100,000) and increased as the level of urbanization declined, with noncore (nonmetropolitan) areas having the highest rate (20.1 per 100,000); this stepped pattern occurred among both females and males. Rates declined from 2018 to 2019 in two county urbanization levels: large fringe metropolitan (3.1%) and micropolitan (nonmetropolitan) (5.7%). Rates also declined among females in micropolitan (nonmetropolitan) areas.

In 2019, the largest proportion of suicides occurred by use of firearms (50.4%), with a rate of 6.8 per 100,000. Whereas males were most likely to die from a firearm-related injury (55.6%) females were equally likely to die from firearm use (31.4%), poisoning (30.0%), and suffocation (e.g., hanging) (29.0%). The rate of firearm suicides declined significantly from 2018 to 2019, by 2.9% (from 7.0 to 6.8 per 100,000), overall, likely driven by a 2.4% decline in their use among males (from 12.6 to 12.3 per 100,000); the rate of firearm suicide among females did not change. The rate of suicide by suffocation among females decreased significantly (10.0%; from 2.0 to 1.8 per 100,000). Rates of suicide by all other mechanisms did not change significantly overall or among females or males.

Firearms were the most common mechanism of suicide in 2019 in all county urbanization levels (Figure 1). The percentage of suicides by firearm in 2019 increased in a stepped pattern from the most urban counties (41.7%) to the most rural

TABLE. (*Continued*) Annual number and age-adjusted* rate of suicide† per 100,000 population, by selected characteristics — National Vital Statistics System, United States, 2018 and 2019

Characteristic	2018 No. (rate) [95% CI]	2019 No. (rate) [95% CI]	Absolute change§	Relative change¶
Female				
Total	**10,583 (6.2) [6.1–6.3]**	**10,255 (6.0) [5.9–6.1]**	**–0.2****	**–3.2****
Race/Ethnicity††				
American Indian/Alaska Native	136 (11.1) [9.2–13.0]	145 (12.1) [10.1–14.1]	1.0	9.0
Asian	394 (3.8) [3.4–4.2]	392 (3.7) [3.3–4.0]	–0.1	–2.6
Black or African American	616 (2.9) [2.6–3.1]	624 (2.9) [2.7–3.2]	0	0
Native Hawaiian/Other Pacific Islander	12 (—)	18 (—)	—	—
White	8,418 (8.0) [7.8–8.2]	8,046 (7.7) [7.5–7.9]	–0.3**	–3.8**
Multiracial	132 (4.5) [3.7–5.3]	122 (3.9) [3.2–4.7]	–0.6	–13.3
Hispanic	844 (2.9) [2.7–3.0]	886 (3.0) [2.8–3.2]	0.1	3.4
Unknown	31 (—)	22 (—)	—	—
Age group, yrs§§				
10–14	206 (2.0) [1.7–2.3]	203 (2.0) [1.7–2.3]	0	0
15–24	1,222 (5.8) [5.5–6.2]	1,154 (5.5) [5.2–5.9]	–0.3	–5.2
25–34	1,670 (7.4) [7.1–7.8]	1,526 (6.8) [6.4–7.1]	–0.6**	–8.1**
35–44	1,742 (8.4) [8.0–8.8]	1,710 (8.2) [7.8–8.6]	–0.2	–2.4
45–54	2,143 (10.2) [9.7–10.6]	2,156 (10.4) [10.0–10.9]	0.2	2.0
55–64	2,069 (9.5) [9.1–9.9]	1,948 (8.9) [8.5–9.3]	–0.6**	–6.3**
65–74	1,011 (6.2) [5.8–6.6]	985 (5.9) [5.5–6.2]	–0.3	–4.8
75–84	364 (4.2) [3.8–4.6]	410 (4.6) [4.1–5.0]	0.4	9.5
≥85	151 (3.6) [3.0–4.2]	158 (3.7) [3.2–4.3]	0.1	2.8
Urbanization¶¶				
Large central metropolitan	2,701 (5.1) [4.9–5.3]	2,682 (5.0) [4.8–5.2]	–0.1	–2.0
Large fringe metropolitan	2,555 (5.9) [5.6–6.1]	2,457 (5.6) [5.4–5.9]	–0.3	–5.1
Medium metropolitan	2,428 (6.8) [6.5–7.1]	2,400 (6.7) [6.4–7.0]	–0.1	–1.5
Small metropolitan	1,094 (7.3) [6.8–7.7]	1,106 (7.3) [6.9–7.8]	0	0
Micropolitan (nonmetropolitan)	1,070 (7.9) [7.4–8.4]	918 (6.9) [6.4–7.3]	–1.1**	–12.7**
Noncore (nonmetropolitan)	735 (8.2) [7.6–8.8]	692 (7.9) [7.3–8.5]	–0.3	–3.7
Mechanism of injury				
Cut/Pierce	162 (0.1) [0.1–0.1]	152 (0.1) [0.1–0.1]	0	0
Drowning	195 (0.1) [0.1–0.1]	187 (0.1) [0.1–0.1]	0	0
Fall	308 (0.2) [0.2–0.2]	333 (0.2) [0.2–0.2]	0**	0**
Fire/Flame	61 (0) [0–0.1]	59 (0) [0–0.1]	0	0
Firearm	3,331 (1.9) [1.8–2.0]	3,216 (1.9) [1.8–1.9]	0	0
Poisoning	3,100 (1.7) [1.7–1.8]	3,079 (1.7) [1.7–1.8]	0	0
Suffocation	3,163 (2.0) [1.9–2.0]	2,971 (1.8) [1.8–1.9]	–0.2**	–10.0**
Other†††	263 (0.2) [0.1–0.2]	258 (0.2) [0.1–0.2]	0	0

See table footnotes on page 265.

(i.e., least urban) counties (62.5%). Conversely, suffocation, the second most prevalent mechanism of suicide, followed a largely stepped decrease from most urban (31.4%) to least urban (28.5%) counties; suicides by poisoning followed a similar pattern, from 14.5% (most urban) to 12.9% (least urban).

The overall suicide rate declined significantly from 2018 to 2019 in five states (Idaho, Indiana, Massachusetts, North Carolina, and Virginia) (Figure 2). The suicide rate among females declined significantly in three states (Indiana, Missouri, and Washington), and rates among males declined significantly in five states (Florida, Kentucky, Massachusetts, North Carolina, and West Virginia) (Supplementary Table, https://stacks.cdc.gov/view/cdc/102794). The largest significant overall decline occurred in Idaho (14.6%). Among females, the largest significant decline occurred in Indiana (29.7%). Among males, the largest significant decline occurred in West Virginia (16.1%). The suicide rate increased significantly overall in Hawaii (30.3%) and Nebraska (20.1%), among females in Minnesota (39.6%), and among males in Hawaii (35.1%) and Wyoming (39.6%).

Discussion

The declines in suicide rates in 2019 are encouraging after 13 consecutive years of rate increases (*1*). From 2018 to 2019, the suicide rate decreased by 2.1%, with significant declines among both females and males and among multiple age groups. Suicide rates declined in large fringe metropolitan areas and micropolitan areas and in five states, overall. Particularly encouraging was the significant decline in firearm suicides, the mechanism of suicide that is most common and most

TABLE. (*Continued*) Annual number and age-adjusted* rate of suicide† per 100,000 population, by selected characteristics — National Vital Statistics System, United States, 2018 and 2019

Characteristic	2018 No. (rate) [95% CI]	2019 No. (rate) [95% CI]	Absolute change§	Relative change¶
Male				
Total	**37,761 (22.8) [22.6–23.0]**	**37,256 (22.4) [22.1–22.6]**	**–0.4****	**–1.8****
Race/Ethnicity††				
American Indian/Alaska Native	409 (33.6) [30.3–36.9]	401 (33.0) [29.7–36.3]	–0.6	–1.8
Asian	921 (10.0) [9.3–10.6]	950 (10.1) [9.4–10.7]	0.1	1.0
Black or African American	2,406 (12.2) [11.7–12.7]	2,491 (12.5) [12.0–13.0]	0.3	2.5
Native Hawaiian/Other Pacific Islander	61 (19.8) [15.0–25.6]	72 (22.1) [17.3–28.0]	2.3	11.6
White	29,997 (28.6) [28.3–29.0]	29,382 (28.1) [27.7–28.4]	–0.5**	–1.7**
Multiracial	382 (13.8) [12.3–15.3]	405 (14.2) [12.7–15.7]	0.4	2.9
Hispanic	3,469 (12.1) [11.7–12.5]	3,445 (11.6) [11.2–12.0]	–0.5	–4.1
Unknown	116 (—)	110 (—)	—	—
Age group, yrs§§				
10–14	390 (3.7) [3.3–4.0]	331 (3.1) [2.8–3.5]	–0.6**	–16.2**
15–24	4,989 (22.7) [22.1–23.3]	4,800 (22.0) [21.4–22.6]	–0.7	–3.1
25–34	6,350 (27.4) [26.7–28.0]	6,533 (28.0) [27.3–28.7]	0.6	2.2
35–44	5,779 (28.1) [27.4–28.8]	5,815 (28.0) [27.3–28.7]	–0.1	–0.4
45–54	6,202 (30.2) [29.4–30.9]	5,856 (29.0) [28.3–29.8]	–1.2**	–4.0**
55–64	6,471 (31.7) [31.0–32.5]	6,290 (30.7) [29.9–31.4]	–1.0	–3.2
65–74	3,963 (27.8) [27.0–28.7]	3,882 (26.4) [25.6–27.2]	–1.4**	–5.0**
75–84	2,516 (37.4) [35.9–38.8]	2,567 (36.7) [35.3–38.1]	–0.7	–1.9
≥85	1,097 (47.2) [44.4–50.0]	1,171 (49.3) [46.5–52.1]	2.1	4.4
Urbanization¶¶				
Large central metropolitan	9,277 (18.3) [18.0–18.7]	9,080 (17.8) [17.5–18.2]	–0.5	–2.7
Large fringe metropolitan	8,473 (20.5) [20.1–21.0]	8,383 (20.0) [19.6–20.5]	–0.5	–2.4
Medium metropolitan	8,434 (24.5) [24.0–25.0]	8,389 (24.3) [23.7–24.8]	–0.2	–0.8
Small metropolitan	4,279 (28.3) [27.4–29.1]	4,221 (27.9) [27.0–28.7]	–0.4	–1.4
Micropolitan (nonmetropolitan)	4,267 (30.6) [29.6–31.5]	4,091 (29.5) [28.6–30.4]	–1.1	–3.6
Noncore (nonmetropolitan)	3,031 (31.0) [29.8–32.1]	3,092 (32.1) [31.0–33.3]	1.1	3.5
Mechanism of injury				
Cut/Pierce	735 (0.4) [0.4–0.4]	769 (0.4) [0.4–0.5]	0	0
Drowning	327 (0.2) [0.2–0.2]	319 (0.2) [0.2–0.2]	0	0
Fall	841 (0.5) [0.5–0.5]	850 (0.5) [0.5–0.5]	0	0
Fire/Flame	153 (0.1) [0.1–0.1]	128 (0.1) [0.1–0.1]	0	0
Firearm	21,101 (12.6) [12.4–12.7]	20,725 (12.3) [12.1–12.4]	–0.3**	–2.4**
Poisoning	3,137 (1.9) [1.8–1.9]	3,046 (1.8) [1.7–1.9]	–0.1	–5.3
Suffocation	10,677 (6.7) [6.5–6.8]	10,592 (6.6) [6.5–6.7]	–0.1	–1.5
Other†††	790 (0.5) [0.4–0.5]	827 (0.5) [0.5–0.5]	0	0

Abbreviation: CI = confidence interval.

* Age-adjusted death rates (per 100,000) were calculated by using the direct method and the 2000 U.S. standard population. Rates and CIs are rounded to one digit and as a result might not exactly match similar rates published elsewhere. Suicides for persons aged <10 years were included in the total numbers and age-adjusted rates but are not shown as part of age groups because determining suicidal intent in younger children can be difficult, and case counts were <20, indicating unstable rates.

† Suicide deaths were identified by using *International Classification of Diseases, Tenth Revision* underlying cause-of-death codes U03, X60–X84, and Y87.0.

§ The rate in 2019 minus the rate in 2018.

¶ The (2019 rate minus 2018 rate) divided by 2018 rate multiplied by 100.

** P≤0.05 for difference between 2018 and 2019. Z-tests were used if the number of deaths was ≥100 in both 2018 and 2019; nonoverlapping confidence intervals based on the gamma method were used if the number of deaths was <100 in 2018 or 2019.

†† Data for Hispanic origin should be interpreted with caution; studies comparing Hispanic origin on death certificates and on Census surveys have shown inconsistent reporting on Hispanic ethnicity. Potential racial misclassification might lead to underestimates for certain categories, primarily non-Hispanic American Indian/Alaska Native and non-Hispanic Asian/Pacific Islander decedents. Single-race estimates are presented and might not be comparable to earlier years produced by bridging multiple races to a single race choice. Hispanic and unknown ethnicity include persons of any race. Racial groups exclude persons of Hispanic or unknown ethnicity.

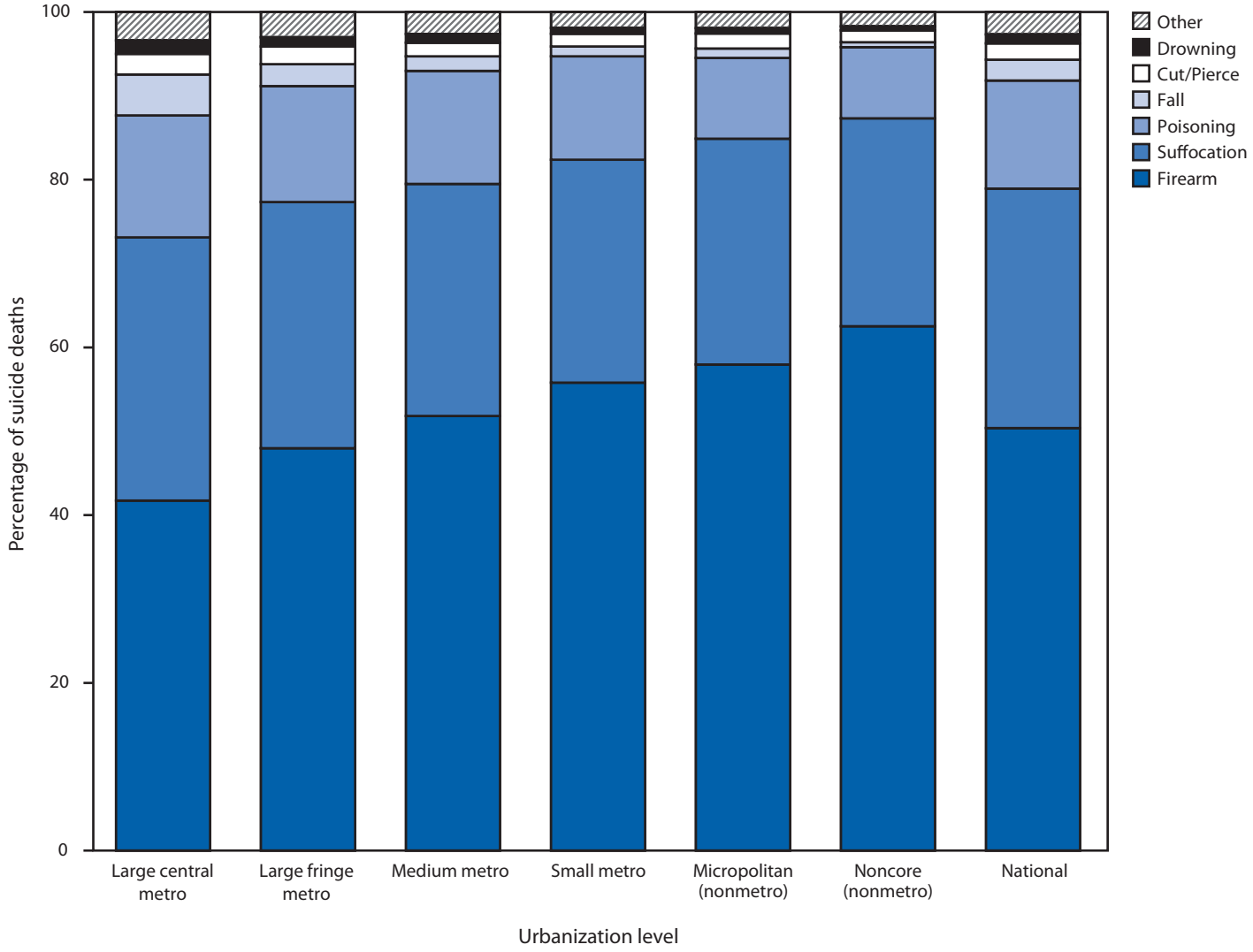
§§ Crude rates per 100,000 are presented for age groups.

