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Use of Real-Time PCR for *Chlamydia psittaci* Detection in Human Specimens During an Outbreak of Psittacosis — Georgia and Virginia, 2018

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Psittacosis is typically a mild febrile respiratory illness caused by infection with the bacterium *Chlamydia psittaci* and usually transmitted to humans by infected birds (*1*). On average, 11 psittacosis cases per year were reported in the United States during 2000–2017. During August–October 2018, the largest U.S. psittacosis outbreak in 30 years (82 cases identified*) occurred in two poultry slaughter plants, one each in Virginia and Georgia, that shared source farms (*2*). CDC used *C. psittaci* real-time polymerase chain reaction (PCR) to test 54 human specimens from this outbreak. This was the largest number of human specimens from a single outbreak ever tested for *C. psittaci* using real-time PCR, which is faster and more sensitive than commercially available serologic tests. This represented a rare opportunity to assess the utility of multiple specimen types for real-time PCR detection of *C. psittaci*. *C. psittaci* was detected more frequently in lower respiratory specimens (59% [10 of 17]) and stool (four of five) than in upper respiratory specimens (7% [two of 28]). Among six patients with sputum and nasopharyngeal swabs tested, *C. psittaci* was detected only in sputum in five patients. Cycle threshold (Ct) values suggested bacterial load was higher in lower respiratory specimens than in nasopharyngeal swabs. These findings support prioritizing lower respiratory specimens for real-time PCR detection of *C. psittaci*. Stool specimens might also have utility for diagnosis of psittacosis.

Use of primarily serologic tests for laboratory confirmation of psittacosis might contribute to underdiagnosis. The most commonly available diagnostic tests for psittacosis are commercially available serologic tests. These tests have poor specificity and require testing of paired sera collected weeks apart, delaying or preventing confirmation of clinical diagnoses (*3*). Real-time PCR assays are sensitive, specific, and can be performed in hours. However, in the United States, real-time

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* Although 80 cases had been reported previously, a retrospective review of CDC and medical records and discussion with state partners led to an increase of the case count to 82. During September 19–20, 2018, a health hazard evaluation was conducted at the Virginia plant by the National Institute for Occupational Safety and Health at the request of the U.S. Department of Agriculture Food Safety and Inspection Service. Recommendations to reduce worker risk included repositioning cooling fans, ensuring proper function of evisceration tools, and other changes to workplace practices to reduce bacterial contamination and aerosolization.

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PCR assays for diagnosis of psittacosis using human respiratory specimens are currently available only at CDC (*4*).

During August 31–September 12, 2018, the Virginia Department of Health and Georgia Department of Public Health were each notified of a cluster of patients hospitalized with symptoms consistent with psittacosis; all worked in one of two chicken slaughter plants that shared source farms, one in Virginia and one in Georgia (*2*). In Virginia and Georgia, local and state public health officials conducted active case finding to identify illness consistent with psittacosis in persons who worked at one of the plants during August–September 2018. Workers were classified as having probable or confirmed cases of illness based on case definitions. Probable cases were identified based on symptoms and epidemiologic exposures, and confirmed cases were identified based on detection of *C. psittaci* by real-time PCR in at least one clinical specimen.[†] Clinical specimens for *C. psittaci* testing were collected from workers seeking medical care, at the discretion of local clinicians, and sent to CDC for real-time PCR testing; no diagnostic testing for psittacosis was performed elsewhere. CDC recommended collection of lower respiratory specimens whenever possible, but all available specimens were accepted and tested.[§] Testing was performed in triplicate using extracted total nucleic acid[¶] and oligonucleotides targeting the *C. psittaci* locus tag CPSIT_RS01985 on an ABI 7500 real-time PCR system (*4*,*5*). A specimen was considered positive for *C. psittaci* if amplification of the CPSIT_RS01985 locus tag was detected. Patient demographic, clinical, and specimen characteristics among the subset of workers who submitted specimens to CDC were determined by patient interview, medical chart abstraction, and laboratory record review.

[†] Among those who worked at the Virginia plant during August 1–September 7, 2018, or at the Georgia plant during August 13–September 28, 2018, persons with probable cases had physician-diagnosed pneumonia, fever, or chills with two or more of the following: headache, cough, or muscle aches. Patients with confirmed cases had real-time PCR detection of *C. psittaci* in at least one clinical specimen with or without meeting the probable case definition.

[§] A total of seven specimen types were tested, including upper respiratory specimens (nasopharyngeal swab or oropharyngeal swab), lower respiratory specimens (sputum or bronchoalveolar lavage), and nonrespiratory specimens (stool, blood, and cerebrospinal fluid).

[¶] Total nucleic acid was extracted from all specimens using a MagNA Pure Compact instrument (Roche Diagnostics) with the Roche Total Nucleic Acid Isolation Kit I according to manufacturer instructions; elution volume was 100 μL. Stool, whole blood, and sputum specimens were preprocessed before nucleic acid extraction. For stool specimens, 200 mg of stool were first resuspended in 2 mL of phosphate buffered saline (PBS). Then, 400 μL of the resuspended stool specimen was inactivated by combining with 400 μL MagNA Pure Bacteria Lysis Buffer and 40 μL Proteinase K (25 mg/mL; Thermo Fisher Scientific). Inactivated specimens were subject to mechanical lysis by bead-beat with 0.5 mm glass beads using a Precellys 24 Homogenizer (Bertin Corp.) at 5,000 rpm for 60 seconds twice with a 5-second hold in between. The specimen was then centrifuged at 10,000×g for 1 minute, and 700 μL of supernatant was used for total nucleic acid extraction. Whole blood was not resuspended with PBS, but otherwise underwent the same preprocessing as stool. For sputum specimens, 300 μL of the specimen was combined with 300 μL of 1,4-Dithiothreitol (12.5mM; Fisher Scientific) and incubated at room temperature for 1 hour.

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Frequency of *C. psittaci* detection among all specimens and mean Ct value among *C. psittaci*–positive specimens were evaluated for each specimen type. Frequency of demographic and clinical characteristics were determined for probable and confirmed cases. All analyses were performed using SAS (version 9.4; SAS Institute). This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.**

Among 82 ill workers identified by Virginia and Georgia departments of health, 33 (40%) submitted a total of 54 specimens for real-time PCR testing. Thirteen of the 33 (39%) workers tested had confirmed cases of psittacosis, and 20 (61%) had probable cases of psittacosis (Table 1). Compared with probable cases, confirmed cases tended to be identified among older patients. A higher proportion of persons with confirmed cases were male, had a diagnosis of pneumonia, were hospitalized, or required intensive care unit admission. The most commonly submitted specimen type was nasopharyngeal swab (18 of 20 [90%] of probable and eight of 13 confirmed cases). Nasopharyngeal swab specimens only were submitted by 13 (65%) of 20 persons with probable cases and one of 13 persons with confirmed cases. Lower respiratory specimens were submitted by six (30%) of 20 persons with probable cases and most (10 of 13) persons with confirmed cases. Timing of specimen collection relative to illness onset was similar for persons with probable (mean = 7 days; range = 2–13 days) and confirmed (mean = 6 days; range = 1–14 days) cases. Most patients received antibiotic treatment before or on the same day as specimen collection for *C. psittaci* testing (Table 1).

C. psittaci was most commonly detected in stool (four of five specimens) and lower respiratory specimens of bronchoalveolar lavage (two of two) and sputum (eight of 15), and less frequently in upper respiratory specimens of nasopharyngeal swabs (two [7%] of 27) and oropharyngeal swabs (zero of one) (Table 2). Among *C. psittaci*–positive specimens, lower respiratory specimens had lower Ct values (mean = 29; range = 26–31), indicating higher bacterial load, than did nasopharyngeal swabs (Ct values 31 and 33) and stool specimens (mean = 34; range = 32–37).