¶¶ Urbanization level of the decedent's county of residence was categorized by using the 2013 National Center for Health Statistics Urban–Rural Classification Scheme for Counties (https://www.cdc.gov/nchs/data_access/urban_rural.htm). The classification levels for counties are as follows: 1) large central metropolitan: part of a metropolitan statistical area with ≥1 million population and covers a principal city; 2) large fringe metropolitan: part of a metropolitan statistical area with ≥1 million population but does not cover a principal city; 3) medium metropolitan: part of a metropolitan statistical area with ≥250,000 but <1 million population; 4) small metropolitan: part of a metropolitan statistical area with <250,000 population; 5) micropolitan: part of a micropolitan statistical area (has an urban cluster of ≥10,000 but <50,000 population); and 6) noncore (nonmetropolitan): not part of a metropolitan or micropolitan statistical area.

*** Because of the change in the composition of the population during 2018–2019, the rounded age-adjusted rate increased 100%, from 0.1 to 0.2, as the number of drowning deaths decreased from 522 to 506. Confidence intervals are the same for both age-adjusted rate estimates.

††† "Other" mechanisms of injury include other land transport, struck by/against, other specified, and unspecified.

FIGURE 1. Suicide* mechanism of injury,† by level of urbanization§ — National Vital Statistics System, United States, 2019



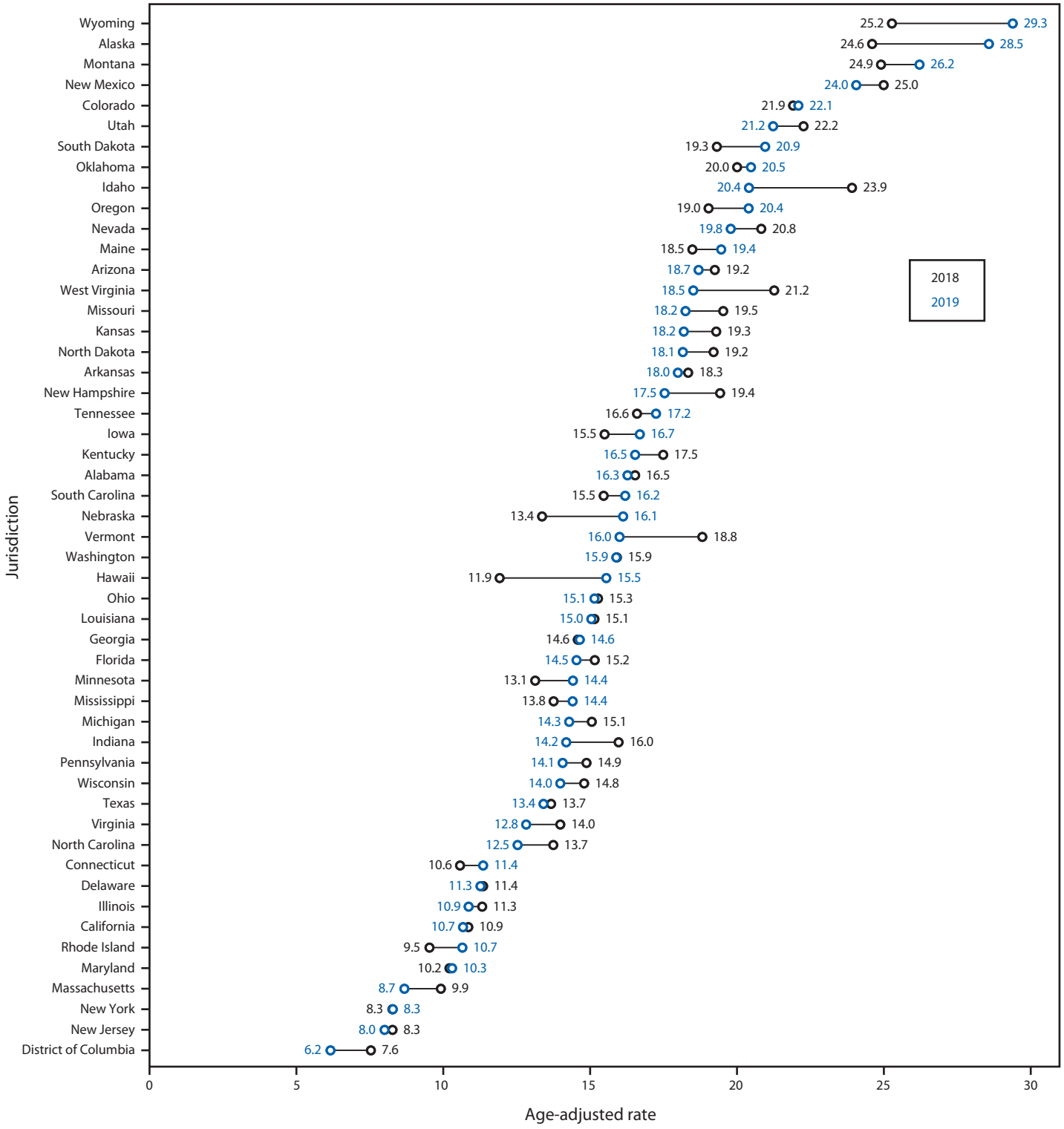
* Suicide deaths were identified by using *International Classification of Diseases, Tenth Revision* underlying cause-of-death codes U03, X60–X84, and Y87.0.
† "Other" mechanisms of injury include other land transport, struck by/against, other specified, and unspecified.
§ Urbanization level of the decedent's county of residence was categorized by using the 2013 National Center for Health Statistics Urban–Rural Classification Scheme for Counties (https://www.cdc.gov/nchs/data_access/urban_rural.htm). The classification levels for counties are as follows: 1) large central metropolitan (large central metro): part of a metropolitan statistical area with ≥1 million population and covers a principal city; 2) large fringe metropolitan (large fringe metro): part of a metropolitan statistical area with ≥1 million population but does not cover a principal city; 3) medium metropolitan (medium metro): part of a metropolitan statistical area with ≥250,000 but <1 million population; 4) small metropolitan (small metro): part of a metropolitan statistical area with <250,000 population; 5) micropolitan (nonmetro): part of a micropolitan statistical area (has an urban cluster of ≥10,000 but <50,000 population); and 6) noncore (nonmetro): not part of a metropolitan or micropolitan statistical area.

lethal (*6*). However, few significant declines were observed by race/ethnicity, most states did not experience significant changes, and a small number of states experienced increased rates, underscoring persisting disparities in 2019.

Research has shown that suicide is preventable and that risks for suicide extend beyond mental health and lack of access to mental health treatment alone (*7*). Suicide prevention must focus on the constellation of associated factors, including mental illness, substance misuse, high conflict or violent relationships, social isolation, job and financial problems, lack of community connectedness, barriers to suicide-related care, and access to lethal means among persons at risk (*7*).

As the United States continues to respond to the coronavirus disease 2019 (COVID-19) pandemic and its long-term impacts on isolation, stress, economic insecurity, and worsening mental health and wellness, prevention is more important than ever. Past research indicates that suicide rates remain stable or decline during infrastructure disruption (e.g., natural disasters), only to rise afterwards as the longer-term sequalae unfold in persons, families, and communities (*8*).

FIGURE 2. Overall age-adjusted rate*,† of suicide,§ by state — National Vital Statistics System, United States, 2018 and 2019



* Age-adjusted death rates per 100,000 population were calculated by using the direct method and the 2000 U.S. standard population. Rates are rounded to one digit.
† States with statistically significant changes ($p \leq 0.05$); Z-tests were used if the number of deaths was ≥100 in both 2018 and 2019; nonoverlapping confidence intervals based on the gamma method were used if the number of deaths was <100 in 2018 or 2019. States with statistically significant changes were Hawaii, Idaho, Indiana, Massachusetts, Nebraska, North Carolina, and Virginia.
§ Suicide deaths were identified by using *International Classification of Diseases, Tenth Revision* underlying cause-of-death codes U03, X60–X84, and Y87.0.

A comprehensive approach to suicide prevention is urgently needed in all states to continue the initial progress made in 2019. A comprehensive approach is one that relies on use of data to drive decision-making and robust implementation and evaluation of prevention strategies with the best available evidence that address the range of factors associated with suicide, especially among populations disproportionately affected (https://www.cdc.gov/injury/fundedprograms/comprehensive-suicide-prevention/index.html). Such strategies are all the more relevant in the midst of the COVID-19 pandemic and include those focused on strengthening economic supports, expanding access to and delivery of care (e.g., telehealth), promoting social connectedness, creating protective environments including reducing access to lethal means among persons at risk, teaching coping and problem-solving skills, identifying and supporting persons at risk, and lessening harms and preventing future risk (e.g., safe media reporting on suicide) (*3*).

The findings in this report are subject to at least two limitations. First, caution must be used when interpreting rate decreases from 1 year to the next because rates might be unstable, especially in smaller segments of the population, and declines observed in a single year cannot be interpreted as a trend. Second, evidence over several decades suggests that suicides are undercounted on death certificates for various reasons, including the higher burden of proof to classify a death as a suicide (versus proof needed to classify other manners of death), stigma, and lack of autopsies or thorough investigations (*9*); thus, suicide rates might be underestimated in 2018 and 2019.

Suicide is preventable, and effective approaches to both reduce suicide risk factors and increase protective factors are available. Comprehensive prevention efforts are critical to realize further declines in suicide and to reach the national goal to reduce suicide rates by 20% by 2025 (*10*). Resources are available that states and communities can use to better understand suicide, prioritize evidence-based comprehensive suicide prevention, and save lives (*3*).

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Summary

What is already known about this topic?

Suicide is preventable. In 2019, approximately 47,500 lives were attributed to suicide. From 2018 to 2019, the suicide rate declined for the first time in more than a decade.

What is added by this report?

Suicide rates declined overall by 2.1%, among females by 3.2%, and among males by 1.8%, as well as in five states, certain demographic groups, and by certain mechanisms of suicide; however, disparities persist.

What are the implications for public health practice?

To build on 2019 progress, CDC's Preventing Suicide: A Technical Package of Policy, Programs, and Practices supports a comprehensive approach to prevention. Implementing such an approach, especially in disproportionately affected populations (e.g., American Indian/Alaska Natives), is needed in all states.

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Estimated Medicaid Costs Associated with Hepatitis A During an Outbreak — West Virginia, 2018–2019

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Hepatitis A is a vaccine-preventable disease caused by the hepatitis A virus (HAV). Transmission of the virus most commonly occurs through the fecal-oral route after close contact with an infected person. Widespread outbreaks of hepatitis A among persons who use illicit drugs (injection and noninjection drugs) have increased in recent years (*1*). The Advisory Committee on Immunization Practices (ACIP) recommends routine hepatitis A vaccination for children and persons at increased risk for infection or severe disease, and, since 1996, has recommended hepatitis A vaccination for persons who use illicit drugs (*2*). Vaccinating persons who are at-risk for HAV infection is a mainstay of the public health response for stopping ongoing person-to-person transmission and preventing future outbreaks (*1*). In response to a large hepatitis A outbreak in West Virginia, an analysis was conducted to assess total hepatitis A–related medical costs during January 1, 2018–July 31, 2019, among West Virginia Medicaid beneficiaries with a confirmed diagnosis of HAV infection. Among the analysis population, direct clinical costs ranged from an estimated $1.4 million to $5.6 million. Direct clinical costs among a subset of the Medicaid population with a diagnosis of a comorbid substance use disorder ranged from an estimated $1.0 million to $4.4 million during the study period. In addition to insight on preventing illness, hospitalization, and death, the results from this study highlight the potential financial cost jurisdictions might incur when ACIP recommendations for hepatitis A vaccination, especially among persons who use illicit drugs, are not followed (*2*).

Historically, hepatitis A infections have been rare in West Virginia, with an average of eight cases reported annually to the state Bureau for Public Health during 2007–2013 (*3*). Since March 2018, West Virginia has experienced a series of hepatitis A outbreaks, primarily among persons who use illicit drugs (*4*). As of February 2020, a total of 2,702 outbreak-related cases had been reported; approximately two thirds of patients reported illicit drug use, approximately one half of the outbreak-related patients were hospitalized, and 23 deaths were reported (*4*). The cost of West Virginia's hepatitis A outbreak has not been previously quantified.