Among 13 patients with confirmed psittacosis, nine submitted multiple specimen types, allowing comparison of *C. psittaci* detection by specimen type (Table 3). Six patients had nasopharyngeal swab and sputum specimens tested; all sputa tested positive for *C. psittaci*, but only one nasopharyngeal swab tested positive. Three patients submitted stool and sputum specimens; all three sputum specimens tested positive for *C. psittaci,* and two stool specimens tested positive. *C. psittaci* was also detected in stool specimens of two patients with *C. psittaci*–negative nasopharyngeal swabs, including patient A, who had positive sputum and stool specimens but a negative nasopharyngeal swab. Ct values were lower in sputum than in stool specimens or nasopharyngeal swabs from the same patient (patients A, F, and G).

TABLE 1. Characteristics of persons with probable and confirmed cases associated with a psittacosis outbreak — Georgia and Virginia, 2018

Characteristic	Cases, no. (%) Probable* (n = 20)	Cases, no. (%) Confirmed† (n = 13)
Age, yrs, mean (range)	36 (22–55)	48 (29–57)
Male	11 (55)	10 (77)
Clinical characteristic		
Physician-diagnosed pneumonia	15 (75)	12 (92)
Hospitalized	12 (60)	11 (85)
Admitted to intensive care unit	0 (—)	2 (15)
Specimen type submitted§		
Upper respiratory		
Nasopharyngeal swab	18 (90)	8 (62)
Oropharyngeal swab	1 (5)	0 (—)
Lower respiratory		
Sputum	6 (30)	8 (62)
Bronchoalveolar lavage	0 (—)	2 (15)
Nonrespiratory		
Stool	0 (—)	5 (38)
Blood	2 (10)	0 (—)
Cerebrospinal fluid	1 (5)	0 (—)
Only nasopharyngeal specimens submitted	12 (60)	1 (8)
Days from illness onset to specimen collection, mean (range)	7 (2–13)	6 (1–14)
Antibiotic treatment relative to specimen collection¶		
Before	9 (45)	10 (77)
Same day	8 (40)	3 (23)
After	3 (15)	0 (—)

Abbreviation: PCR = polymerase chain reaction.

* Cases of illness in persons who worked at the Virginia plant during August 1–September 7, 2018, or at the Georgia plant during August 13–September 28, 2018, and had physician-diagnosed pneumonia, fever, or chills with two or more of the following: headache, cough, or muscle aches. All probable cases in this analysis were real-time PCR–negative for *Chlamydia psittaci*.

† Cases of illness in persons who had real-time PCR detection of *C. psittaci* in at least one clinical specimen with or without meeting the probable case definition.

§ A total of 18 patients submitted multiple specimens; therefore, the sum of patients submitting each specimen type exceeds 33.

¶ The percentage of patients with doxycycline or a macrolide antibiotic treatment, first- and second-line antibiotics against psittacosis, initiated before, on the same day as, or after specimens for *C. psittaci* testing were collected. It could not be distinguished whether antibiotic treatment occurred before or after specimen collection for patients with antibiotic treatment initiation and specimen collection occurring on the same day.

Discussion

This was the largest U.S. psittacosis outbreak in 30 years, the first U.S. outbreak in which human specimens were tested exclusively by real-time PCR, and the first that included testing of stool specimens. In this outbreak investigation, as in other

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** 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 2. Real-time PCR test results, by specimen type, for all specimens tested in association with a psittacosis outbreak — Georgia and Virginia, 2018

Specimen type	No. of specimens tested	*C. psittaci*–positive specimens, no. (%)	Ct value among *C. psittaci*–positive specimens, mean (range)
Upper respiratory			32 (31–33)[*]
Nasopharyngeal swab	27	2 (7)	
Oropharyngeal swab	1	0 (—)	
Lower respiratory			29 (26–31)
Sputum	15	8 (53)	
Bronchoalveolar lavage	2	2 (100)	
Nonrespiratory			34 (32–37)[†]
Stool	5	4 (80)	
Blood	3	0 (—)	
Cerebrospinal fluid	1	0 (—)	

Abbreviations: *C. psittaci* = *Chlamydia psittaci*; Ct = cycle threshold; PCR = polymerase chain reaction.

[*] Data are from two nasopharyngeal swabs with Ct values 31 and 33.

[†] Data are only from stool specimens because there were no *C. psittaci*–positive blood or cerebrospinal fluid specimens.

published studies with real-time PCR–based detection of *C. psittaci* (*3*), *C. psittaci* was more frequently detected in lower respiratory specimens than in upper respiratory specimens, as reflected by detection in sputum but not nasopharyngeal swabs in five confirmed cases. Ct values in *C. psittaci*–positive specimens also suggest that bacterial load is higher in lower respiratory specimens than in nasopharyngeal swab specimens. This analysis suggests that lower respiratory specimens are more useful than upper respiratory specimens for *C. psittaci* detection by real-time PCR. Although submission of lower respiratory specimens is encouraged, upper respiratory specimens are easier to collect, which could explain why nasopharyngeal swab was the most frequently submitted specimen type. Given that 60% of patients with probable cases submitted only nasopharyngeal swab specimens, *C. psittaci* might have been underdetected in this outbreak; it is possible that more confirmed cases would have been detected if lower respiratory specimens were collected for testing in these patients.

Although only five stool specimens were tested in this outbreak, the frequency of *C. psittaci* detection in stool specimens was high, and in two patients *C. psittaci* was detected in stool and sputum specimens. Gastrointestinal symptoms have been reported among psittacosis patients (*6*–*8*), and three of four patients with *C. psittaci* detection in stool specimens in this investigation also had gastrointestinal symptoms. However, whether these symptoms correspond with detection of *C. psittaci* in stool specimens has not been documented. Additional studies are needed to validate whether detection of *C. psittaci* DNA in stool specimens alone indicates presence of infectious bacteria in humans. Nonetheless, this investigation provides promising evidence that stool specimens might have utility for diagnosis of psittacosis using real-time PCR.

The findings in this report are subject to at least two limitations. First, specimens were not systematically collected and

TABLE 3. Clinical findings, hospitalization status, and real-time PCR test results in patients[*] with confirmed psittacosis cases (n = 13) associated with a psittacosis outbreak — Georgia and Virginia, 2018

	Clinical findings and hospitalization status			Real-time PCR result by specimen type (Ct value)[†]			
Patient	**Pneumonia[§]**	**Hospitalized**	**Admitted to ICU**	**Sputum**	**BAL**	**NP swab**	**Stool**
A	Yes	Yes	No	Pos (30)	—[¶]	Neg	Pos (37)
B	Yes	Yes	No	Pos (30)	—	Neg	—
C	Yes	No	No	Pos (28)	—	Neg	—
D[**]	Yes	Yes	No	Pos (26)	—	Neg	—
E	Yes	Yes	No	Pos (26)	—	Neg	—
F[††]	Yes	Yes	Yes	Pos (27)	—	Pos (33)	—
G	Yes	Yes	No	Pos (28)	—	—	Pos (32)
H	Yes	Yes	No	Pos (30)	—	—	Neg
I	Yes	Yes	No	—	Pos (31)	—	—
J	Yes	Yes	Yes	—	Pos (30)	—	—
K[§§]	No	Yes	No	—	—	Pos/Neg (31)	—
L	Yes	Yes	No	—	—	Neg	Pos (38)
M	Yes	No	No	—	—	—	Pos (32)

Abbreviations: BAL = bronchoalveolar lavage; Ct = cycle threshold; ICU = intensive care unit; Neg = negative; NP = nasopharyngeal; PCR = polymerase chain reaction; Pos = positive.

[*] All specimens associated with an individual patient were collected on the same day unless otherwise noted. For example, sputum, NP swab, and stool specimens for patient A were all collected on the same day, but specimens from patient A were not necessarily collected on the same day as were those from patient B.

[†] "Pos" indicates *Chlamydia psittaci* was detected. "Neg" indicates *C. psittaci* was not detected. Ct values represent the real-time PCR amplification cycle at which CPSIT_RS01985 amplification was first detected. Ct values are displayed only for *C. psittaci*–positive specimens, because CPSIT_RS01985 was not detected in *C. psittaci*–negative specimens.

[§] Radiograph confirmed pneumonia.

[¶] Dashes indicate specimen type was not submitted to CDC.

[**] Sputum was collected 3 days after the NP swab.

[††] Sputum was collected 1 day after the NP swab.

[§§] Two NP swabs were tested; one tested positive and one tested negative. The negative NP swab was collected 2 days after the positive NP swab.

Summary

What is already known about this topic?

Real-time polymerase chain reaction (PCR) testing for *Chlamydia psittaci*, the bacterium that causes psittacosis, is faster and more specific than widely available serologic tests. However, the utility of diverse specimen types for *C. psittaci* detection by real-time PCR is unknown.

What is added by this report?

During a large psittacosis outbreak in 2018, *C. psittaci* was most frequently detected in lower respiratory and stool specimens using real-time PCR.

What are the implications for public health practice?

It is important for clinicians and public health professionals to prioritize collection of lower respiratory specimens for *C. psittaci* real-time PCR testing. Findings of this outbreak investigation provide preliminary evidence that stool specimens might have utility for diagnosis of psittacosis.

were available from only a subset of patients. Because of this, the sample size overall and per specimen type was small. The small sample size limited ability to assess how severity of illness and antibiotic treatment affect *C. psittaci* detection for each specimen type. Second, although lower respiratory specimen collection was encouraged, psittacosis is characterized by dry cough, and lower respiratory specimens are difficult to obtain from mildly ill patients unless sputum collection is induced. Patients with severe illness, who likely also have higher bacterial load, might have been more likely to submit lower respiratory specimens.

Many factors influence *C. psittaci* detection in human clinical specimens; these include specimen type, timing of collection relative to illness onset and treatment with tetracycline or macrolide antibiotics, and severity of illness. Collecting information about these factors and systematic, serial testing of multiple specimen types from suspected cases might help inform optimal conditions for *C. psittaci* detection using real-time PCR. Public health professionals and health care providers should be aware that *C. psittaci* might not be detected if nasopharyngeal swab specimens alone are tested and that collection of respiratory specimens from multiple sites can improve detection by real-time PCR. Although lower respiratory specimens collected shortly after symptom onset might have the highest yield to diagnose psittacosis using real-time PCR, stool specimens might also have utility for diagnosis of psittacosis.

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COVID-19 Incidence and Mortality Among American Indian/Alaska Native and White Persons — Montana, March 13–November 30, 2020

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Geographic differences in infectious disease mortality rates have been observed among American Indian or Alaska Native (AI/AN) persons in the United States (*1*), and aggregate analyses of data from selected U.S. states indicate that COVID-19 incidence and mortality are higher among AI/AN persons than they are among White persons (*2*,*3*). State-level data could be used to identify disparities and guide local efforts to reduce COVID-19–associated incidence and mortality; however, such data are limited. Reports of laboratory-confirmed COVID-19 cases and COVID-19–associated deaths reported to the Montana Department of Public Health and Human Services (MDPHHS) were analyzed to describe COVID-19 incidence, mortality, and case-fatality rates among AI/AN persons compared with those among White persons. During March–November 2020 in Montana, the estimated cumulative COVID-19 incidence among AI/AN persons (9,064 cases per 100,000) was 2.2 times that among White persons (4,033 cases per 100,000).* During the same period, the cumulative COVID-19 mortality rate among AI/AN persons (267 deaths per 100,000) was 3.8 times that among White persons (71 deaths per 100,000). The AI/AN COVID-19 case-fatality rate (29.4 deaths per 1,000 COVID-19 cases) was 1.7 times the rate in White persons (17.0 deaths per 1,000). State-level surveillance findings can help in developing state and tribal COVID-19 vaccine allocation strategies and assist in local implementation of culturally appropriate public health measures that might help reduce COVID-19 incidence and mortality in AI/AN communities.

Reports of COVID-19 cases and COVID-19–associated deaths were analyzed to assess the number, percentage, and crude rates of COVID-19 cases and deaths occurring among AI/AN persons and White persons in Montana during March 13–November 30, 2020. Case data were derived from the Montana Infectious Disease Information System. Montana residents who met the definition of a confirmed case (i.e., having received a positive test result for SARS-CoV-2, the virus that causes COVID-19, from a respiratory specimen, using a molecular amplification test and reported to MDPHHS) were included in the analysis. COVID-19–associated deaths were identified from death certificates reported to the MDPHHS Office of Vital Records; COVID-19 deaths were identified by using *International Classification of Diseases, Tenth Revision* code U07.1, listed as either the underlying or a contributing cause of death. This activity was reviewed by MDPHHS and was conducted for public health surveillance purposes and consistent with applicable state and federal law.†

Information on race was available for 49,426 (78%) of 63,339 persons who had received a diagnosis of COVID-19 and for 903 (100%) COVID-19–associated deaths reported to MDPHHS. Persons of AI/AN race were defined as those whose race was reported as AI/AN alone or in combination with other races. Persons of White race were defined as those whose race was reported as White with no other race selected. Ethnicity was not included in this analysis because data on ethnicity was missing for 37% of reported cases. The 2019 National Center for Health Statistics bridged-race population estimates for AI/AN and White persons in Montana were used as denominators to calculate crude cumulative incidence (cumulative cases per 100,000 population) and cumulative mortality rates (cumulative deaths per 100,000 population).§,¶ These population estimates were used to determine that 90.6% of Montana residents were White and that 7.3% were AI/AN. All rates were calculated separately for AI/AN and White persons, overall and by sex and age group. Age group was assessed both categorically (<65 and ≥65 years) and by using medians with interquartile ranges (IQRs). Rate ratios (COVID-19 cumulative incidence and mortality rates among AI/AN persons divided by corresponding rates among White persons) and case-fatality rates (the number of COVID-19–associated deaths per 1,000 reported COVID-19 cases) were also calculated. Corresponding 95% confidence intervals (CIs) were calculated using the Poisson Exact method (*4*). Analyses were conducted using SPSS (version 23; IBM) for incidence estimates and SAS (version 9.4; SAS Institute) for mortality estimates.

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* Race data were missing for 13,913 of 63,339 (22%) patients, and ethnicity data were missing for 23,435 of 63,339 (37%) patients. Race and ethnicity data were complete for all deaths. Cumulative incidences by race were considered estimates because of the large proportion of missing race/ethnicity data.

† Mont. Code Ann. Sect. 50–15–122 and 50–16–103; 45 C.F.R. part 46.102(l)(2).

§ https://www.cdc.gov/nchs/nvss/bridged_race/data_documentation.htm

¶ The number of COVID-19 cases or deaths by race and by race and sex/age group per 100,000 in the same race or race and sex/age group.

During March 13–November 30, 2020, among 49,426 persons in Montana who had received a diagnosis of COVID-19 and for whom information on race was available, 7,069 (14.3%) were AI/AN, and 39,040 (79.0%) were White. The estimated cumulative incidence among AI/AN persons (9,064 cases per 100,000) was 2.2 times the rate among White persons (4,033) (Table). The estimated cumulative incidence was also higher among AI/AN persons than that among White persons by sex and age group. Among AI/AN persons, the estimated cumulative incidence was higher among persons aged ≥65 years (10,321 per 100,000) compared with that among persons aged <65 years (8,947).[**] Among White persons, incidence was higher among persons aged <65 years (4,137) than among those aged ≥65 years (3,632). The median age of AI/AN persons with COVID-19 was 34 years (IQR = 20–51 years) compared with 42 years (IQR = 26–60 years) among White persons. Among both AI/AN and White persons, estimated cumulative incidence by race was higher among women (9,517 and 4,272 per 100,000, respectively) than among men (8,405 and 3,687, respectively).