Paid claims for West Virginia Medicaid beneficiaries with a diagnosis of hepatitis A* during January 1, 2018–July 31, 2019 were examined. These data were extracted from the West Virginia Bureau for Medical Services' Data Warehouse on request by the West Virginia Bureau for Public Health. A total of 64 patients who had a claim with a procedure code for hepatitis A vaccination† during the study period were excluded (*5*) (Figure). Pharmacy claims were also excluded because no specific pharmacologic treatment exists for hepatitis A (*6*). Total hepatitis A–related medical costs were assessed in three of the following ways: 1) scenario 1, in which costs associated with claims that had any diagnosis (i.e., primary or secondary diagnosis) of hepatitis A were summed to obtain the least conservative estimate of hepatitis A–related costs, 2) scenario 2, in which costs associated with claims that had a primary diagnosis of hepatitis A were summed to obtain a more conservative cost estimate, and 3) scenario 3, in which costs associated with inpatient hospital claims that had both a primary diagnosis of hepatitis A and a diagnosis-related group (DRG) code indicating disorders of the liver§ were summed to obtain the most conservative cost estimate. Hepatitis A–related costs were also measured for the subgroup of patients in each scenario with comorbid substance use disorder. Persons who had at least one claim with a primary or secondary diagnosis related to substance use disorder (excluding nicotine- or alcohol-related substance use disorders¶) during the study period were classified as having comorbid substance use disorder. Analyses were conducted using SAS (version 9.4; SAS Institute). This study was deemed not to be human subjects research by CDC and was exempt from Institutional Review Board review; the

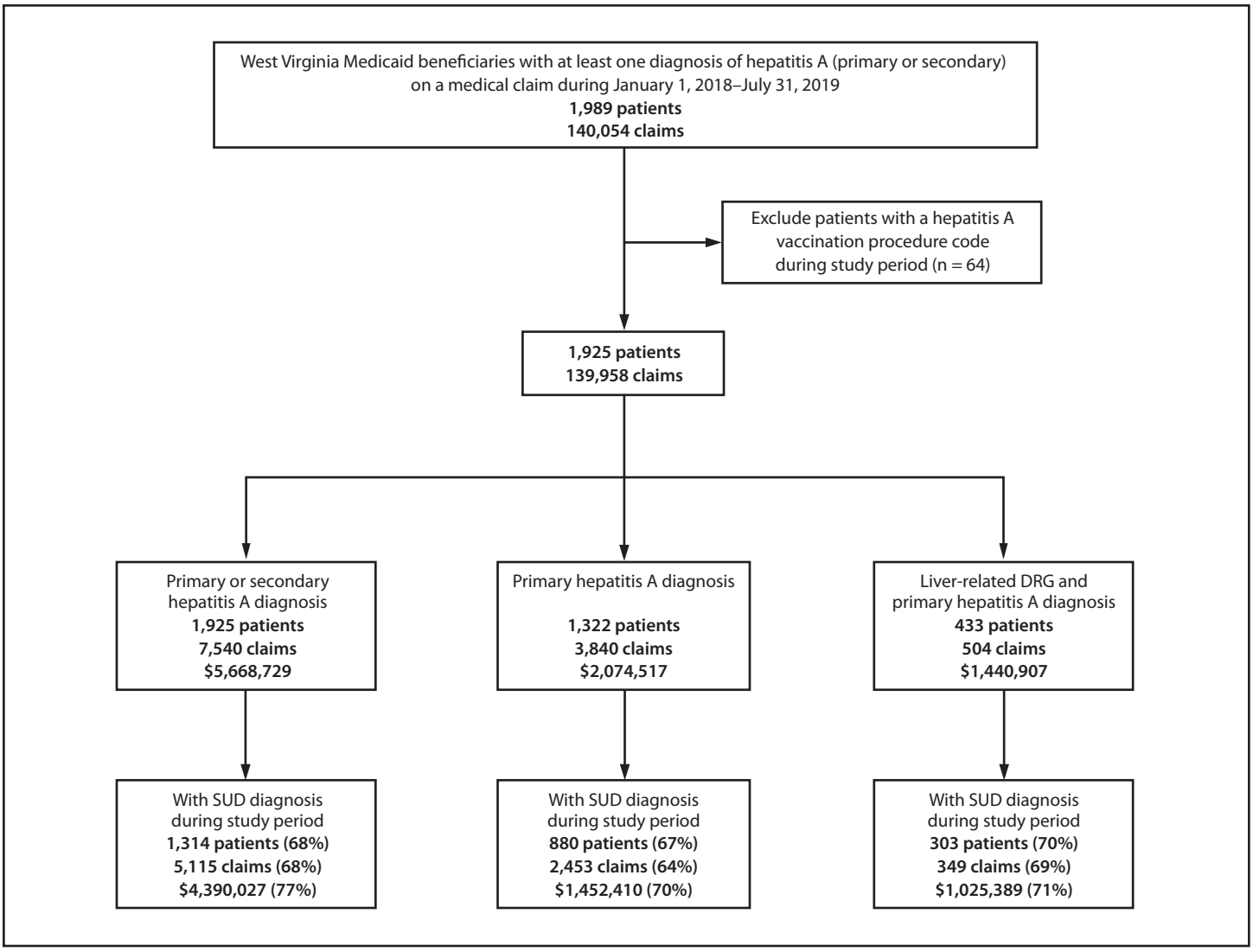
* Hepatitis A patients were identified using the following *International Classification of Diseases, Tenth Revision* (ICD-10), diagnostic codes: B150 and B159.

† American Medical Association, Current Procedural Terminology, vaccine procedures codes 90632, 90633, 90634, 90636, and 90730.

§ *International Classification of Diseases, Tenth Revision, Clinical Modification*, liver-related diagnosis-related groups 441, 442, and 443.

¶ ICD-10/*Diagnostic and Statistical Manual of Mental Disorders, Fifth Edition*, substance use disorder diagnosis codes (excluding nicotine- and alcohol-related codes): F11.1, F11.2, F11.9, F12.1, F12.2, F12.9, F13.1 F13.2, F13.9, F14.1, F14.2. F14.9, F15.1, F15.2, F15.9, F16.1, F16.2, F16.9, F18.1, F18.2, F18.9, F19.1, F19.2, F19.9, F55[.0-.4], F55.8, O35.5, O99.3, P04.4, P96.1, P96.2, T40.0 , T40.1, T40.5, T40[0.7-0.9].

FIGURE. Inclusion criteria for analysis of Medicaid beneficiaries with at least one hepatitis A diagnosis* on a medical claim — West Virginia, January 1, 2018–July 31, 2019†



Abbreviations: DRG = diagnosis-related group; SUD = substance use disorder.
* Direct clinical costs are shown for each hepatitis A diagnosis/SUD group.
† SUD diagnoses exclude those related to alcohol or nicotine.

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

A total of 1,989 Medicaid beneficiaries with a diagnosis of hepatitis A (primary or secondary) were identified; 1,925 patients met study inclusion criteria for scenario 1, 1,322 patients met the criteria for scenario 2, and 433 patients met the criteria for scenario 3 (Figure). The median age of the 1,925 patients in scenario 1 was 37 years (range = 3–83 years) and the majority were male (54%) (Table 1). Approximately two thirds of study patients had a comorbid substance use disorder diagnosis on a claim at some point during the study period.

Total hepatitis A–related clinical costs among all Medicaid beneficiaries with a diagnosis of hepatitis A ranged from $1,440,907 (scenario 3) to $5,668,729 (scenario 1) (Table 2). Among the 1,314 patients with a comorbid substance use disorder diagnosis, the total hepatitis A–related clinical costs ranged from $1,025,389 (scenario 3) to $4,390,027 (scenario 1) (Table 2).

Discussion

This analysis identified 1,925 West Virginia Medicaid beneficiaries whose medical claims included a hepatitis A diagnosis

** 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.

TABLE 1. Demographic and risk factor characteristics of Medicaid beneficiaries with a hepatitis A diagnosis* — West Virginia, January 1, 2018–July 31, 2019

Characteristic	No. (%)		
	Scenario 1†: primary or secondary hepatitis A diagnosis	Scenario 2§: primary hepatitis A diagnosis	Scenario 3¶: liver-related DRG and primary hepatitis A diagnosis
Overall sample			
Unique patients	**1,925**	**1,322**	**433**
Median age, yrs (range)	37 (3–83)	37 (3–83)	38 (18–68)
Male	1,036 (54)	738 (56)	259 (60)
Female	889 (46)	584 (44)	174 (40)
Nonalcohol or nicotine SUD patients during the study period	1,314 (68)	880 (67)	303 (70)
Subgroup with nonalcohol or nicotine SUD during the study period			
Unique patients	**1,314**	**880**	**303**
Median age, yrs (range)	35 (13–71)	35 (13–71)	35 (18–66)
Male	735 (56)	512 (58)	189 (62)
Female	579 (44)	368 (42)	114 (38)

Abbreviations: DRG = diagnosis-related group; SUD = substance use disorder.
* Hepatitis A–related clinical costs were assessed in three ways.
† Scenario 1: costs associated with medical claims that had a primary or secondary diagnosis of hepatitis A were summed to obtain the least conservative estimate of hepatitis A–related costs.
§ Scenario 2: costs associated with medical claims that had a primary diagnosis of hepatitis A were summed to obtain a more conservative cost estimate.
¶ Scenario 3: costs associated with inpatient hospital claims that had both a primary diagnosis of hepatitis A and a diagnosis-related group code indicating disorders of the liver were summed to obtain the most conservative cost estimate.

TABLE 2. Hepatitis A–related Medicaid direct clinical costs* — West Virginia, January 1, 2018–July 31, 2019

Characteristic	Scenario 1†: primary or secondary hepatitis A diagnosis	Scenario 2§: primary hepatitis A diagnosis	Scenario 3¶: liver-related DRG and primary hepatitis A diagnosis
Overall sample			
No. of unique patients	1,925	1,322	433
Total hepatitis A–related direct clinical costs, $	5,668,729	2,074,517	1,440,907
Subgroup with nonalcohol or nicotine SUD during study period			
No. of unique patients	1,314	880	303
Total hepatitis A–related direct clinical costs, $	4,390,027	1,452,410	1,025,389

Abbreviations: DRG = diagnosis-related group; SUD = substance use disorder.
* Hepatitis A–related clinical costs were assessed in three ways.
† Scenario 1: costs associated with medical claims that had a primary or secondary diagnosis of hepatitis A were summed to obtain the least conservative estimate of hepatitis A–related costs.
§ Scenario 2: costs associated with medical claims that had a primary diagnosis of hepatitis A were summed to obtain a more conservative cost estimate.
¶ Scenario 3: costs associated with inpatient hospital claims that had both a primary diagnosis of hepatitis A and a diagnosis-related group code indicating disorders of the liver were summed to obtain the most conservative cost estimate.

during January 1, 2018–July 31, 2019, and met the study inclusion criteria. During the study period, the total expenditure for medical claims with a hepatitis A diagnosis exceeded $5.6 million, including approximately $1.4 million spent on hepatitis A–related inpatient hospital admissions alone. Illicit drug use is a known risk factor for HAV infection (*1*); claims for 68% of persons in this study included a substance use disorder diagnosis. The total hepatitis A–related costs for this group was approximately $4.4 million during the study period.

The findings in this report are subject to at least four limitations. First, administrative claims data used for this analysis were generated for reimbursement purposes, not research. One previous study assessing the usefulness of claims data for hepatitis surveillance reported higher rates of false positive diagnoses in claims data relative to other data sources (*7*). Second, costs were assumed to be directly attributable to the hepatitis A diagnosis on the claims. Presumably, most services were directly related to the primary diagnosis recorded on the claim; however, this might not always have been the case. The three scenarios described previously were used to mitigate this limitation. Third, the hepatitis A–related costs assessed in this analysis incorporated only direct clinical costs to the West Virginia Medicaid agency for persons with a diagnosis of hepatitis A in the context of an outbreak. These are conservative cost estimates that do not include expenses associated with the public health outbreak response, productivity loss,

Summary

What is already known about this topic?

Widespread outbreaks of hepatitis A among persons who use illicit drugs (injection and noninjection) have increased in recent years. Hepatitis A is a vaccine-preventable disease.

What is added by this report?

During January 1, 2018–July 31, 2019, hepatitis A–related clinical costs among West Virginia Medicaid beneficiaries ranged from $1.4 million to $5.6 million. Among those with a substance use disorder diagnosis, costs ranged from $1.0 million to $4.4 million.

What are the implications for public health practice?

In addition to insight on preventing illness, hospitalization, and death, the results from this study highlight the potential financial cost jurisdictions might incur when Advisory Committee on Immunization Practices recommendations for hepatitis A vaccination, especially among persons who use illicit drugs, are not followed.

other indirect costs, or direct costs from pharmacy claims. In addition, by focusing on direct clinical costs to the West Virginia Medicaid agency, this analysis did not consider hepatitis A–related clinical costs borne by private insurers, Medicare, and other payers, or account for costs borne from treatment of the uninsured. Thus, the hepatitis A–related clinical costs presented in this report likely underestimate the total clinical costs of West Virginia's outbreak. Finally, this analysis was limited to the West Virginia Medicaid population; therefore, the results might not be directly generalizable to other states or demographic groups.

The large hepatitis A outbreak in West Virginia has acutely affected the state's Medicaid program. The costs associated with hepatitis A clinical care alone during a person-to-person outbreak are substantial. The results presented in this report suggest that the West Virginia Medicaid agency incurred a minimum of $1.4 million in costs directly associated with the first 19 months of this outbreak. Although improving, this outbreak is ongoing as of February 2021 and has resulted in hospitalizations for approximately one half of persons with cases of HAV and 23 reported deaths. In addition to insight on preventing illness, hospitalization, and death, the results from this study highlight the potential financial cost jurisdictions might incur when ACIP recommendations for hepatitis A vaccination, especially among persons who use illicit drugs, are not followed (*2*).

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Suspected Recurrent SARS-CoV-2 Infections Among Residents of a Skilled Nursing Facility During a Second COVID-19 Outbreak — Kentucky, July–November 2020

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Reinfection with SARS-CoV-2, the virus that causes coronavirus disease 2019 (COVID-19), is believed to be rare (*1*). Some level of immunity after SARS-CoV-2 infection is expected; however, the evidence regarding duration and level of protection is still emerging (*2*). The Kentucky Department for Public Health (KDPH) and a local health department conducted an investigation at a skilled nursing facility (SNF) that experienced a second COVID-19 outbreak in October 2020, 3 months after a first outbreak in July. Five residents received positive SARS-CoV-2 reverse transcription–polymerase chain reaction (RT-PCR) test results during both outbreaks. During the first outbreak, three of the five patients were asymptomatic and two had mild symptoms that resolved before the second outbreak. Disease severity in the five residents during the second outbreak was worse than that during the first outbreak and included one death. Because test samples were not retained, phylogenetic strain comparison was not possible. However, interim period symptom resolution in the two symptomatic patients, at least four consecutive negative RT-PCR tests for all five patients before receiving a positive test result during the second outbreak, and the 3-month interval between the first and the second outbreaks, suggest the possibility that reinfection occurred. Maintaining physical distance, wearing face coverings or masks, and frequent hand hygiene are critical mitigation strategies necessary to prevent transmission of SARS-CoV-2 to SNF residents, a particularly vulnerable population at risk for poor COVID-19–associated outcomes.* Testing, containment strategies (isolation and quarantine), and vaccination of residents and health care personnel (HCP) are also essential components to protecting vulnerable residents. The findings of this study highlight the importance of maintaining public health mitigation and protection strategies that reduce transmission risk, even among persons with a history of COVID-19 infection.

First Outbreak: Investigation and Findings

In July, a Kentucky SNF notified the local health department of a case of COVID-19 in one of the facility's HCP; KDPH was also notified. RT-PCR testing was performed in accordance with state protocol to identify additional cases among residents and HCP. A confirmed COVID-19 case was defined as a positive RT-PCR test result for a SNF resident or HCP. The index patient in this outbreak was a symptomatic HCP. Initially, symptomatic persons and exposed residents who had received direct care and HCP who had close contact with the infected HCP were tested.† Facility-wide testing for all residents and HCP began when additional positive test results were received. Residents and HCP who received negative results were retested weekly; in addition, anyone experiencing symptoms was tested at the time of symptom onset. Residents with positive test results were cohorted in a separate COVID-19 unit with dedicated HCP who used appropriate personal protective equipment. The SNF required the receipt of two negative test results collected >24 hours apart to release patients from the COVID-19 unit. HCP with positive test results could not return to work until completion of their isolation period.§ Residents who had been exposed to COVID-19 with negative test results were cohorted in a separate unit, primarily in double-occupancy rooms. Weekly testing of all noninfected HCP and residents continued for >14 days after the final case of the initial outbreak was identified. In total, 20 (17.4%) of 115 residents and five (3.5%) of 143 HCP in this facility received positive test results during July 16–August 11, representing an overall attack rate of 9.7%. Eight (40.0%) residents with COVID-19 were hospitalized, and five (25.0%) residents with COVID-19 died. No hospitalizations or deaths occurred among HCP with COVID-19.