During March 13–November 30, 2020, among 903 COVID-19–associated deaths in Montana, 208 (23.0%) occurred among AI/AN persons compared with 664 (73.5%) among White persons. The cumulative COVID-19 mortality rate among AI/AN persons (267 deaths per 100,000) was 3.8 times the rate among White persons (71 deaths per 100,000). Cumulative mortality was also higher among AI/AN persons than among White persons by sex and age group. The median age of death among AI/AN persons who died from COVID-19 was 68 years (IQR = 58–75) compared with 82 years (IQR = 73–89) among White persons. The case-fatality rate among AI/AN persons (29.4 deaths per 1,000 COVID-19 cases) was 1.7 times (95% CI = 1.7–1.8) the rate among White persons (17.0 deaths per 1,000 COVID-19 cases).

Discussion

During March 13–November 30, 2020, COVID-19 incidence and mortality among AI/AN persons in Montana were approximately twice and nearly four times those among White persons, respectively. In addition, the case-fatality rate among AI/AN persons was close to twice that among White persons. Several factors might have contributed to the higher COVID-19 incidence and mortality among AI/AN persons. AI/AN communities in Montana have higher levels of social vulnerability, including living in shared housing, challenges accessing health care and transportation, and lower household incomes.[††] As well, AI/AN persons might be more likely than

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[**] A total of 681 cases of COVID-19 were reported among 6,598 AI/AN persons aged ≥65 years, and 6,388 cases were reported among 71,395 AI/AN persons aged <65 years.

[††] https://svi.cdc.gov/map.html

TABLE. COVID-19 incidence and mortality rates[*] among American Indian or Alaska Native (AI/AN) and White persons,[†,§] by age group and sex[¶] — Montana, March 13–November 30, 2020

	AI/AN		White		
Characteristic	No. (%)	Rate (95% CI)	No. (%)	Rate (95% CI)	AI/AN to White rate ratio (95% CI)
Cumulative incidence					
Total	**7,069 (100)**	**9,064 (8,852–9,275)**	**39,040 (100)**	**4,033 (3,993–4,073)**	**2.2 (2.1–2.5)**
Sex					
Female	3,752 (53)	9,517 (9,212–9,821)	20,498 (52)	4,272 (4,213–4,330)	2.2 (2.1–2.4)
Male	3,242 (46)	8,405 (8,116–8,695)	17,995 (46)	3,687 (2,633–3,741)	2.3 (2.1–2.5)
Age group, yrs					
<65	6,388 (90)	8,947 (8,728–9,167)	31,842 (82)	4,137 (4,091–4,182)	2.2 (2.0–2.4)
≥65	681 (10)	10,321 (9,546–1,097)	7,198 (18)	3,632 (3,549–3,716)	2.8 (2.6–3.1)
Cumulative mortality					
Total	**208 (100)**	**267 (232–306)**	**664 (100)**	**71 (66–77)**	**3.8 (3.2–4.4)**
Sex					
Female	88 (42)	223 (179–275)	306 (46)	66 (59–74)	3.4 (2.7–4.3)
Male	120 (58)	311 (258–372)	358 (54)	76 (68–84)	4.1 (3.3–5.0)
Age group, yrs					
<65	87 (42)	122 (98–150)	72 (11)	10 (8–12)	12.5 (9.1–17.1)
≥65	121 (58)	1,834 (1,522–2,191)	592 (89)	302 (278–328)	6.1 (5.0–7.4)

Abbreviation: CI = confidence interval.

[*] The number of COVID-19 cases or deaths by race and by race and sex/age group per 100,000 in the same race or race and sex/age group.

[†] Includes Hispanic and non-Hispanic persons.

[§] Race data were missing for 13,913 of 63,339 (22%) patients, and ethnicity data were missing for 23,435 of 63,339 (37%) patients; race and ethnicity data were complete for all deaths.

[¶] Sex data were missing for 75 (1%) AI/AN patients and for 547 (1%) White patients.

White persons to live in multigenerational households or be unable to work from home because of the nature of their work (e.g., being frontline workers) or because they are not able to telework due to the lack of Internet access, which might increase the risk for SARS-CoV-2 infection (*5*). AI/AN persons in Montana also have a high prevalence of chronic health conditions and risk factors for severe illness from COVID-19, including heart disease, type 2 diabetes mellitus, and cigarette smoking.[§§]

An assessment of the impact of COVID-19 among AI/AN persons from 23 states made early during the pandemic (January–July 2020) found that the cumulative incidence rate ratio between AI/AN and White persons was 3.5 (*2*), similar to the current study's finding. In addition, a study comparing age-adjusted COVID-19 mortality rates among AI/AN and White persons in 14 states during January–June 2020 reported a mortality rate ratio of 1.8 for AI/AN persons compared with that for White persons (*3*), which was lower than that identified in a supplementary analysis conducted by MDPHHS.[¶¶]

The findings in this report are subject to at least three limitations. First, the case-level surveillance and death certificate data might not have been complete at the time of the analysis and are subject to change. Therefore, this analysis likely underestimated the number of persons who had received a diagnosis of COVID-19 and the number of deaths that occurred, particularly more recently. Second, information on race and ethnicity was missing for 22% and 37% of cases, respectively. Because of the large proportion of COVID-19 cases with missing ethnicity information, ethnicity was not included in the analyses. Therefore, COVID-19 patients and decedents whose race was listed as White include some persons whose ethnicity is Hispanic or non-Hispanic. Previous reports have documented that Hispanic populations have disproportionality higher COVID-19 mortality compared with White populations (*6*). However, the extent of bias introduced as a result of this limitation is expected to be minimal because Hispanic persons represent a small proportion of Montana's population (4.1%). Finally, previous studies suggest that AI/AN persons might be misclassified as non–AI/AN races and ethnicities. However, studies conducted in Montana and northern plains states indicate that race misclassification is relatively less common in these states than it is in other areas of the United States (*7*,*8*).

Understanding the higher COVID-19 incidence, mortality, and case-fatality rates among AI/AN persons can help develop state and tribal COVID-19 vaccine allocation strategies, including adapting the current interim CDC Advisory Committee on Immunization Practices' COVID-19 vaccine allocation recommendations to prioritize persons at increased risk for poor outcomes or at high risk for exposure to SARS-CoV-2 in AI/AN communities, such as tribal elders, persons living in multigenerational or congregate households, and persons with high-risk medical conditions (*9*). These findings also reinforce the importance of using state-level surveillance to identify disparities among AI/AN or other minority communities to help develop local implementation of culturally informed public health measures and enhanced community education to prevent or limit community transmission of SARS-CoV-2 (*10*).

Summary

What is already known about this topic?

Aggregate analyses of data from selected U.S. states indicate that COVID-19 incidence and mortality are higher among American Indian or Alaska Native (AI/AN) persons than they are among White persons.

What is added by this report?

COVID-19 incidence and mortality rates among AI/AN persons in Montana were 2.2 and 3.8 times, respectively, those among White persons. The case-fatality rate among AI/AN persons was 1.7 times that among White persons.

What are the implications for public health practice?

These findings reinforce importance of using state-level surveillance to develop state and tribal COVID-19 vaccine allocation strategies and to inform local implementation of culturally appropriate public health measures that might help reduce COVID-19 incidence and mortality in AI/AN communities.

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[§§] https://dphhs.mt.gov/Portals/85/ahealthiermontana/2017SHAFinal.pdf

[¶¶] The MDPHHS calculated age-adjusted COVID-19 mortality rate for AI/AN persons (374 deaths per 100,000; 95% CI = 322–433) was 7.8 times (95% CI = 6.7–9.1) that among White persons (48 deaths per 100,000; 95% CI = 44–52). Rates were age-adjusted to the 2000 U.S. standard population.