KDPH and the local health department encouraged the facility to continue to monitor hand hygiene of residents and HCP, emphasize environmental cleaning and disinfection, practice universal masking, use standard precautions for general resident contact, quarantine newly-admitted and readmitted patients for 14 days, employ testing, and restrict visitation based on county-level incidence rates. The facility continued to monitor all residents and HCP for signs and symptoms of COVID-19 and to test symptomatic persons. The SNF

* https://www.cdc.gov/coronavirus/2019-ncov/hcp/long-term-care.html

† https://www.cdc.gov/coronavirus/2019-ncov/hcp/nursing-homes-responding.html

§ At the time of the first outbreak, KDPH guidance for return to work for HCP recommended a time- and symptom-based approach. https://chfs.ky.gov/agencies/dph/covid19/Guidanceforreleasefromisolation.pdf

continued to test HCP at least every other week between the two outbreaks. A total of 597 facility-ordered RT-PCR tests were performed in September, and 331 tests were performed during October 1–29; all results were negative.

Second Outbreak: Investigation and Findings

On October 30, 2020, the same SNF notified the local health department and KDPH of two COVID-19 cases after two symptomatic residents received positive test results. Testing and cohorting practices similar to those implemented during the first outbreak were initiated, and testing of residents and HCP was increased to twice weekly. During October 30–December 7, a total of 85 (74.6%) of 114 residents and 43 (29.5%) of 146 HCP received positive SARS-CoV-2 RT-PCR test results, representing an attack rate of 49.2% among the 260 SNF residents and HCP present at the start of the outbreak in October. Among the 85 resident cases identified in the second outbreak, 15 (17.6%) patients died. No HCP died.

Among 12 residents who received positive test results during the first outbreak (July–August) and were still living in the facility in October, five also received positive results during the second outbreak >90 days after the date that their first specimens were collected. These patients were classified as having recurrent cases of COVID-19. Among the five HCP who had received a positive SARS-CoV-2 test result during the July outbreak, only one was working at the facility at the time of the second outbreak. This staff member did not have a positive SARS-CoV-2 test result during the second outbreak. KDPH performed SNF interviews, reviewed testing results from the National Electronic Disease Surveillance System, and contacted the testing laboratories to investigate exposures, testing history, and course of illness of the five patients identified as having recurrent COVID-19. The activity was reviewed by CDC and conducted consistent with applicable federal law and CDC policy.¶

The five patients with recurrent COVID-19 ranged in age from 67 to 99 years; four were women (Table). Each of the five patients had more than three chronic underlying health conditions, and all were permanent residents of the SNF. None of the patients with recurrent COVID-19 had an immunosuppressive condition or was taking immunosuppressive medications that might have hindered clearance of the virus or predisposed them to virus reactivation (*3*).

Among these five patients, only two (patients C and D) were symptomatic during the first outbreak; neither had fever or respiratory symptoms, and neither was hospitalized (Figure). Both had complete resolution of symptoms between the two outbreaks. All residents with recurrent COVID-19 had at least four consecutive negative RT-PCR test results between their two positive tests. All five patients received their positive RT-PCR results for the second COVID-19 diagnosis in the midst of the second facility outbreak and therefore after facility exposure to SARS-CoV-2. Three patients (patients A, C, and D) with recurrent infection had roommates who received positive SARS-CoV-2 RT-PCR results before they received their own positive test results, confirming direct exposure. Patient B was in a private room, and patient E had a roommate who did not have COVID-19. Although no direct route of exposure was identified for patients B or E, exposure to SARS-CoV-2 was very likely because of the large number of infected persons in the facility during the second outbreak. Cycle threshold (Ct) values ≤30 were reported for positive test results for the five patients in each infectious episode, which suggests at least moderate upper respiratory tract viral loads (*4*). Although three of the five patients with recurrent COVID-19 were asymptomatic during their first infectious episode, all five experienced symptoms during their second infectious episode; the two patients who were symptomatic during the first outbreak experienced more severe symptoms during the second infectious episode compared with the symptoms they had during the first outbreak (Table). One resident patient required hospitalization and subsequently died.

Discussion

After receiving positive COVID-19 test results during a SNF outbreak and subsequently receiving four to five negative SARS-CoV-2 RT-PCR test results, five residents received positive results >90 days later during the facility's second COVID-19 outbreak, suggesting SARS-CoV-2 reinfection. All patients with recurrent COVID-19 experienced more severe disease during the second outbreak, and one died. The exposure history, including the timing of roommates' infections and the new onset of symptoms during the second outbreak, suggest that the second positive RT-PCR results represented new infections after the patients apparently cleared the first infection.

The finding that all five patients with recurrent COVID-19 had either asymptomatic or mildly symptomatic courses during their first infections is noteworthy, suggesting the possibility that asymptomatic or mildly symptomatic initial infections do not produce a sufficiently robust immune response to prevent reinfection (*5*). The patients with recurrent illness ranged in age from 67 to 99 years; a decline in immune system function with aging is well-documented, but little scientific evidence is available to date regarding whether or how an aging immune system might affect response to initial SARS-CoV-2 infection, likelihood of reinfection upon new exposure, and illness

¶ 45 C.F.R. part 46.102(l)(2).

TABLE. Demographic and clinical characteristics and laboratory test results among five skilled nursing facility residents with recurrent COVID-19 — Kentucky, 2020

		First outbreak (Jul–Aug)		Second outbreak (Oct–Dec)		
Patient	Sex (age group, yrs)	Ct values*	Symptoms	No. of days since positive test result in first outbreak	Ct values*	Symptoms
A	M (80–89)	N1: 28.5 N2: 29.0 RNAse P: 24.4	Asymptomatic	101	N1: 30.0 N2: 31.0 RNAse P: 32.0	Functional decline, lethargy, decreased appetite, dry cough; onset 1 day before test, persisted 14 days
B	F (80–89)	N1: 28.2 N2: 28.8 RNAse P: 25.8	Asymptomatic	103	N1: 17.5 N2: 19.1 RNAse P: 25.0	Congestion, SOB, respiratory failure; onset and hospitalization 1 day after test, death 8 days later
				104†	E: 18.2 N: 19.8	
C	F (60–69)	N1: 28.9 N2: 28.9 RNAse P: 24.9	Nausea at day 13 after positive test, persisted 1 day	109	N1: 19.3 N2: 20.4 RNAse P: 27.2	Cough, SOB, sore throat, loss of appetite, malaise, muscle aches; onset day of test, persisted 17 days
D	F (70–79)	N1: 29.2 N2: 29.6 RNAse P: 25.7	Gastrointestinal symptoms, onset 4 days prior to test, persisted 17 days, no fever or respiratory symptoms	109	N1: 18.5 N2: 18.9 RNAse P: 22.2	Loss of appetite, malaise; onset 3 days after test, persisted 12 days
E	F (90–99)	N1: 28.9 N2: 29.9 RNAse P: 33.0	Asymptomatic	110	N1: 17.2 N2: 17.9 RNAse P: 21.1	Cough, loss of appetite, malaise, muscle aches; onset day of test, persisted 6 days

Abbreviations: COVID-19 = coronavirus disease 2019; Ct = cycle threshold; F = female; M = male; RT-PCR = reverse transcription–polymerase chain reaction; SOB = shortness of breath.

* E and N genes are gene targets used to detect infection with SARS-CoV-2, the virus that causes COVID-19. One or both of the N1 and N2 gene targets must be detected with a Ct value ≤37 for a positive result. Lower Ct values indicate higher concentrations of SARS-CoV-2. RNAse P is a control that is used to assess specimen quality. Ct values ≤37 indicate the presence of human RNAse P gene.

† Patient B was retested with RT-PCR on hospital admission.

severity associated with reinfection (*6*). As with any diagnostic test, false-positive results are possible. The absence of symptoms in three of five patients during the initial episode could support the argument that the test results during the first outbreak were false positives, although it is known that up to 40%–50% of infections are asymptomatic (*7*,*8*). The probability that all five tests were false positives is a less likely explanation, especially in the context of a facility outbreak with associated severe morbidity and mortality. In addition, Ct values for the positive test results in the first outbreak were within the cutoff for limit of detection, suggesting virus titers consistent with infection.

These findings highlight the importance of maintaining public health practices that reduce transmission risk, even among persons who have previously received a positive SARS-CoV-2 test result. These findings support the possibility of reinfection in this population, though more definitive evidence with genomic sequencing is missing. The findings also suggest the possibility that disease can be more severe during a second infection.

The findings in this report are subject to at least three limitations. First, because specimens were not stored, genomic sequencing to confirm a reinfection was not possible (*9*). Second, no additional testing was performed during the first outbreak until at least 10 days after the first RT-PCR positive test result for the five residents later identified to have recurrent COVID-19. Therefore, no additional test results exist to support the initial test result as a true positive. Finally, no serologic testing was performed after the first outbreak, which could have helped confirm infection before the second infectious episode.

Five SNF residents received positive SARS-CoV-2 test results during two separate facility outbreaks that occurred

Summary

What is already known about this topic?

Case reports of reinfection with SARS-CoV-2 exist; however, data are limited as to the frequency and outcomes of reinfection.

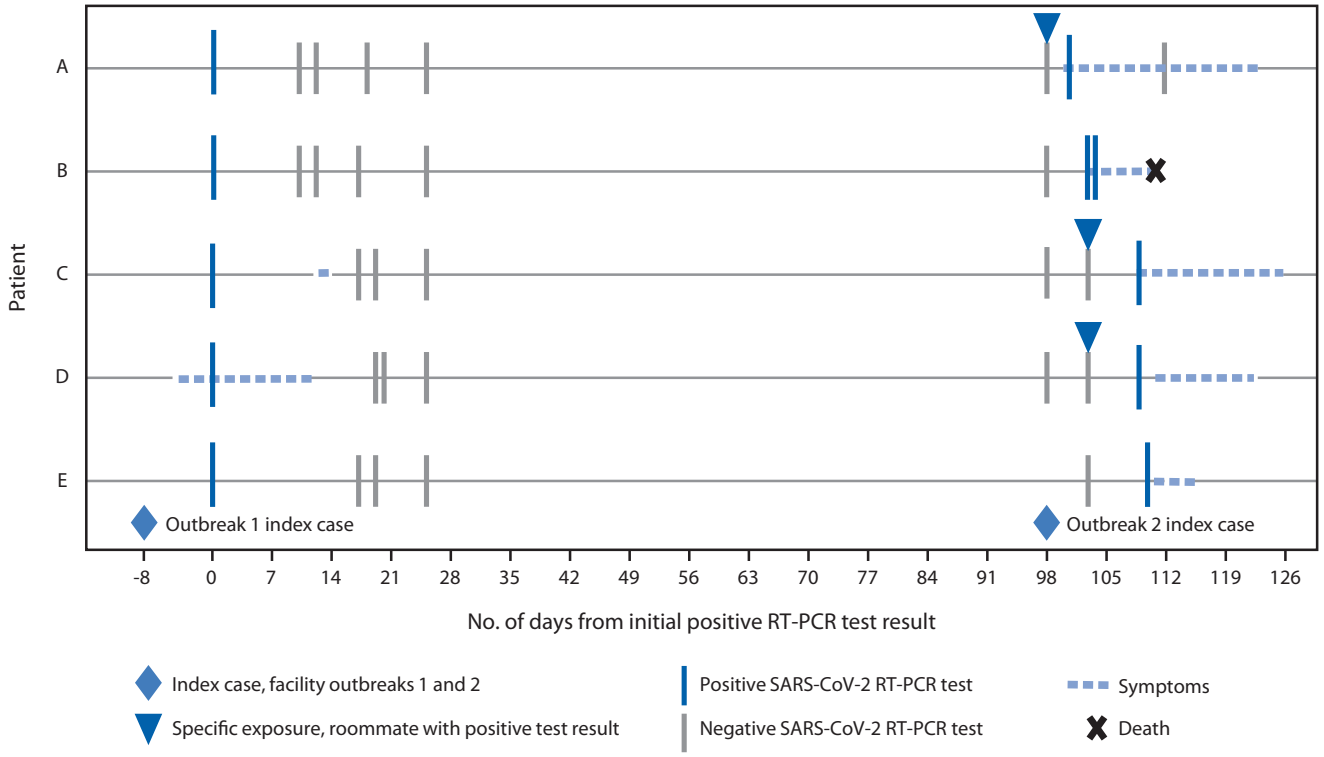
What is added by this report?

Five residents of a skilled nursing facility received positive SARS-CoV-2 nucleic acid test results in two separate COVID-19 outbreaks separated by 3 months. Residents received at least four negative test results between the two outbreaks, suggesting the possibility of reinfection. Severity of disease in the five residents during the second outbreak was worse than that during the first outbreak and included one death.

What are the implications for public health practice?

Skilled nursing facilities should use strategies to reduce the risk for SARS-CoV-2 transmission among all residents, including among those who have previously had a COVID-19 diagnosis. Vaccination of residents and health care personnel in this setting is particularly important to protect residents.

FIGURE. Exposure, symptom onset, and testing timeline for five patients with recurrent COVID-19 cases in a skilled nursing facility — Kentucky, July–December 2020*



Abbreviations: COVID-19 = coronavirus disease 2019; RT-PCR = reverse transcription–polymerase chain reaction.
* Dates indicate day of specimen collection.

in July and October 2020, suggesting possible reinfection. Affected persons experienced more severe illness during their second SARS-CoV-2 infection. Reinfection risk to the general population is suspected to be low, but SNF residents might have higher risk for new exposures, given the congregate nature of these settings and ongoing interactions with HCP and other residents. In addition, the level and duration of postinfection immunity in persons with an aging immune system is unknown, but the potential health consequences of reinfection among SNF populations remain serious. Therefore, steps to protect this population from the ongoing potential of SARS-CoV-2 exposures should be implemented. Based on the observations of this study, testing and cohorting practices in SNFs should not assume that residents infected >90 days earlier are immune to COVID-19. Public health interventions to limit transmission are vital for all persons in SNFs, including those who have previously been infected with SARS-CoV-2; these include physical distancing, use of masks (including by SNF residents, if tolerated), and frequent hand hygiene using hand sanitizer with 60%–95% alcohol or washing with soap and water for at least 20 seconds. Vaccination in these settings, as recommended by the Advisory Committee on Immunization Practices, is particularly important to optimally protect these vulnerable persons (*10*).

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First Identified Cases of SARS-CoV-2 Variant B.1.1.7 in Minnesota — December 2020–January 2021

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On February 17, 2021, this report was posted as an MMWR *Early Release on the* MMWR *website (https://www.cdc.gov/mmwr).*

On January 9, 2021, the Minnesota Department of Health (MDH) announced the identification of the SARS-CoV-2 variant of concern (VOC) B.1.1.7, also referred to as 20I/501Y.V1 and VOC 202012/01, in specimens from five persons; on January 25, MDH announced the identification of this variant in specimens from three additional persons. The B.1.1.7 variant, which is reported to be more transmissible than certain other SARS-CoV-2 lineages*,† (*1*), was first reported in the United Kingdom in December 2020 (*1*). As of February 14, 2021, a total of 1,173 COVID-19 cases of the B.1.1.7 variant had been identified in 39 U.S. states and the District of Columbia (*2*). Modeling data suggest that B.1.1.7 could become the predominant variant in the United States in March 2021 (*3*).