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Use of Stay-at-Home Orders and Mask Mandates to Control COVID-19 Transmission — Blackfeet Tribal Reservation, Montana, June–December 2020

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COVID-19 has disproportionately affected persons who identify as non-Hispanic American Indian or Alaska Native (AI/AN) (*1*). The Blackfeet Tribal Reservation, the northern Montana home of the sovereign Blackfeet Nation, with an estimated population of 10,629 (*2*), detected the first COVID-19 case in the community on June 16, 2020. Following CDC guidance,[*] and with free testing widely available, the Indian Health Service and Blackfeet Tribal Health Department began investigating all confirmed cases and their contacts on June 25. The relationship between three community mitigation resolutions passed and enforced by the Blackfeet Tribal Business Council and changes in the daily COVID-19 incidence and in the distributions of new cases was assessed. After the September 28 issuance of a strictly enforced stay-at-home order and adoption of a mask use resolution, COVID-19 incidence in the Blackfeet Tribal Reservation decreased by a factor of 33 from its peak of 6.40 cases per 1,000 residents per day on October 5 to 0.19 on November 7. Other mitigation measures the Blackfeet Tribal Reservation used included closing the east gate of Glacier National Park for the summer tourism season, instituting remote learning for public school students throughout the fall semester, and providing a Thanksgiving meal to every household to reduce trips to grocery stores. CDC has recommended use of routine public health interventions for infectious diseases, including case investigation with prompt isolation, contact tracing, and immediate quarantine after exposure to prevent and control transmission of SARS-CoV-2, the virus that causes COVID-19 (*3*). Stay-at-home orders, physical distancing, and mask wearing indoors, outdoors when physical distancing is not possible, or when in close contact with infected or exposed persons are also recommended as nonpharmaceutical community mitigation measures (*3,4*). Implementation and strict enforcement of stay-at-home orders and a mask use mandate likely helped reduce the spread of COVID-19 in the Blackfeet Tribal Reservation.

The potential effects of community mitigation measures on changes in the number and incidence of new COVID-19 cases in the Blackfeet Tribal Reservation during June 16–December 10, 2020, were assessed using deidentified laboratory and case investigation data. The tribal health clinic, the Indian Health Service, a dialysis clinic, and a long-term care facility performed testing for SARS-CoV-2 and used various data collection tools. Local public health nurses abstracted case investigation data, including patient age, sex, race, ethnicity, test date, and exposure information. A case was defined as receipt of a positive SARS-CoV-2 result from either a nucleic acid amplification test, such as a polymerase chain reaction test, or a rapid antigen detection test by a resident of the Blackfeet Tribal Reservation. Incidence was calculated as the daily number of new COVID-19 cases per 1,000 residents. Analyses were conducted using SAS (version 9.4; SAS Institute). Population estimates for the Blackfeet Tribal Reservation and for Montana were obtained from the U.S. Census Bureau (*2,5*). This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.[†]

During 2020, the Blackfeet Nation implemented three stay-at-home orders; mask use in public was required by all three orders. The first was a mandatory stay-at-home order,[§] which was in place during June 29–July 31; violations of isolation or quarantine orders could result in a fine up to $500.[¶,**] The second was a recommended stay-at-home order,[††] which began August 19. The third was an enforced stay-at-home order,[§§] which began September 28. Under this third order, breaking quarantine or isolation orders could result in up to 3 years in jail and a fine up to $5,000.[¶¶] Patients unable to isolate at home were provided temporary housing in two local hotels. A COVID-19 dispatch team delivered medications and food to community members, as needed.

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[*] https://www.cdc.gov/coronavirus/2019-ncov/php/contact-tracing/contact-tracing-plan/overview.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.

[§] http://www.blackfeetnation.com/wp-content/uploads/2020/07/22.-Blackfeet-Tribe_Resolution_Re-affirming-Closure-of-Blackfeet-Tribe-in-Response-to-COVID-19-Outreach_June-29_2020.pdf

[¶] http://www.blackfeetnation.com/wp-content/uploads/2020/07/24.-Blackfeet_Resolution-282-200_Approving-Amende-Quarantine-Order.pdf

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[††] http://www.blackfeetnation.com/wp-content/uploads/2020/08/20.-Blackfeet-Resolution_Extending-closure-until-further-notice.pdf#:~:text

[§§] http://blackfeetnation.com/covid19/

[¶¶] http://www.blackfeetnation.com/wp-content/uploads/2020/10/Blackfeet-Tribe-Resolution_Continuing-Current-Fines-and-Offenses-beginning-on-October-26-2020-until-Further-Notice-Under-Current-Phase-Restrictions.pdf

During June 16–December 10, 2020, a total of 1,180 COVID-19 cases were reported in the Blackfeet Tribal Reservation (Table). The median age of patients was 36 years (range = 0–96 years); 50.5% of cases occurred in females, and 91.9% of patients self-identified as AI/AN. After the first COVID-19 case was reported in the community on June 16, the Blackfeet Tribal Business Council voted not to open the east gate of Glacier National Park, which borders the reservation, through the end of the 2020 tourist season (*6*). The Blackfeet Tribal Reservation recorded few cases during July, when mandatory stay-at-home orders and ongoing case investigation and contact tracing were in effect, with an average daily incidence of 0.10 cases per 1,000 residents (Figure 1). On July 31, the Blackfeet Tribal Reservation opened its campgrounds to residents when the mandatory stay-at-home orders expired. In August, a slight increase in incidence was observed, to 0.19 cases per 1,000.

The second, or recommended, stay-at-home order commenced on August 19. However, the number of cases increased after gatherings at the Northwest Montana Fair and Rodeo (August 19–23) in Kalispell, outside of the reservation, and during Labor Day weekend (September 5–7). Daily incidence peaked at 6.40 cases per 1,000 residents on October 5, which was 63 times the incidence in July.

On September 28, a third stay-at-home order was issued, with strict enforcement and substantial fines for violation. Afterward, incidence decreased to 0.19 cases per 1,000 by November 7. A gradual increase in newly identified cases among persons aged 5–17 years and 30–39 years began the week of August 9, after the campgrounds opened on July 31, and peaked the week of August 16 (Figure 2). During August, the numbers of cases in these age groups were higher than those in other age groups. Incident cases among persons aged 18–39 years and 50–64 years increased after the Northwest Montana Fair and Rodeo (week of August 16) and Labor Day weekend (week of September 6), and peaked during the week of September 27, before the enforced stay-at-home order was issued.

Among 142 (12.0%) of 1,180 patients with available household exposure data, 121 (85.2%) reported at least one household contact with COVID-19. Workplace exposure data were available for 198 (16.8%) patients, 12 (6.1%) of whom reported a workplace exposure. Community exposure data were available for 133 (11.3%) patients; among these, 53 (39.8%) reported known community exposure. Twelve patients (1.0%) reported exposure in an adult congregate living facility.

TABLE. Characteristics of Blackfeet Tribal Reservation residents and COVID-19 cases — Blackfeet Tribal Reservation, Montana, June–December 2020

Characteristics	No. (%)	
	All residents* (N = 10,629)	COVID-19 patients† (N = 1,180)
Age, yrs		
Mean (SD)	N/A	37.8 (20.7)
Range	N/A	0–96
Median (IQR)	30.4	36 (21–54)
Sex		
Female	5,257 (49.5)	596 (50.5)
Male	5,372 (50.5)	564 (47.8)
Unknown	0 (—)	20 (1.7)
Race§		
American Indian or Alaska Native	8,865 (83.4)	772 (91.9)
Asian	8 (0.1)	1 (0.1)
Black or African American	24 (0.2)	1 (0.1)
Multiple races	112 (1.1)	20 (2.4)
Other race	125 (1.2)	23 (2.7)
Unknown	0 (—)	18 (2.2)
White	1,482 (13.9)	5 (0.6)
Ethnicity¶		
Hispanic	206 (1.9)	1 (0.1)
Non-Hispanic	10,423 (98.1)	548 (74.2)
Unknown	0 (—)	190 (25.8)

Abbreviations: IQR = interquartile range; N/A = not available; SD = standard deviation.

* https://www.census.gov/tribal/?aianihh=0305

† Blackfeet case investigation report.

§ Unknown for 340 COVID-19 patients.

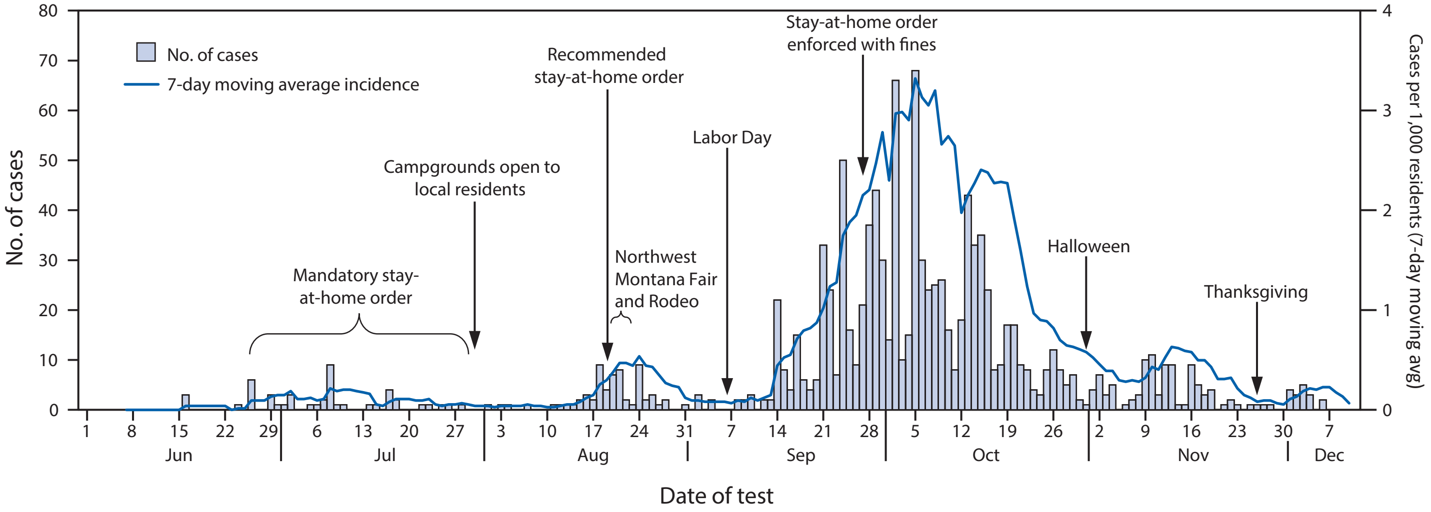
¶ Unknown for 441 COVID-19 patients.

Discussion

After implementation of mitigation measures, including case investigation, contact tracing, a mandatory stay-at-home order, and required mask use in public, the average reported daily COVID-19 incidence in the Blackfeet Tribal Reservation remained low (0.10 cases per 1,000 residents) during July. When the mandatory stay-at-home order expired on July 31, the Tribal Business Council issued a recommended stay-at-home order on August 19. After the opening of local campgrounds and Northwest Montana Fair and Rodeo and Labor Day weekend gatherings, daily COVID-19 incidence increased sharply, peaking October 5, and representing a sixty-three-fold increase over the daily average incidence in July. The continued increase in newly identified cases after September 28, when the enforced stay-at-home order commenced, reflects exposures that occurred in the preceding 2 weeks.*** The strictly enforced stay-at-home order, with increased penalties, likely contributed to the more than thirtyfold decrease in incidence by November 7.

*** https://www.cdc.gov/coronavirus/2019-ncov/hcp/clinical-guidance-management-patients.html

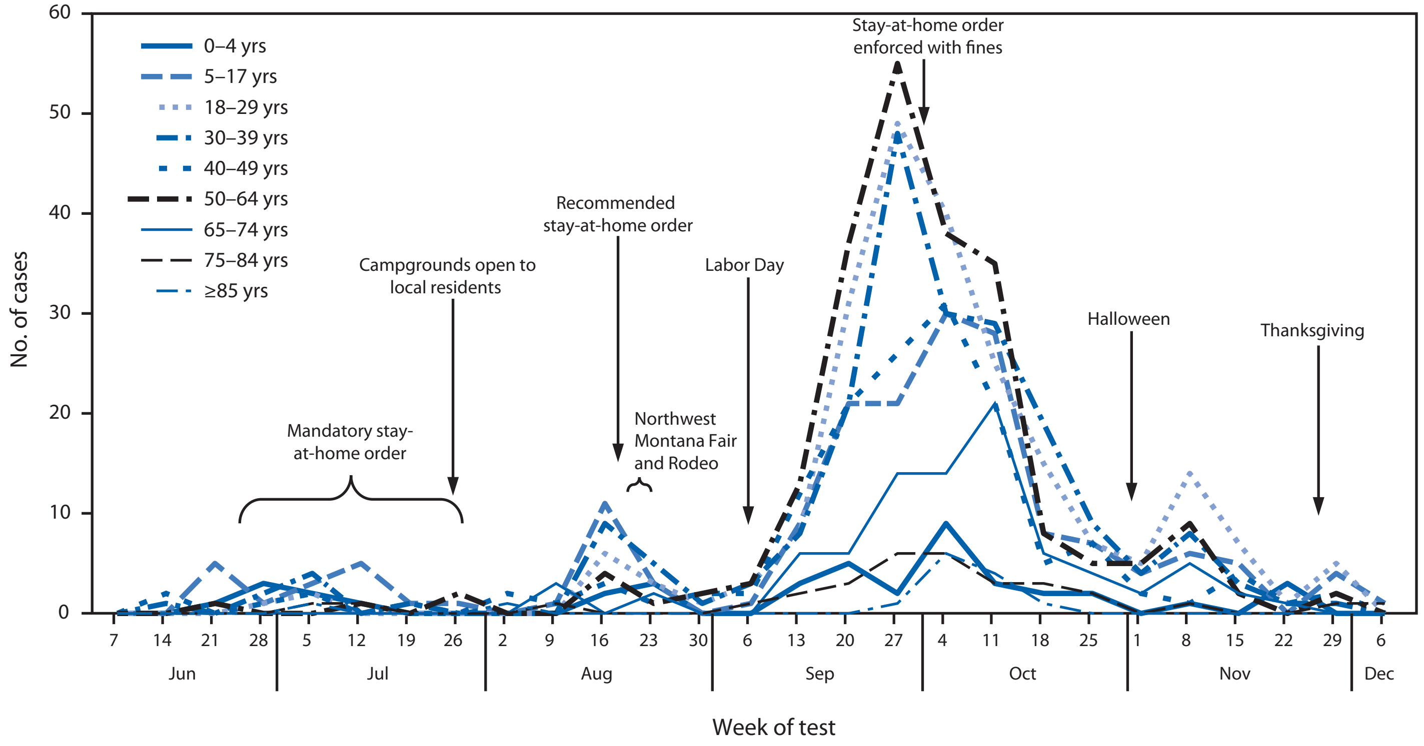
FIGURE 1. Number of COVID-19 cases, by test date and 7-day moving average incidence (N = 1,150) — Blackfeet Tribal Reservation, Montana, June 1–December 10, 2020*,†



* Case data collected and recorded by Blackfeet and Indian Health Service public health nurses.

† Among 1,180 total cases, 30 were missing test date and are not included in the figure.

FIGURE 2. Number of weekly COVID-19 cases, by week of test and age group (N = 1,150) — Blackfeet Tribal Reservation, Montana, June 1–December 10, 2020*,†



* Case data collected and recorded by Blackfeet and Indian Health Service public health nurses.

† Among 1,180 total cases, 30 were missing test date and are not included in the figure.

The steep declines in COVID-19 incidence in the Blackfeet Tribal Reservation might not have occurred without widespread and consistent enforcement of the mandate for mask use in public and stay-at-home orders. Wearing a mask reduces SARS-CoV-2 transmission from persons with symptomatic or asymptomatic infection and offers some protection for the wearer.[†††] On July 15, Montana first implemented a limited mask use mandate, which only applied to counties with four or more active COVID-19 cases,[§§§] but enforcement across the state was inconsistent (*7*). COVID-19 incidence in Montana increased throughout September and October, peaking November 14, at 1.54 cases per 1,000 residents (*8*). After the mask use mandate was applied to all Montana counties on November 17 (*9*), incidence in the state decreased (*8*).