The B.1.1.7 variant has a mutation in the spike protein that causes S-gene target failure (SGTF) in the Thermo Fisher Scientific TaqPath COVID-19 reverse transcription–polymerase chain reaction (RT-PCR) assay. The overall RT-PCR result is positive but is negative for the S-gene target and positive for the other two assay targets; SGTF has served as a proxy for identifying the B.1.1.7 variant (*1*). The MDH Public Health Laboratory (MDH-PHL) requested SARS-CoV-2 RT-PCR–positive specimens with SGTFs collected during November 1, 2020–January 12, 2021, from clinical laboratories that used the TaqPath assay, and 30 specimens were received. An additional specimen that had been collected from a household contact of a person with an SGTF specimen was requested and obtained from a clinical laboratory using another COVID-19 assay that does not detect SGTFs. MDH-PHL conducted whole genome sequencing to analyze the 31 specimens.§

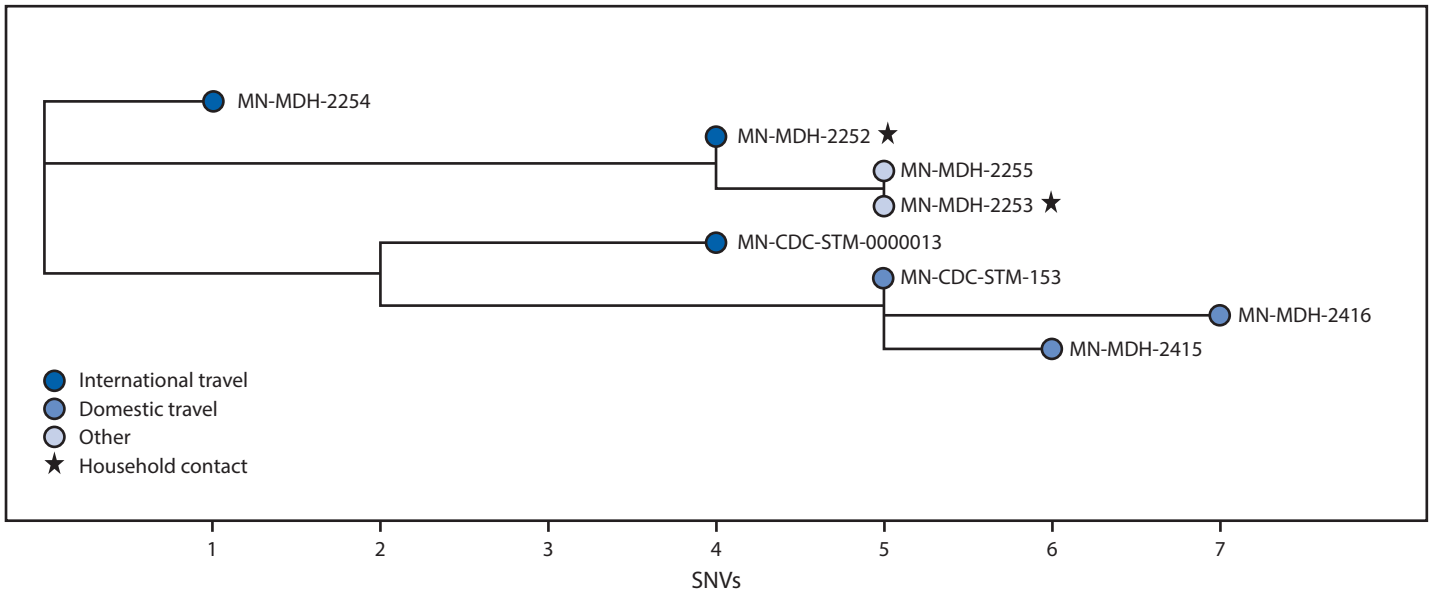
The SARS-CoV-2 variant B.1.1.7 was identified in eight specimens from Minnesota residents, including six (19%) of the 31 specimens sequenced by MDH-PHL and two specimens sequenced through CDC's national SARS-CoV-2 surveillance system.¶ The eight specimens were collected during December 18, 2020–January 11, 2021, from eight Minnesota residents in five counties in the Minneapolis–St. Paul metropolitan area. Seven persons were interviewed after receiving positive SARS-CoV-2 test results; after those with the B.1.1.7 variant were identified, MDH case investigators recontacted the patients to obtain additional information on exposures and close contacts. Six of the eight patients were successfully contacted, including one who had not been interviewed previously. This activity was reviewed by CDC and was conducted consistent with applicable federal law and policy.**

The eight persons from whom the specimens were collected ranged in age from 15 to 41 years. Three persons had a history of international travel during the 14 days before illness onset, including two who traveled to West Africa (MN-MDH-2252 and MN-MDH-2254) (Figure) and one who traveled to the Dominican Republic (MN-CDC-STM-0000013). Three additional persons traveled to California (MN-MDH-2415, MN-MDH-2416, and MN-CDC-STM-153) in the 14 days before illness onset or specimen collection, including one who received a positive test result while in California and isolated there before returning to Minnesota. Five persons reported COVID-19–like symptoms and had illness onset dates during December 16, 2020–January 10, 2021; three were asymptomatic. Two sequences (MN-MDH-2253 and MN-MDH-2255) were identical, and the MN-MDH-2252 sequence differed by one single nucleotide variant (SNV). The three sequences for cases from California clustered together within one to three SNVs and are genetically distinct from the other sequences. Two specimens from international travelers, MN-MDH-2254 and MN-CDC-STM-0000013, did not have sequences similar to those identified in Minnesota.

Persons identified with the variant B.1.1.7 in Minnesota had exposure histories related to travel (six), the household (one), and others in the community (one). None had a history of

* https://www.medrxiv.org/content/10.1101/2020.12.30.20249034v1.full.pdf
† https://www.biorxiv.org/content/10.1101/2020.12.14.422555v3.full.pdf
§ https://virological.org/t/tracking-sars-cov-2-voc-202012-01-lineage-b-1-1-7-dissemination-in-portugal-insights-from-nationwide-rt-pcr-spike-gene-drop-out-data/600
¶ https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance.html
** 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.

FIGURE. Phylogenetic tree* showing genetic distance† between SARS-CoV-2–positive specimens with the B.1.1.7 variant (n = 8) and exposure histories related to travel,§ household contacts, and others in the community



Abbreviation: SNV = single nucleotide variant.

* Phylogenetic tree created using Interactive Tree of Life (version 5.7; European Molecular Biology Laboratory). https://itol.embl.de/

† MN-MDH-2253 and MN-MDH-2255 were identical, and MN-MDH-2252 was within one SNV. MN-MDH-2252 and MN-MDH-2253 were collected from persons who were household contacts. Two specimens from international travelers, MN-MDH-2254 and MN-CDC-STM-0000013, did not have sequences similar to those identified in Minnesota.

§ International and domestic travel occurred during the 14 days before illness onset or specimen collection, including onset of illness in persons who received positive SARS-CoV-2 test results while away from Minnesota. MN-CDC-STM-153, MN-MDH-2416, and MN-MDH-2415 were clustered together within one to three SNVs. These three specimens were from persons who reported travel to California in the 14 days before illness onset or specimen collection, including one who received a positive test result while in California and isolated there before returning to Minnesota.

travel to the United Kingdom, although three persons traveled internationally and three persons traveled domestically in the 14 days before illness onset or specimen collection, including one who received a positive test result before returning to Minnesota. Identification of this variant in Minnesota, a variant that epidemiologic and genomic evidence suggests has increased transmissibility, highlights the importance of mitigation measures such as mask use, physical distancing, avoiding crowds and poorly ventilated indoor spaces, isolation of persons with diagnosed COVID-19, quarantine of close contacts of persons with COVID-19,†† and adherence to CDC travel guidance§§ to slow transmission. As SARS-CoV-2 continues to evolve, timely genomic surveillance and disease mitigation strategies will be critical for monitoring variant emergence and protecting public health.

†† https://www.cdc.gov/coronavirus/2019-ncov/your-health/need-to-know.html

§§ https://www.cdc.gov/coronavirus/2019-ncov/travelers/travel-during-covid19.html

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Detection of B.1.351 SARS-CoV-2 Variant Strain — Zambia, December 2020

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The first laboratory-confirmed cases of coronavirus disease 2019 (COVID-19), the illness caused by SARS-CoV-2, in Zambia were detected in March 2020 (*1*). Beginning in July, the number of confirmed cases began to increase rapidly, first peaking during July–August, and then declining in September and October (Figure). After 3 months of relatively low case counts, COVID-19 cases began rapidly rising throughout the country in mid-December. On December 18, 2020, South Africa published the genome of a SARS-CoV-2 variant strain with several mutations that affect the spike protein (*2*). The variant included a mutation (N501Y) associated with increased transmissibility.[†,§] SARS-CoV-2 lineages with this mutation have rapidly expanded geographically.[¶,**] The variant strain (PANGO [Phylogenetic Assignment of Named Global Outbreak] lineage B.1.351[††]) was first detected in the Eastern Cape Province of South Africa from specimens collected in early August, spread within South Africa, and appears to have displaced the majority of other SARS-CoV-2 lineages circulating in that country (*2*). As of January 10, 2021, eight countries had reported cases with the B.1.351 variant. In Zambia, the average number of daily confirmed COVID-19 cases increased 16-fold, from 44 cases during December 1–10 to 700 during January 1–10, after detection of the B.1.351 variant in specimens collected during December 16–23. Zambia is a southern African country that shares substantial commerce and tourism linkages with South Africa, which might have contributed to the transmission of the B.1.351 variant between the two countries.

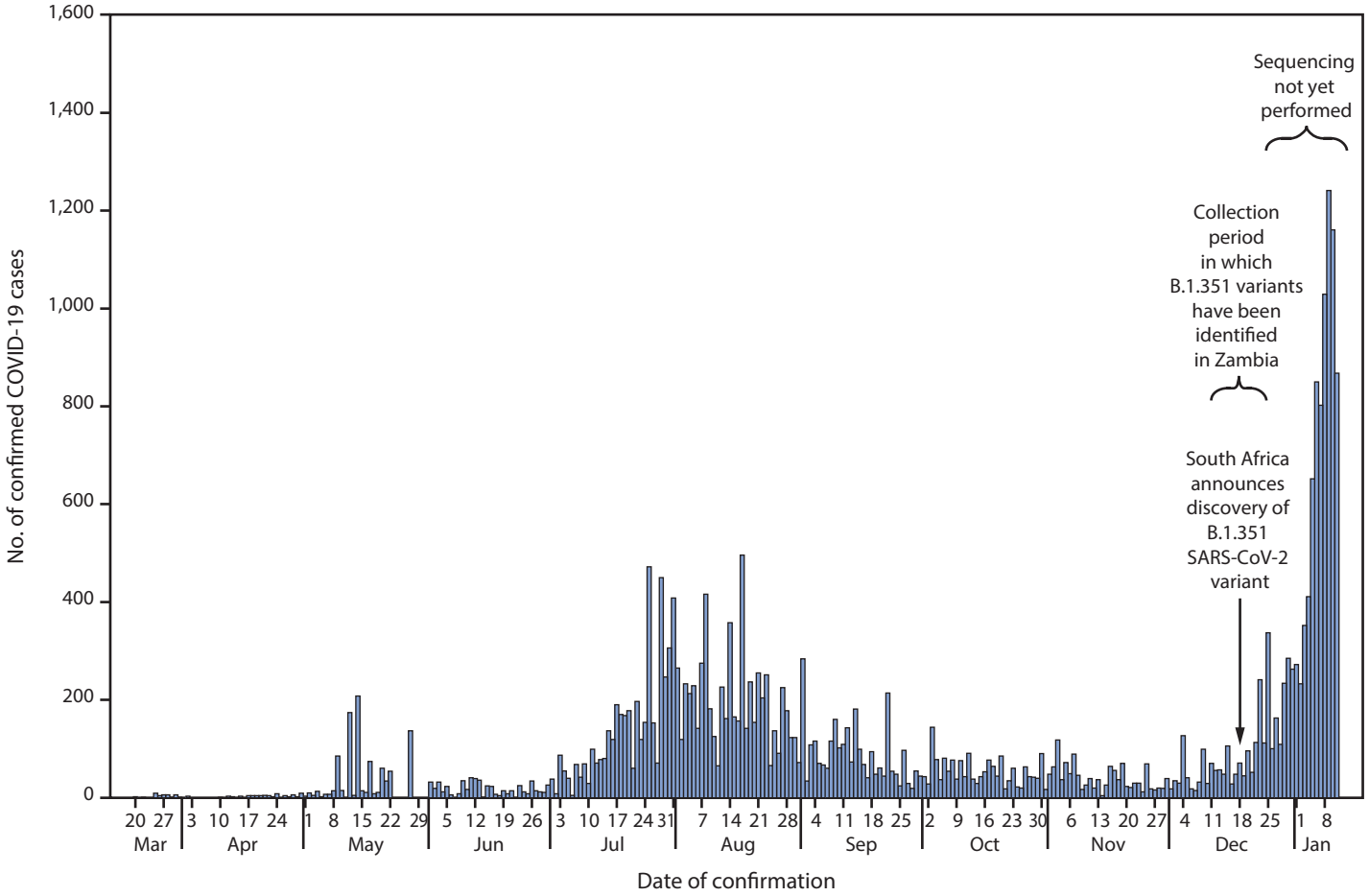
Since September 2020, University of Zambia and PATH (https://www.path.org) have routinely been conducting genetic epidemiologic studies using whole genome sequencing (WGS) on SARS-CoV-2–positive specimens. A subset of specimens collected during March 18–December 23, 2020, were sequenced, from which 268 high-quality genomes were generated. Specimens were selected for WGS based on availability and real-time reverse transcription–polymerase chain reaction (RT-PCR) diagnostic test cycle threshold (Ct) values of <30; lower Ct values are correlated with larger amounts of virus in the sample. Sequences were linked to case investigation information including patient age, sex, and geographic location from routine public health data maintained by the Zambia National Public Health Institute. For WGS, complementary DNA was prepared using random primers from viral RNA extracted from SARS-CoV-2 real-time RT-PCR–positive specimens. Multiplex PCR was then performed using custom primers (*3*) to generate overlapping amplicons for nanopore sequencing on a MinION (Oxford Nanopore Technology, United Kingdom).[§§] Consensus sequence reads were generated using the standard ARTIC Network bioinformatic pipeline,[¶¶] a system for processing samples from viral disease outbreaks to generate real-time, actionable epidemiologic information.

Among the 23 specimens collected during December 16–23, 22 (96%) were the B.1.351 variant. None of the 245 previously sequenced genomes was from this lineage. Among the 22 specimens containing the variant strain, 21 (95%) contained all nine B.1.351 lineage-defining mutations. Thirteen (57%) were from males, and the median patient age was 32 years (interquartile range = 27–45 years). Specimens with the B.1.351 variant were obtained from persons in four districts (Lusaka, 16; Livingstone, four; Chingola, one; and Chibombo, one) across four provinces (Lusaka, Southern, Copperbelt, and Central). Five (23%) specimens were obtained from persons in two different clusters, with no known epidemiologic links among other cases.

Detection of the B.1.351 variant coincided with a rapid rise in confirmed cases in Zambia. This detection establishes an epidemiologic linkage between COVID-19 outbreaks in Zambia and South Africa. Spread of the B.1.351 variant is of public health concern because of the potential for increased transmissibility and, thus, increases in cases, hospitalizations,

* These authors contributed equally to this work.
† https://khub.net/documents/135939561/338928724/SARS-CoV-2%20variant%20under%20investigation,%20meeting%20minutes.pdf/962e866b-161f-2fd5-1030-32b6ab467896?t = 1608470511452
§ https://virological.org/t/mutations-arising-in-sars-cov-2-spike-on-sustained-human-to-human-transmission-and-human-to-animal-passage/578
¶ https://cmmid.github.io/topics/covid19/uk-novel-variant.html
** https://www.who.int/csr/don/31-december-2020-sars-cov2-variants/en/
†† https://github.com/cov-lineages/pangolin/
§§ https://www.protocols.io/view/ncov-2019-sequencing-protocol-v3-locost-bh42j8ye
¶¶ https://artic.network/ncov-2019/ncov2019-bioinformatics-sop.html

FIGURE. Reported laboratory-confirmed COVID-19 cases, by date of confirmation — Zambia, March 20, 2020–January 11, 2021



Abbreviation: COVID-19 = coronavirus disease 2019.

and deaths.*** The B.1.351 variant might be associated with higher viral loads and contains another spike protein mutation (E484K) that might hinder antibody binding,†††,§§§ which could blunt naturally developed immunity or reduce vaccine efficacy. The predominance of the B.1.351 variant in a small cohort of recent specimens suggests that it might have become the dominant lineage in Zambia, although additional WGS of specimens from other districts is needed to characterize the full extent of its spread. Further, the available genomic data could not identify when and from where the B.1.351 variant was introduced to Zambia. Because the B.1.351 variant has been detected in Zambia, it might be circulating elsewhere in southern Africa, where many countries reported rapid increases in numbers of COVID-19 cases during December 2020–January 2021.¶¶¶ Phylogenetic analysis and additional sequencing are ongoing to better understand the origin, prevalence, and transmission characteristics of this lineage in Zambia. Expanding capacity for genetic epidemiology in Africa will help strengthen surveillance for the B.1.351 variant as well as early detection of emerging variants that might affect the implementation of vaccination programs.

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All authors have completed and submitted the International Committee of Medical Journal Editors form for disclosure of potential conflicts of interest. Edgar Simulundu reports receipt of reagents from Hokkaido University during the course of the study. No other potential conflicts of interest were disclosed.

*** https://www.cdc.gov/coronavirus/2019-ncov/transmission/variant.html
††† https://www.biorxiv.org/content/10.1101/2020.12.31.425021v1.full.pdf
§§§ https://www.biorxiv.org/content/10.1101/2020.12.28.424451v1.full.pdf
¶¶¶ https://africacdc.org/download/outbreak-brief-52-coronavirus-disease-2019-covid-19-pandemic/

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First Month of COVID-19 Vaccine Safety Monitoring — United States, December 14, 2020–January 13, 2021

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On February 19, 2021, this report was posted as an MMWR *Early Release on the* MMWR *website (https://www.cdc.gov/mmwr).*

Two coronavirus disease 2019 (COVID-19) vaccines are currently authorized for use in the United States. The Food and Drug Administration (FDA) issued Emergency Use Authorization (EUA) for the Pfizer-BioNTech COVID-19 vaccine on December 11, 2020, and for the Moderna COVID-19 vaccine on December 18, 2020; each is administered as a 2-dose series. The Advisory Committee on Immunization Practices issued interim recommendations for Pfizer-BioNTech and Moderna COVID-19 vaccines on December 12, 2020 (*1*), and December 19, 2020 (*2*), respectively; initial doses were recommended for health care personnel and long-term care facility (LTCF) residents (*3*). Safety monitoring for these vaccines has been the most intense and comprehensive in U.S. history, using the Vaccine Adverse Event Reporting System (VAERS), a spontaneous reporting system, and v-safe,* an active surveillance system, during the initial implementation phases of the COVID-19 national vaccination program (*4*). CDC conducted descriptive analyses of safety data from the first month of vaccination (December 14, 2020–January 13, 2021). During this period, 13,794,904 vaccine doses were administered, and VAERS received and processed† 6,994 reports of adverse events after vaccination, including 6,354 (90.8%) that were classified as nonserious and 640 (9.2%) as serious.§ The symptoms most frequently reported to VAERS were headache (22.4%), fatigue (16.5%), and dizziness (16.5%). A total of 113 deaths were reported to VAERS, including 78 (65%) among LTCF residents; available information from death certificates, autopsy reports, medical records, and clinical descriptions from VAERS reports and health care providers did not suggest any causal relationship between COVID-19 vaccination and death. Rare cases of anaphylaxis after receipt of both vaccines were reported (4.5 reported cases per million doses administered). Among persons who received Pfizer-BioNTech vaccine, reactions reported to the v-safe system were more frequent after receipt of the second dose than after the first. The initial postauthorization safety profiles of the two COVID-19 vaccines in current use did not indicate evidence of unexpected serious adverse events. These data provide reassurance and helpful information regarding what health care providers and vaccine recipients might expect after vaccination.

VAERS is an existing national passive surveillance system for adverse events after vaccination that accepts reports from health care providers, vaccine manufacturers, and the public. Reported signs and symptoms are coded using Medical Dictionary for Regulatory Activities (MedDRA) terminology.¶ Serious adverse events are followed up by the VAERS program to obtain additional information, including medical records, information from health care providers, and, in the case of death, death certificates and autopsy reports (*4*).

V-safe is a safety monitoring system established by CDC specifically for the COVID-19 vaccination program. V-safe participants voluntarily self-enroll and receive smartphone text messages providing hyperlinks to web surveys.** During the first week after vaccination, enrollees complete daily surveys asking about local injection site and systemic reactions. Enrollees are asked if they missed work, were unable to perform normal daily activities, or received care from a medical professional because of reported symptoms or heath conditions. Enrollees who report seeking medical care are contacted, and a VAERS report is completed if clinically indicated. Persons who do not report their sex as male are asked about pregnancy status at time of vaccination (initial survey) and about a positive pregnancy test result (3- and 6-week surveys); reported pregnancies are followed up through the v-safe pregnancy registry.††

CDC conducted descriptive analyses of data from VAERS and v-safe during December 14, 2020–January 13, 2021, a

* https://www.cdc.gov/coronavirus/2019-ncov/vaccines/safety/vsafe.html

† Processed VAERS reports are those that have been MedDRA-coded, been deduplicated, and undergone quality assurance and quality control.

§ Based on the Code of Federal Regulations, a serious adverse event is defined as occurring if one of the following is reported: death, life-threatening illness, hospitalization or prolongation of hospitalization, permanent disability, congenital anomaly, or birth defect. https://www.accessdata.fda.gov/scripts/cdrh/cfdocs/cfcfr/cfrsearch.cfm?fr

¶ A single VAERS report might be assigned more than one MedDRA Preferred Term; not all terms are medically confirmed diagnoses. https://www.meddra.org/how-to-use/basics/hierarchy

** V-safe enrollees receive daily health check-ins via smartphone text messages that link to web-based surveys for the first 7 days after vaccination, then weekly through 6 weeks postvaccination and then at 3, 6, and 12 months. The health check-in process resets when a person receives a second dose of vaccine.

†† https://www.cdc.gov/vaccinesafety/pdf/vsafe-pregnancy-surveillance-protocol-508.pdf

period when the first and second doses of Pfizer-BioNTech vaccine and the first dose of Moderna vaccine were administered. Because LTCF staff members were vaccinated at LTCF facilities, residents of LTCFs were presumptively identified by restricting examination of VAERS reports to adults aged ≥65 years with a documented vaccination at an LTCF. To ensure that LTCF residents with serious adverse events were identified, manual review was conducted of all reports of serious adverse events among those vaccinated in LTCFs, regardless of vaccine recipient's age. Administered vaccine doses were reported to CDC.[§§] These activities were reviewed by CDC and are consistent with applicable federal law and CDC policy.[¶¶] All analyses were conducted using SAS software (version 9.4; SAS Institute).

During December 14, 2020–January 13, 2021, a total of 13,794,904 COVID-19 vaccine doses were administered in the United States; 8,436,863 (61.2%) doses were administered to women. VAERS received 6,994 reports of COVID-19–associated adverse events during this period. Among all reports, 6,354 (90.8%) were classified as nonserious and 640 (9.2%) as serious, including 113 (1.6%) deaths. The median age of vaccine recipients in VAERS reports was 42 years (range = 15–104 years); 5,505 (78.7%) reports were submitted for adverse events in women. Headache (22.4%), fatigue (16.5%), and dizziness (16.5%) were the most frequently reported symptoms after vaccination with either vaccine (Table 1). Sixty-two reports of anaphylaxis have been confirmed, 46 (74.2%) after receipt of the Pfizer-BioNTech vaccine and 16 (25.8%) after receipt of the Moderna vaccine.

VAERS Reports Involving Non-LTCF Residents

Among the 6,994 VAERS reports received and processed, 6,844 (97.9%) involved persons not residing in LTCFs; among these, 5,533 (80.8%) received the Pfizer-BioNTech vaccine and 1,311 (19.2%) received the Moderna vaccine. Most reports concerned women (5,413; 79.1%), and the median age of persons reporting adverse events was 42 years (range = 15–96 years). The most frequently reported symptoms were headache (1,564; 22.9%), dizziness (1,149; 16.8%), and fatigue (1,147; 16.8%). Among these reports, 6,326 (92.4%) were classified as nonserious. Included among the 518 (7.6%) serious reports were 35 reports of death: 16 (45.7%) after the Pfizer-BioNTech vaccine and 19 (54.3%) after the Moderna vaccine. Decedents ranged in age from 25 to 91 years (median = 62 years); 15 (42.9%) were women. The median interval from vaccination to death was 3 days (range = 0–20 days). Among 19 persons whose deaths were reported to VAERS after receiving COVID-19 vaccine, record collection and evaluation are ongoing; for the remaining 16 reported deaths, review of death certificates or other data indicated underlying heart disease, cancer, stroke, probable pulmonary embolism, and otherwise frail health as the cause of death.

VAERS Reports Involving LTCF Residents

Among residents of LTCFs who received COVID-19 vaccine, 150 (2.1%) reports of adverse events were submitted to VAERS, including 88 (58.7%) after receipt of the Pfizer-BioNTech vaccine and 62 (41.3%) after receipt of the Moderna vaccine. The median vaccine recipient age was 83 years (range = 17–104 years), and 92 (61%) reports concerned women. Among 122 (81.3%) reports of serious adverse events in LTCF residents, 78 (52.0%) deaths have been reported and investigated; 42 (53.8%) occurred in residents in hospice care or with a do-not-resuscitate status. Death certificate data were available for 17 (22.0%) deaths; causes of death included cardiac disease, dementia, pneumonia, and failure to thrive. Nineteen (24.3%) reported deaths are currently awaiting additional records to establish cause of death. Reported deaths occurred 0–20 days after vaccination (median = 2 days).

v-safe Reports

During December 14, 2020–January 13, 2021, v-safe enrolled 1,602,065 vaccine recipients who completed at least one survey; 814,648 (50.8%) received Pfizer-BioNTech, and 787,417 (49.2%) received Moderna vaccines. The median recipient age was 46 years (range = 16–110 years); 1,106,656 (69.1%) were women. There were 10,825 (0.68%) enrollees who reported that they were pregnant at the time of vaccination, and 262 (0.02%) reported a positive pregnancy test result after vaccination. Solicited local and systemic reactions were similar between persons receiving first doses of Pfizer-BioNTech and Moderna vaccines. Injection site pain, fatigue, headache, myalgia, and chills were most frequently reported (Figure). Enrollees reported more reactions on the day after vaccination than on any other day. For the Pfizer-BioNTech vaccine, reactions were more frequent after the second dose than the first; the reported rate of fever and chills was more than four times higher after the second dose than after the first (Table 2).

Discussion

After administration of 13.8 million doses of Pfizer-BioNTech and Moderna COVID-19 vaccines to the U.S. population during the first month of the vaccination program, the postauthorization safety profiles for both vaccines are reassuring. Most (90.9%) VAERS reports were for nonserious events

[§§] https://covid.cdc.gov/covid-data-tracker/#datatracker-home

[¶¶] 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.

TABLE 1. Reports of adverse events after receipt of Pfizer-BioNTech and Moderna COVID-19 vaccines, by recipients' demographic characteristics and reported symptoms — Vaccine Adverse Event Reporting System, United States, December 14, 2020–January 13, 2021

Characteristic	No. (%) reporting adverse events			
	All COVID-19 vaccine doses (N = 6,994)	Pfizer-BioNTech vaccine		Moderna vaccine
		Dose 1 (N = 5,428)	Dose 2 (N = 193)	Dose 1 (N = 1,373)
Nonserious adverse event reports	6,354 (90.9)	5,087 (93.7)	152 (78.6)	1,115 (81.2)
Serious adverse event reports*†	640 (9.2)	341 (6.3)	41 (21.2)	258 (18.8)
Sex				
Female	5,505 (78.7)	4,296 (79.2)	142 (73.6)	1,067 (77.7)
Male	1,408 (20.1)	1,056 (19.5)	51 (26.4)	301 (21.9)
Unknown	81 (1.2)	76 (1.4)	0 (—)	5 (0.4)
Age group (yrs)				
0–17	12 (0.2)	4 (0.1)	0 (—)	8 (0.6)
18–49	4,539 (64.9)	3,568 (65.7)	119 (61.7)	852 (62.1)
50–64	1,772 (25.3)	1,351 (24.9)	51 (26.4)	370 (27.0)
65–74	255 (3.7)	184 (3.4)	11 (5.7)	60 (4.4)
75–84	85 (1.2)	48 (0.9)	5 (2.6)	32 (2.3)
≥85	93 (1.3)	46 (0.9)	4 (2.1)	43 (3.1)
Unknown	238 (3.4)	227 (4.2)	3 (1.6)	8 (0.1)
Most frequently reported symptoms				
Headache	1,566 (22.4)	1,184 (21.8)	35 (18.1)	347 (25.3)
Fatigue	1,154 (16.5)	912 (16.8)	14 (7.3)	228 (16.6)
Dizziness	1,151 (16.5)	907 (16.7)	16 (8.3)	228 (16.6)
Chills	1,040 (14.9)	760 (14.0)	19 (9.8)	261 (19.0)
Nausea	1,037 (14,8)	790 (14.6)	18 (9.3)	229 (16.7)

Abbreviation: COVID-19 = coronavirus disease 2019.

* Based on the Code of Federal Regulations, classification of a serious adverse event includes a report of one of the following: death, life-threatening illness, hospitalization or prolongation of hospitalization, permanent disability, congenital anomaly, or birth defect. https://www.accessdata.fda.gov/scripts/cdrh/cfdocs/cfcfr/cfrsearch.cfm?fr

† Includes 113 deaths.