The increases in COVID-19 cases among Blackfeet residents aged 5–17 years and 30–39 years followed relaxation of stay-at-home orders, the opening of campgrounds, and gatherings at the Northwest Montana Fair and Rodeo and during Labor Day weekend. The peaks in COVID-19 incidence in these groups were followed approximately 6 weeks later by a peak among persons aged 50–64 years. The average household size in the Blackfeet Tribal Reservation (3.4 persons) is higher than that in Montana (2.4 persons) (*2,5*). Using limited available household data (available for 12% of all cases), a household COVID-19 contact was reported for a larger proportion of cases among the Blackfeet (85%) than for cases among other Montana residents (22%) (*10*). Multigenerational households might contribute to COVID-19 transmission between age groups in the Blackfeet Tribal Reservation; however, information on multigenerational households for the Blackfeet was not available. Future planning for mitigation measures and data collection should take multigenerational households into account.

The findings in this report are subject to at least five limitations. First, the different performance characteristics of the two diagnostic tests (rapid antigen detection and molecular SARS-CoV-2 tests) created potential misclassification of cases. Second, complete standardized data were not available because the various entities conducting testing did not use the same data collection tools. Third, the lack of consistently collected data on contact tracing, exposures, order compliance, and relationships between COVID-19 cases prevented the assessment of secondary transmission. Fourth, data on household, workplace, and community exposure was limited; comparison with other populations should be made with caution. Finally, the relative contribution of each mitigation measure to the changes in COVID-19 rates could not be ascertained.

Summary

What is already known about this topic?

Community mitigation measures (e.g., stay-at-home orders and mask use), coupled with case investigation and contact tracing with immediate isolation or quarantine, are primary approaches to preventing and controlling community SARS-CoV-2 transmission.

What is added by this report?

In the Blackfeet Tribal Reservation, enforcement of stay-at-home orders and mandated use of face coverings in public, with potential fines and jail for noncompliance, were associated with a thirty-three-fold reduction in COVID-19 incidence from its peak of 6.40 cases per 1,000 residents per day on October 5 to 0.19 on November 7, 2020.

What are the implications for public health practice?

Enforcement of stay-at-home orders and mask use mandates, coupled with robust public health investigations, have been shown to reduce COVID-19 incidence.

The enforcement of stay-at-home orders, coupled with a mandate for mask use in public, likely contributed to a reduction in COVID-19 incidence, potentially helping to control the pandemic in the Blackfeet Tribal Reservation. A combination of mitigation measures, including case investigation, contact tracing, and enforced stay-at-home and mask use orders, will likely reduce COVID-19 transmission by limiting potential exposure to SARS-CoV-2. As of 2021, vaccination is available and recommended as another effective method of COVID-19 mitigation. In communities disproportionately affected by COVID-19, these mitigation strategies are likely to help reduce some COVID-19–associated health disparities.

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[†††] https://www.cdc.gov/coronavirus/2019-ncov/prevent-getting-sick/cloth-face-cover-guidance.html

[§§§] https://dphhs.mt.gov/aboutus/news/2020/directiverequiringfacecoverings

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Provisional Mortality Data — United States, 2020

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On March 31, 2021, this report was posted as an MMWR *Early Release on the* MMWR *website (https://www.cdc.gov/mmwr).*

CDC's National Vital Statistics System (NVSS) collects and reports annual mortality statistics using data from U.S. death certificates. Because of the time needed to investigate certain causes of death and to process and review data, final annual mortality data for a given year are typically released 11 months after the end of the calendar year. Daily totals reported by CDC COVID-19 case surveillance are timely but can underestimate numbers of deaths because of incomplete or delayed reporting. As a result of improvements in timeliness and the pressing need for updated, quality data during the global COVID-19 pandemic, NVSS expanded provisional data releases to produce near real-time U.S. mortality data.* This report presents an overview of provisional U.S. mortality data for 2020, including the first ranking of leading causes of death. In 2020, approximately 3,358,814 deaths† occurred in the United States. From 2019 to 2020, the estimated age-adjusted death rate increased by 15.9%, from 715.2 to 828.7 deaths per 100,000 population. COVID-19 was reported as the underlying cause of death or a contributing cause of death for an estimated 377,883 (11.3%) of those deaths (91.5 deaths per 100,000). The highest age-adjusted death rates by age, race/ethnicity, and sex occurred among adults aged ≥85 years, non-Hispanic Black or African American (Black) and non-Hispanic American Indian or Alaska Native (AI/AN) persons, and males. COVID-19 death rates were highest among adults aged ≥85 years, AI/AN and Hispanic persons, and males. COVID-19 was the third leading cause of death in 2020, after heart disease and cancer. Provisional death estimates provide an early indication of shifts in mortality trends and can guide public health policies and interventions aimed at reducing numbers of deaths that are directly or indirectly associated with the COVID-19 pandemic.

CDC analyzed provisional NVSS death certificate data for deaths occurring among U.S. residents in the United States during January–December 2020. The numbers and rates of overall deaths and COVID-19 deaths were assessed by age, sex, and race/ethnicity (categorized as Hispanic, non-Hispanic White [White], Black, non-Hispanic Asian, non-Hispanic AI/AN, non-Hispanic Native Hawaiian or other Pacific Islander [NH/PI], non-Hispanic multiracial, and unknown). Causes of death were coded according to the *International Classification of Diseases, Tenth Revision* (ICD-10), which describes disease classification and the designation of underlying cause of death (*1*,*2*). Numbers and rates of COVID-19 deaths include deaths for which COVID-19 was listed on the death certificate as a confirmed or presumed underlying cause of death or contributing cause of death (ICD-10 code U07.1). COVID-19 was the underlying cause of approximately 91% (345,323) of COVID-19–associated deaths during 2020 (*3*). Leading underlying causes of death were calculated and ranked (*4*). Deaths that occurred in the United States among residents of U.S. territories and foreign countries were excluded.§ Age was unknown for 86 (<0.01%) decedents, and race/ethnicity was unknown for 9,135 (0.27%). There were no records with unknown sex. To describe the trend in deaths during 2020, the number of deaths from all causes and from COVID-19 were calculated for each week. Midyear U.S. Census Bureau population estimates (July 1, 2020) were used to calculate estimated death rates per 100,000 standard population (*5*). Age-adjusted death rates were calculated for deaths by sex and race/ethnicity, and crude death rates were calculated by age. Age-adjusted death rates for 2020 were also compared with those from 2019 (*6*).

In 2020, approximately 3,358,814 deaths occurred in the United States (Table). The age-adjusted rate was 828.7 deaths per 100,000 population, an increase of 15.9% from 715.2 in 2019. The highest overall numbers of deaths occurred during the weeks ending April 11, 2020, (78,917) and December 26, 2020 (80,656) (Figure 1). Death rates were lowest among persons aged 5–14 years (13.6) and highest among persons aged ≥85 years (15,007.4); age-adjusted death rates were higher among males (990.5) than among females (689.2).

During 2020, COVID-19 was listed as the underlying or contributing cause of 377,883 deaths (91.5 per 100,000 population). COVID-19 death rates were lowest among children aged 1–4 years (0.2) and 5–14 years (0.2) and highest among those aged ≥85 years (1,797.8). Similar to the rate of overall deaths, the age-adjusted COVID-19–associated death rate among males (115.0) was higher than that among females (72.5).

Age-adjusted death rates differed by race/ethnicity. Overall age-adjusted death rates were lowest among Asian

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* https://www.cdc.gov/nchs/nvss/deaths.htm

† Based on death records received and processed as of March 21, 2021, for deaths occurring in the United States among U.S. residents. Data included in this analysis include >99% of deaths that occurred in 2020.

§ At the time of analysis, 1.1% of total NVSS deaths and 0.6% of COVID-19 deaths that occurred in the United States were among residents of U.S. territories and foreign countries.