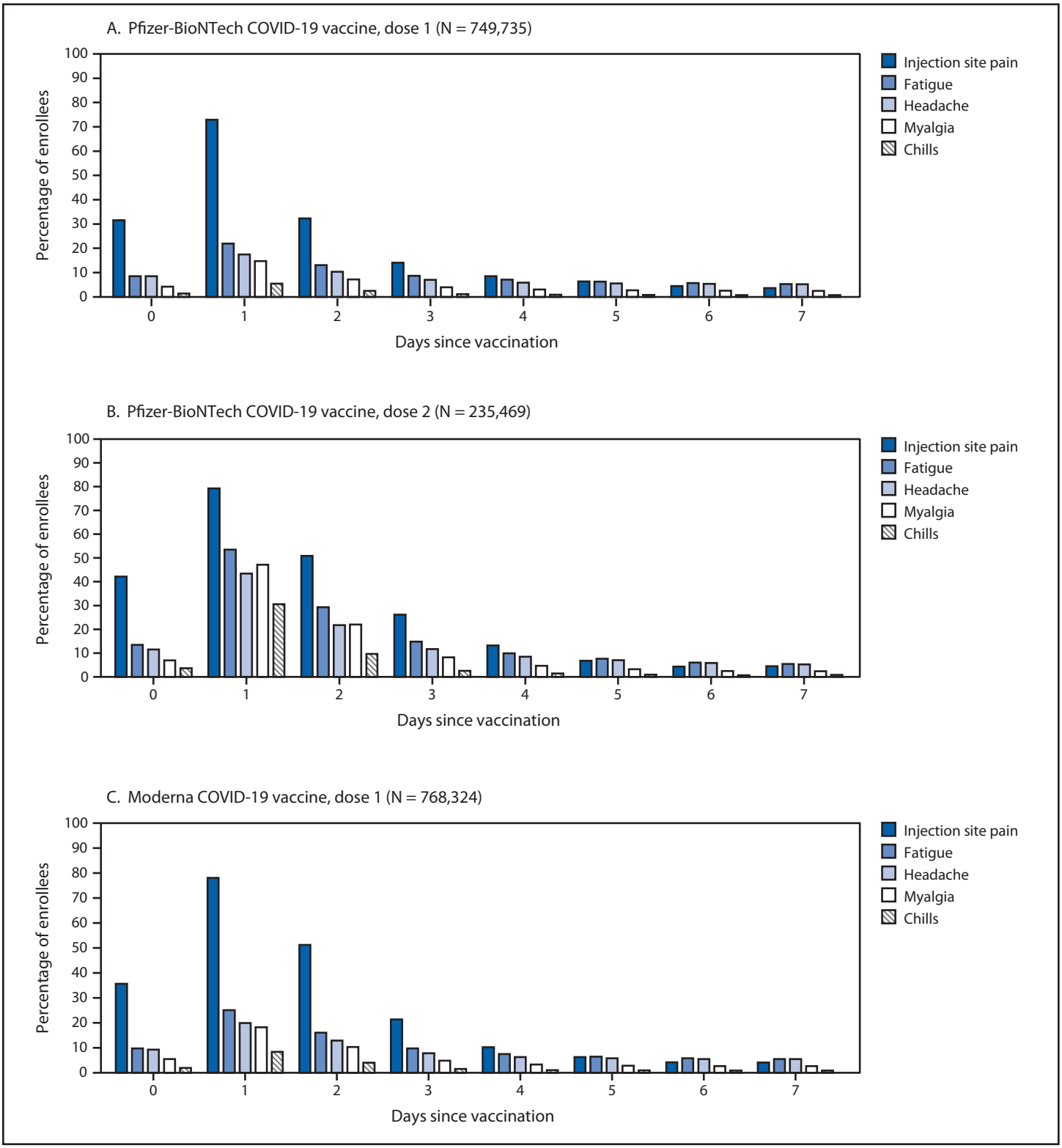
and involved local and systemic symptoms; transient local and systemic reactions were also frequently reported in v-safe. Reports of anaphylaxis have been observed after administration of both vaccines (*5*). The occurrence of anaphylaxis after receipt of COVID-19 vaccines during the analytic period, 4.5 cases per million doses administered, is within the range reported after receipt of inactivated influenza vaccine (1.4 per million), pneumococcal polysaccharide vaccine (2.5 per million), and live attenuated herpes zoster vaccine (9.6 per million); effective treatments for anaphylaxis exist (*6*).

VAERS received 113 reports of death after COVID-19 vaccinations; two thirds of these deaths occurred among LTCF residents. All-cause mortality is high in LTCF populations because underlying medical conditions are common. Based on expected rates of background mortality, among the approximately 1 million LTCF residents vaccinated in the first month of the U.S. COVID-19 vaccination program, approximately 7,000 coincidental, temporally associated deaths from all causes would be expected during the analytic period (*7*). In contrast, VAERS received 78 reports of death after COVID-19 vaccination in LTCF residents, and approximately one half were in residents who were in hospice or who had a do-not-resuscitate status. Reported causes of death in LTCF residents after COVID-19 vaccination are consistent with expected all-cause mortality in this population. Among deaths in persons with available death certificate and autopsy information who were not LTCF residents, causes of death were consistent with background all-cause mortality and did not indicate any unexpected pattern that might suggest a causal relationship with vaccination (*8*).

Findings from v-safe monitoring for both vaccines indicate substantial reactogenicity. More reactogenicity was reported after the second dose of Pfizer-BioNTech than the first, particularly on the day after vaccination (data on second dose of Moderna vaccine were not available because of later availability and the dosing interval). These findings are similar to those from clinical trials from both manufacturers, in which injection site pain, fatigue, headache, and myalgia were most frequently reported, with a higher frequency after the second dose in comparable age groups (*9*,*10*). V-safe's rapid collection of experiences from vaccinated persons provides valuable information that health care providers can use to counsel vaccine recipients about common reactions and what to expect after vaccination.*** V-safe will be able to provide information on vaccination during pregnancy through follow-up in the v-safe pregnancy registry.

*** https://www.cdc.gov/vaccines/covid-19/info-by-product/clinical-considerations.html

FIGURE. Percentage of enrollees who reported common local and systemic reactions by day after receipt of the first dose of Pfizer BioNTech COVID-19 vaccine (A), second dose of Pfizer BioNTech COVID-19 vaccine (B), and first dose of Moderna COVID-19 vaccine (C) — v-safe, United States, December 14, 2020–January 13, 2021



Abbreviation: COVID-19 = coronavirus disease 2019.

TABLE 2. Percentage of v-safe enrollees who completed at least one survey (N = 1,602,065) with local and systemic reactions reported for day 0–7 and for day 1 after receiving Pfizer-BioNTech and Moderna COVID-19 vaccines — v-safe,* United States, December 14, 2020–January 13, 2021

	Percentage of v-safe enrollees reporting reactions			
	Both vaccines	Pfizer-BioNTech vaccine		Moderna vaccine
Local and systemic reaction	Day 0–7	Dose 1, day 1	Dose 2, day 1	Dose 1, day 1
Injection site pain	70.9	72.9	79.3	78.1
Fatigue	33.5	21.9	53.5	25.1
Headache	29.5	17.5	43.4	19.9
Myalgia	22.9	14.7	47.2	18.3
Chills	11.6	5.5	30.6	8.4
Fever	11.4	5.8	29.2	8.2
Injection site swelling	10.8	6.2	8.6	12.6
Joint pain	10.4	5.3	23.5	7.3
Nausea	8.9	4.2	14.0	5.5

Abbreviation: COVID-19 = coronavirus disease 2019.
* https://www.cdc.gov/coronavirus/2019-ncov/vaccines/safety/vsafe.html

The findings in this report are subject to at least three limitations. First, VAERS analyses are based on passive surveillance, and reporting biases are possible, both from underreporting because of lack of awareness or compliance with reporting requirements as well as from stimulated reporting related to increased awareness. Second, LTCF residents might have been undercounted because the search strategy for identifying LTCF residents relied primarily on vaccination facility documentation. Because of challenges in distinguishing LTCF staff members from LTCF residents aged ≤65 years, only serious VAERS reports were reviewed among those aged ≤65 years who were vaccinated in LTCFs. Finally, v-safe is a voluntary self-enrollment program requiring smartphone access, and all vaccination locations might not have offered equal access to v-safe enrollment materials to vaccine recipients; therefore, information from v-safe might not be representative or generalizable.

Mass vaccination with highly effective vaccines is critical to controlling the COVID-19 pandemic. Because of the speed of COVID-19 vaccine development and deployment, there have been concerns among the public about the safety of these new vaccines. In response to these concerns, the U.S. government has implemented the most comprehensive vaccine safety monitoring program in its history. Cases of anaphylaxis after receipt of both authorized vaccines have been observed, though rarely; anaphylaxis rates are comparable with those reported after receipt of other vaccines. No unexpected patterns of reactions or other safety concerns have been identified during early monitoring. CDC and FDA will continue to monitor the safety of COVID-19 vaccines to inform vaccination policy and to maintain public confidence.

Adverse events that occur after COVID-19 vaccination should be reported to VAERS. Providers are encouraged to promote v-safe enrollment and are required under EUA to report to VAERS vaccination administration errors, serious adverse events, cases of multisystem inflammatory syndrome, and cases of COVID-19 that result in hospitalization or death after COVID-19 vaccination.††† These initial findings should provide reassurance to health care providers and to vaccine recipients and promote confidence in the safety of COVID-19 vaccines.

Summary

What is already known about this topic?

Two COVID-19 vaccines have received Emergency Use Authorization for administration in the United States. In preauthorization clinical trials, local and systemic reactions were reported; no serious safety problems were detected.

What is added by this report?

Monitoring, conducted as part of the U.S. vaccination program, indicates reassuring safety profiles for COVID-19 vaccines. Local and systemic reactions were common; rare reports of anaphylaxis were received. No unusual or unexpected reporting patterns were detected.

What are the implications for public health practice?

Health care providers and vaccine recipients can be reassured about the safety of Pfizer BioNTech and Moderna COVID-19 vaccines. Counseling vaccine recipients to expect transient local and systemic reactions might ease concerns and encourage completion of the 2-dose vaccination series.

††† https://vaers.hhs.gov/faq.html

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All authors have completed and submitted the International Committee of Medical Journal Editors form for disclosure of potential conflicts of interest. Geoffrey M. Calvert reports owning 100 shares of Johnson & Johnson stock. No other potential conflicts of interest were disclosed.

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Please note: This report has been corrected. An erratum has been published.

Morbidity and Mortality Weekly Report

Clusters of SARS-CoV-2 Infection Among Elementary School Educators and Students in One School District — Georgia, December 2020–January 2021

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On February 22, 2021, this report was posted as an MMWR *Early Release on the* MMWR *website (https://www.cdc.gov/mmwr).*

In-person learning benefits children and communities (*1*). Understanding the context in which transmission of SARS-CoV-2, the virus that causes coronavirus disease 2019 (COVID-19), occurs in schools is critical to improving the safety of in-person learning. During December 1, 2020–January 22, 2021, Cobb and Douglas Public Health (CDPH), the Georgia Department of Public Health (GDPH), and CDC investigated SARS-CoV-2 transmission in eight public elementary schools in a single school district. COVID-19 cases* among educators and students were either self-reported or identified by local public health officials. Close contacts (contacts)† of persons with a COVID-19 case received testing. Among contacts who received positive test results, public health investigators assessed epidemiologic links, probable transmission directionality, and the likelihood of in-school transmission.§ Nine clusters of three or more epidemiologically linked COVID-19 cases were identified involving 13 educators and 32 students at six of the eight elementary schools. Two clusters involved probable educator-to-educator transmission that was followed by educator-to-student transmission and resulted in approximately one half (15 of 31) of school-associated cases. Sixty-nine household members of persons with school-associated cases were tested, and 18 (26%) received positive results. All nine transmission clusters involved less than ideal physical distancing, and five involved inadequate mask use by students. Educators were central to in-school transmission networks. Multifaceted mitigation measures in schools, including promotion of COVID-19 precautions outside of school, minimizing in-person adult interactions at school, and ensuring universal and correct mask use and physical distancing among educators and students when in-person interaction is unavoidable, are important in preventing in-school transmission of SARS-CoV-2. Although not required for reopening schools, COVID-19 vaccination should be considered as an additional mitigation measure to be added when available.

During the investigation period, which included 24 in-person school days during December 1, 2020–January 22, 2021, approximately 2,600 students (approximately 80% of the district's elementary school students) and 700 staff members attended elementary school in person. During this period, COVID-19 incidence (7-day moving average number of cases per 100,000 persons) in Cobb County, Georgia, increased almost 300%, from 152 to 577 cases.¶ COVID-19 cases among educators and students attending in-person school were either self-reported to the school district or identified by local public health officials through laboratory results. Contacts who were exposed to persons with COVID-19 in school were identified by school officials, advised to quarantine based on local health department guidelines,** and referred to the investigation team.

Reverse transcription–polymerase chain reaction (RT-PCR) testing†† of anterior nasal swab specimens was offered free of charge to all contacts who were exposed in school, within 5–10 days of their last documented in-school exposure; 60% of identified contacts received testing, and 40% either declined testing or could not be reached. Semistructured

* A COVID-19 case was defined as a positive SARS-CoV-2 reverse transcription–polymerase chain reaction or antigen test result in a person who attended school in person.

† Close contacts were defined as persons exposed to an index patient at school within 6 ft for >15 minutes per day during a 24-hour period while the index patient was infectious (48 hours before to 10 days after symptom onset or, if asymptomatic, 48 hours before to 10 days after specimen collection).

§ To be classified as having a school-associated COVID-19 case, a person had to meet three criteria: 1) the timing of symptom onset (if symptoms were present) and testing must have been consistent with acquisition of SARS-CoV-2 infection from the index patient or a person with a school-associated case in the school setting based on the known incubation period, 2) the person must have had close contact at school with the school index patient or another person with a school-associated case according to GDPH guidelines and during that patient's infectious period, and 3) the person must not have had known community or household contact with anyone with confirmed COVID-19 in the 2 weeks before receiving a positive test result, including with the index patient or another person with a school-associated case outside of school.

¶ Incidence was calculated as a 7-day moving average per 100,000 persons and included persons with SARS-CoV-2 infection confirmed by reverse transcription–polymerase chain reaction or antigen testing.

** Students and staff members exposed to a COVID-19 patient were advised to quarantine for a minimum of 7 days if a specimen collected ≥5 days after exposure was negative for SARS-CoV-2 and they remained asymptomatic or for 10 days if they were not tested and remained asymptomatic. Persons with positive SARS-CoV-2 test results were advised to self-isolate for a minimum of 10 days after their positive test date or date of first symptom onset. https://dph.georgia.gov/contact; https://dph.georgia.gov/isolation-contact (accessed February 17, 2021)

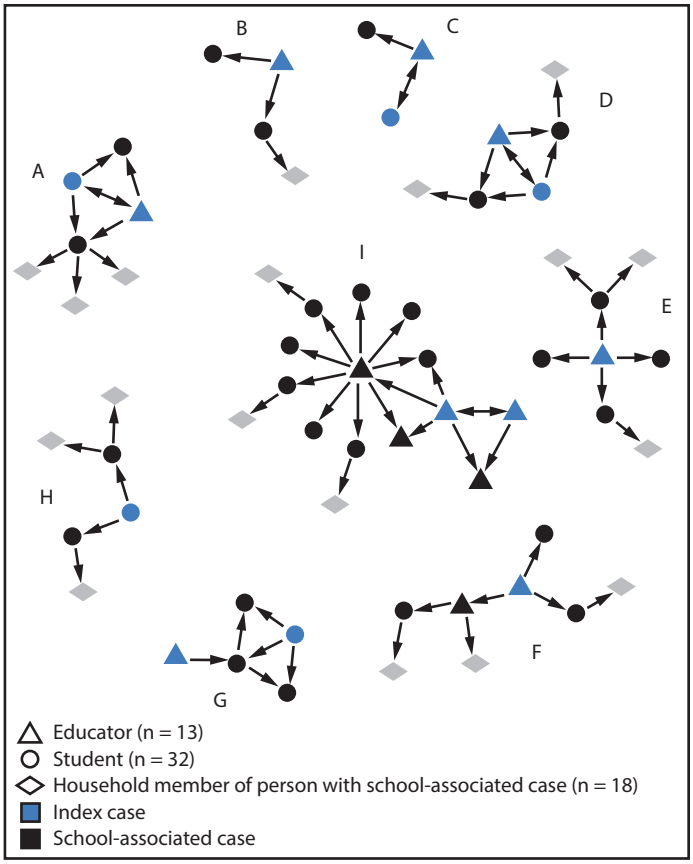
†† Testing was performed at the Georgia Public Health Laboratory using the PerkinElmer COVID assay (Extraction-Chemagic, PCR-7500FastDx).

virtual interviews with parents, educators, and principals were conducted to characterize the settings in which transmission likely occurred. Interviews included a review of symptom onset dates; possible exposures to persons with COVID-19 outside of school; and information on seating charts, classroom layouts, physical distancing, and compliance with recommended mask use during specific classroom interactions. Public health investigators visited four of six schools where SARS-CoV-2 transmission had been identified to observe adherence to recommended mitigation strategies and provide technical assistance. For contacts who received positive test results, epidemiologic links, probable transmission directionality, and the likelihood of in-school transmission were assessed by using interview data, testing dates, and symptom onset dates. Clusters were defined as epidemiologic links between an index patient and two or more persons who likely acquired SARS-CoV-2 infection in school (i.e., school-associated cases). Two contacts with positive test results were excluded because they likely acquired SARS-CoV-2 from household members outside of school. Household members of persons with school-associated cases were offered free RT-PCR testing. This activity was reviewed by CDPH, GDPH, and CDC and was conducted consistent with applicable Georgia law, federal law, and CDC policy.[§§]

During the investigation period, nine clusters of COVID-19 cases were identified, involving 13 educators and 32 students at six of the eight investigated elementary schools (Figure). The median cluster size, including household members, was six persons (range = 3–16). An educator was the index patient in four clusters (B, E, F, and I), a student was the index patient in one cluster (H), and in four clusters (A, C, D, and G), whether the index patient was the student, the educator, or both (i.e., two index cases occurred) could not be determined. Eight clusters (all except H) involved at least one educator and probable educator-to-student transmission. Four clusters (A, D, G, and H) involved probable student-to-student transmission, and three (A, C, and D) involved probable student-to-educator transmission. Two clusters (F and I) involved probable educator-to-educator transmission during in-person meetings or lunches, which was followed by educator-to-student transmission in the classroom and resulted in 15 of 31 (48%) school-associated cases. Sixty-nine household members of persons with school-associated cases were tested, and 18 (26%) received positive results.

Public health investigators identified several COVID-19 mitigation challenges. Although plastic dividers were placed on desks between students, students sat <3 ft apart. Physical distancing of >6 ft was not possible because of the high number

FIGURE. Nine SARS-CoV-2 transmission clusters (A–I)* at six elementary schools in one school district — Georgia, December 2020–January 2021



* The presence of two index cases within a cluster indicates that the index patient could not be determined or that two index patients might have occurred. Arrows indicate epidemiologic links between cases and probable transmission direction, determined by in-depth interviews of persons with cases, exposures outside of school, and symptom onset data.

of in-person students and classroom layouts. In seven clusters (A, B, C, D, E, F, and I), transmission among educators and students might have occurred during small group instruction sessions in which educators worked in close proximity to students. The school district mandated in-classroom mask use except while eating, and both reported and observed compliance during site visits was high. However, information obtained during interviews indicated that specific instances involving lack of or inadequate mask use by students likely contributed to spread in five clusters (A, C, E, G, and I). Students ate lunch in their classrooms, which might have facilitated spread. Opportunities to decrease nonessential in-person interactions among staff members during lesson planning and lunches were noted.

Discussion

These findings suggest that educators can play an important role in in-school transmission and that in-school transmission can occur when physical distancing and mask compliance

[§§] 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.

Summary

What is already known about this topic?

In-person learning provides important benefits to children and communities. Understanding SARS-CoV-2 transmission in schools is critical to improving the safety of in-person learning.

What is added by this report?

An investigation of SARS-CoV-2 transmission in a Georgia school district during December 1, 2020–January 22, 2021, identified nine clusters of COVID-19 cases involving 13 educators and 32 students at six elementary schools. Two clusters involved probable educator-to-educator transmission that was followed by educator-to-student transmission in classrooms and resulted in approximately one half (15 of 31) of school-associated cases.

What are the implications for public health practice?

Educators might play a central role in in-school transmission networks. Preventing SARS-CoV-2 infections through multifaceted school mitigation measures and COVID-19 vaccination of educators is a critical component of preventing in-school transmission.

are not optimal. Previous investigations in other U.S. school districts found that low transmission rates in schools can be maintained in the setting of high community incidence (*2*,*3*). To ensure safer in-person learning during the COVID-19 pandemic, schools should implement multicomponent mitigation strategies, including efforts to prevent infection among educators, and promoting consistent, correct mask use and physical distancing wherever possible, especially during mealtime when masks are not being worn.

The finding that educators play an important role in in-school transmission is consistent with findings from other investigations. A large prospective study of SARS-CoV-2 transmission in schools in the United Kingdom found that the most common type of transmission event was from educator to educator (*4*); in another large prospective study of transmission in German schools, in-school transmission rates were three times higher when the index case occurred in an educator than when the index case occurred in a student.[¶¶] Measures to prevent SARS-CoV-2 infection among educators, including promotion of COVID-19 precautions outside of school, minimizing in-person adult interactions at school, ensuring mask compliance and physical distancing among educators when in-person interaction is unavoidable, and COVID-19 vaccination, when available, will likely reduce in-school transmission, particularly if implemented in a multifaceted approach. Messaging to improve awareness among educators about the risk for acquiring SARS-CoV-2 infections from colleagues in addition to students is needed. The school district has already implemented many of these measures, including administrative changes to prevent nonessential in-person interactions among educators.

The findings in this report are subject to at least three limitations. First, distinguishing in-school transmission from community transmission was challenging, particularly when the 7-day community incidence exceeded 150 cases per 100,000 persons and was increasing. Second, certain clusters and cases within clusters might not have been detected because not all contacts received testing. Finally, because adults with SARS-CoV-2 infection are more likely to have symptoms and be tested (*5*), index cases might have been more frequently identified in educators than in students, possibly resulting in missed instances of student-to-student and student-to-educator transmission.

Consistent with findings from international studies, this report found that initial infections among educators played a substantial role in in-school SARS-CoV-2 transmission and subsequent chains of infection to other educators, students, and households, highlighting the importance of preventing infections among educators in particular. Preventing SARS-CoV-2 infections in educators and students through multifaceted school mitigation measures is a critical component of preventing in-school transmission. Although not a requirement for reopening schools, adding COVID-19 vaccination for educators as an additional mitigation measure, when available, might serve several important functions, including protecting educators at risk for severe COVID-19–associated illness (*6*), potentially reducing in-school SARS-CoV-2 transmission, and minimizing interruptions to in-person learning, all of which have important implications for educational equity and community health. Because most children are not yet eligible for vaccination, continued implementation of multifaceted COVID-19 mitigation strategies in schools, including universal and correct mask use and physical distancing, even after educators are vaccinated, will be critical given the limited available evidence on reduction of transmission postvaccination and vaccine-related long-term protection (*7*).

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[¶¶] https://www.medrxiv.org/content/10.1101/2021.02.04.21250670v1

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Erratum

Vol. 70, No. 6

The report "Decline in COVID-19 Hospitalization Growth Rates Associated with Statewide Mask Mandates — 10 States, March–October 2020" contained several errors.

On page 212, in the first paragraph, the fifth sentence should have read "After mask mandates had been implemented for ≥3 weeks, hospitalization growth rates declined by **5.6** percentage points among persons aged 18–39 years (95% CI = **0.9**–10.4) and those aged 40–64 years (95% CI = **1.0**–10.2)."

On page 213, in the first complete paragraph of the right-hand column, the second sentence should have read "The overall COVID-19–associated hospitalization growth rates among all adults declined 2.4 percentage points (p-value = 0.04) <3 weeks after the implementation week and declined **5.0** percentage points (p-value <0.01) during the period ≥3 weeks after the implementation week (Table 2)."

On pages 213–214, the second complete paragraph of the right-hand column should have read "Among persons aged 18–39 years, the hospitalization growth rates <3 weeks after the implementation week were lower than were those during the <4 weeks before the implementation week and the implementation week (reference period) when no mask mandate existed, but the estimated percentage point difference (**–2.2**) was not statistically significant (p-value = **0.30**) (Figure) (Table 2). However, in this population, mask mandates were associated with a statistically significant **5.6** percentage-point decline in COVID-19 hospitalization growth rates (p-value = **0.02**) ≥3 weeks after the implementation week. Among adults aged 40–64 years, mask mandates were associated with a 2.9 percentage-point reduction in COVID-19 hospitalization growth rates (p-value = 0.03) <3 weeks after the implementation week. Hospitalization growth rates declined by **5.6** percentage points (p-value = 0.02) during ≥3 weeks after the implementation week. Among adults aged ≥65 years, COVID-19 hospitalization growth rates declined <3 weeks after the implementation week (**1.2** percentage points) and ≥3 weeks after the implementation week (**0.7** percentage points); however, the declines were not statistically significant."

On page 214, there were multiple errors in Table 2. The corrected table is as follows:

TABLE 2. Estimated association between mask mandates and COVID-19–associated hospitalization growth rates in sites with statewide mask mandates, by age group — 10 COVID-19–Associated Hospitalization Surveillance Network sites,*,† March–October 2020

	All (≥18 yrs)		18–39 yrs		40–64 yrs		≥65 yrs	
Time relative to week mask mandate was implemented	**Percentage point change* (95% CI)**	**p-value**	**Percentage point change* (95% CI)**	**p-value**	**Percentage point change* (95% CI)**	**p-value**	**Percentage point change* (95% CI)**	**p-value**
≥4 weeks before	−4.3 (**−10.6** to 1.9)	0.17	**−4.8** (**−17.0** to 7.5)	0.43	−4.0 (−13.3 to 5.3)	0.38	−5.3 (**−15.0** to **4.4**)	0.27
<4 weeks before§	Referent	—	Referent	—	Referent	—	Referent	—
<3 weeks after	−2.4 (−4.7 to −0.1)	0.04	**−2.2** (−6.4 to **2.1**)	**0.30**	−2.9 (−5.5 to −0.3)	0.03	**−1.2** (−3.9 to **1.5**)	**0.38**
≥3 weeks after	**−5.0** (**−8.6** to **−1.4**)	<0.01	**−5.6** (−10.4 to **−0.9**)	**0.02**	**−5.6** (−10.2 to **−1.0**)	0.02	**−0.7** (**−5.3** to **3.9**)	**0.76**

Abbreviations: CI = confidence interval; COVID-19 = coronavirus disease 2019.

* Percentage points are coefficients from the regression models. Reported numbers are from regression models, which controlled for state, age group, time (week), and statewide closing and reopening.

† California, Colorado, Connecticut, Maryland, Michigan, Minnesota, New Mexico, New York, Ohio, and Oregon.

§ This period includes the implementation week (i.e., week zero).

On page 215, the second paragraph of the Summary should have read "During March 22–October 17, 2020, 10 sites participating in the COVID-19–Associated Hospitalization Surveillance Network in states with statewide mask mandates reported a decline in weekly COVID-19–associated hospitalization growth rates by up to **5.6** percentage points for adults aged 18–64 years after mandate implementation, compared with growth rates during the 4 weeks preceding implementation of the mandate."

The Supplementary Table (https://stacks.cdc.gov/view/cdc/101127) should have listed the date of statewide reopening for Michigan as **June 1, 2020**.

Erratum

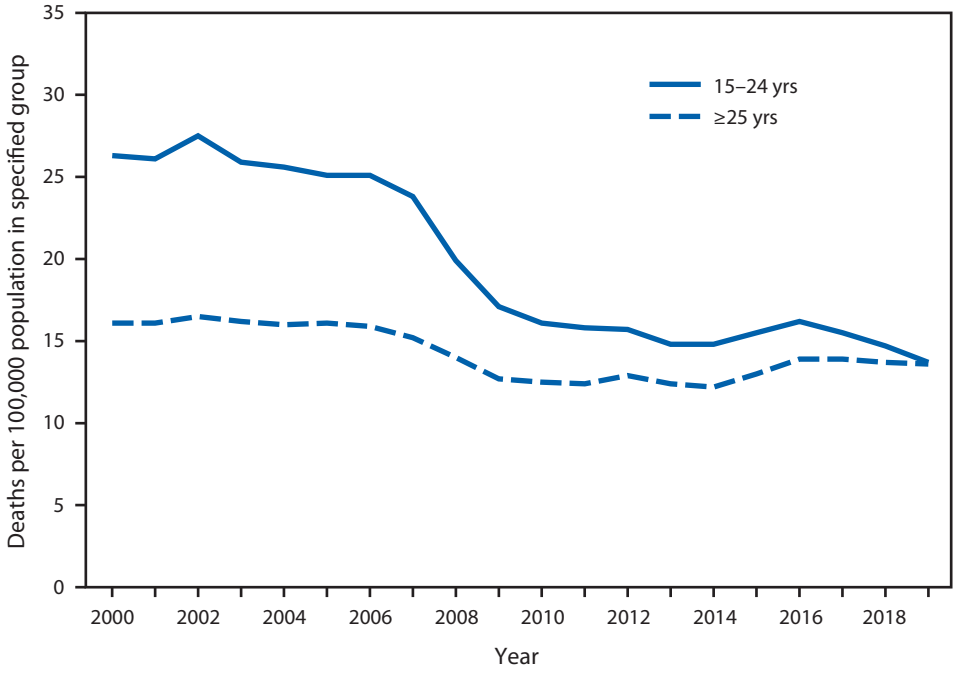
Vol. 69, No. RR-5

In the *MMWR Recommendations and Reports* "Prevention of Hepatitis A Virus Infection in the United States: Recommendations of the Advisory Committee on Immunization Practices, 2020," an error occurred on page 11. In the third sentence of the second paragraph, the vaccines Havrix and Twinrix were incorrectly listed as having preservatives. This sentence should have read "**Havrix, Twinrix, and Vaqta are** formulated without a preservative."

QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Motor-Vehicle–Traffic Death* Rates Among Persons Aged 15–24 Years and ≥25 Years — United States, 2000–2019



* Deaths from motor-vehicle–traffic injuries are identified with *International Classification of Diseases, Tenth Revision* codes V02–V04[.1,.9], V09.2, V12–V14[.3–.9], V19[.4–.6], V20–V28[.3-.9], V29–V79[.4–.9], V80[.3–.5], V81.1, V82.1, V83–V86[.0–.3], V87[.0–.8], and V89.2.

From 2000 to 2006, rates of death caused by motor-vehicle–traffic injuries among persons aged 15–24 years and ≥25 years did not change significantly. From 2006 to 2010, motor-vehicle–traffic death rates per 100,000 population declined among those aged 15–24 years, from 25.1 (2006) to 16.1 (2010), and among those aged ≥25 years, from 15.9 (2006) to 12.5 (2010). Throughout most of the period, motor-vehicle–traffic death rates were higher among persons aged 15–24 years; however, motor-vehicle–traffic death rates began to converge in more recent years, and by 2019, the difference in the rate among those aged 15–24 years (13.7) and those aged ≥25 years (13.6) was not statistically significant.

Source: National Center for Health Statistics, National Vital Statistics System, Mortality Data, 2000–2019. http://www.cdc.gov/nchs/nvss/deaths.htm

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For more information on this topic, CDC recommends the following link: https://www.cdc.gov/transportationsafety

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