TABLE. Provisional* number and rate of total deaths and COVID-19–related deaths, by demographic characteristics — National Vital Statistics System, United States, 2020

	No. (rate)†	
Characteristic	**Total deaths**	**COVID-19 deaths§**
Total	**3,358,814 (828.7)**	**377,883 (91.5)**
Age group, yrs		
<1	19,146 (506.0)	43 (1.1)
1–4	3,469 (22.2)	24 (0.2)
5–14	5,556 (13.6)	67 (0.2)
15–24	35,470 (83.2)	587 (1.4)
25–34	72,678 (157.9)	2,527 (5.5)
35–44	103,389 (246.2)	6,617 (15.8)
45–54	189,397 (467.8)	17,905 (44.2)
55–64	436,886 (1,028.5)	44,631 (105.1)
65–74	669,316 (2,068.8)	80,617 (249.2)
75–84	816,307 (4,980.2)	104,212 (635.8)
≥85	1,007,114 (15,007.4)	120,648 (1,797.8)
Unknown	86 (—)	5 (—)
Sex		
Female	1,602,366 (689.2)	172,689 (72.5)
Male	1,756,448 (990.5)	205,194 (115.0)
Race/Ethnicity		
Hispanic	304,488 (724.1)	68,469 (164.3)
White, non-Hispanic	2,467,419 (827.1)	228,328 (72.5)
Black, non-Hispanic	443,116 (1,105.3)	59,871 (151.1)
Asian, non-Hispanic	90,519 (457.9)	13,334 (66.7)
American Indian or Alaska Native, non-Hispanic	24,279 (1,024.0)	4,504 (187.8)
Native Hawaiian or other Pacific Islander, non-Hispanic	4,424 (828.4)	679 (122.3)
Multiracial, non-Hispanic	15,434 (378.8)	1,125 (31.8)
Unknown	9,135 (—)	1,573 (—)

* National Vital Statistics System provisional data are incomplete. Data from December are less complete due to reporting lags. These data exclude deaths that occurred in the United States among residents of U.S. territories and foreign countries.

† Deaths per 100,000 standard population. Age-adjusted death rates are provided by sex and race/ethnicity.

§ Deaths with confirmed or presumed COVID-19 as an underlying or contributing cause of death, with *International Classification of Diseases, Tenth Revision* code U07.1.

(457.9 per 100,000 population) and Hispanic persons (724.1) and highest among Black (1,105.3) and AI/AN persons (1,024.0). COVID-19–associated death rates were lowest among multiracial (31.8) and Asian persons (66.7) and highest among AI/AN (187.8) and Hispanic persons (164.3). COVID-19 was listed as the underlying cause of 345,323 deaths during 2020 and was the third leading underlying cause of death, after heart disease (690,882 deaths) and cancer (598,932) (Figure 2).

Discussion

During January–December 2020, the estimated 2020 age-adjusted death rate increased for the first time since 2017, with an increase of 15.9% compared with 2019, from 715.2 to 828.7 deaths per 100,000 population. COVID-19 was the underlying or a contributing cause of 377,883 deaths (91.5 deaths per 100,000). COVID-19 death rates were highest among males, older adults, and AI/AN and Hispanic persons. The highest numbers of overall deaths and COVID-19 deaths occurred during April and December. COVID-19 was the third leading underlying cause of death in 2020, replacing suicide as one of the top 10 leading causes of death (*6*).

Summary

What is already known about this topic?

The COVID-19 pandemic caused approximately 375,000 deaths in the United States during 2020.

What is added by this report?

The age-adjusted death rate increased by 15.9% in 2020. Overall death rates were highest among non-Hispanic Black persons and non-Hispanic American Indian or Alaska Native persons. COVID-19 was the third leading cause of death, and the COVID-19 death rate was highest among Hispanics.

What are the implications for public health practice?

Provisional death estimates provide an early indication of shifts in mortality trends. Timely and actionable data can guide public health policies and interventions for populations experiencing higher numbers of deaths that are directly or indirectly associated with the COVID-19 pandemic.

The findings in this report are subject to at least four limitations. First, data are provisional, and numbers and rates might change as additional information is received. Second, timeliness of death certificate submission can vary by jurisdiction. As a result, the national distribution of deaths might be affected by the distribution of deaths from jurisdictions reporting later, which might differ from those in the United States overall. Third, certain categories of race (i.e., AI/AN and Asian) and Hispanic ethnicity reported on death certificates might have been misclassified (*7*), possibly resulting in underestimates of death rates for some groups. Finally, the cause of death for certain persons might have been misclassified. Limited availability of testing for SARS-CoV-2, the virus that causes COVID-19, at the beginning of the COVID-19 pandemic might have resulted in an underestimation of COVID-19–associated deaths.

This report provides an overview of provisional U.S. mortality data for 2020. Provisional death estimates can give researchers and policymakers an early indication of shifts in mortality trends and provide actionable information sooner than the final mortality data that are released approximately 11 months after the end of the data year. These data can guide public health policies and interventions aimed at reducing numbers of deaths that are directly or indirectly associated with the COVID-19 pandemic and among persons most affected, including those who are older, male, or from disproportionately affected racial/ethnic minority groups.

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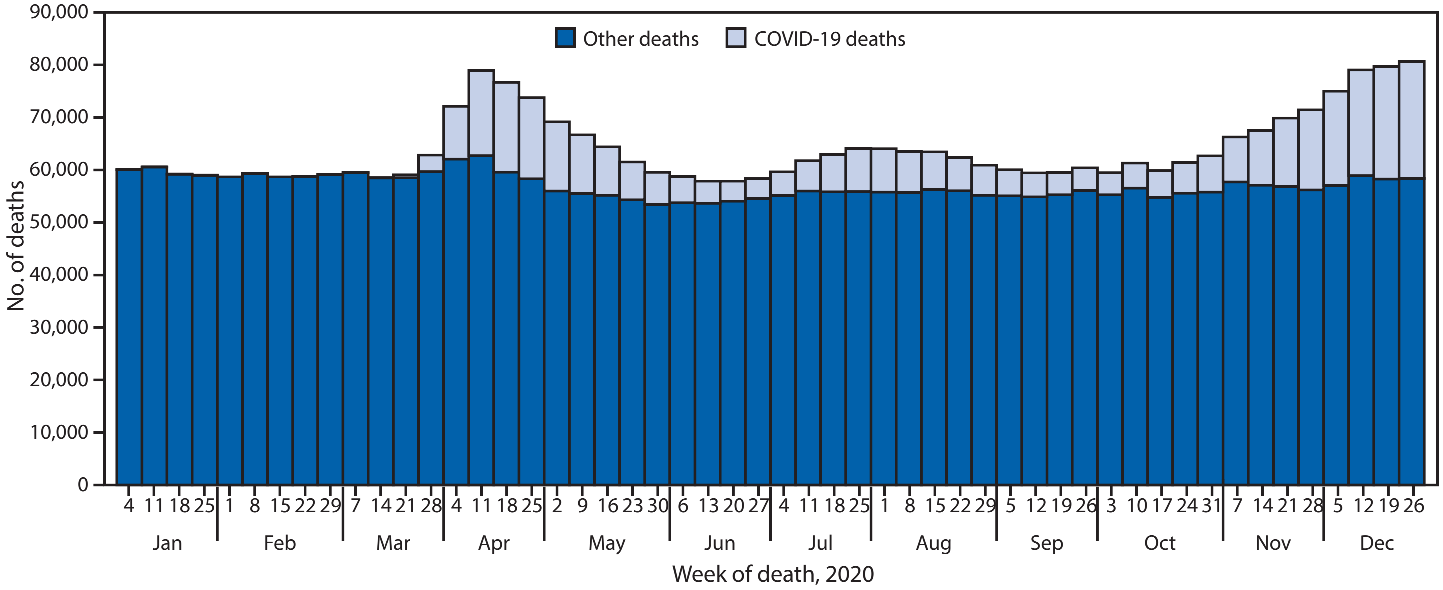
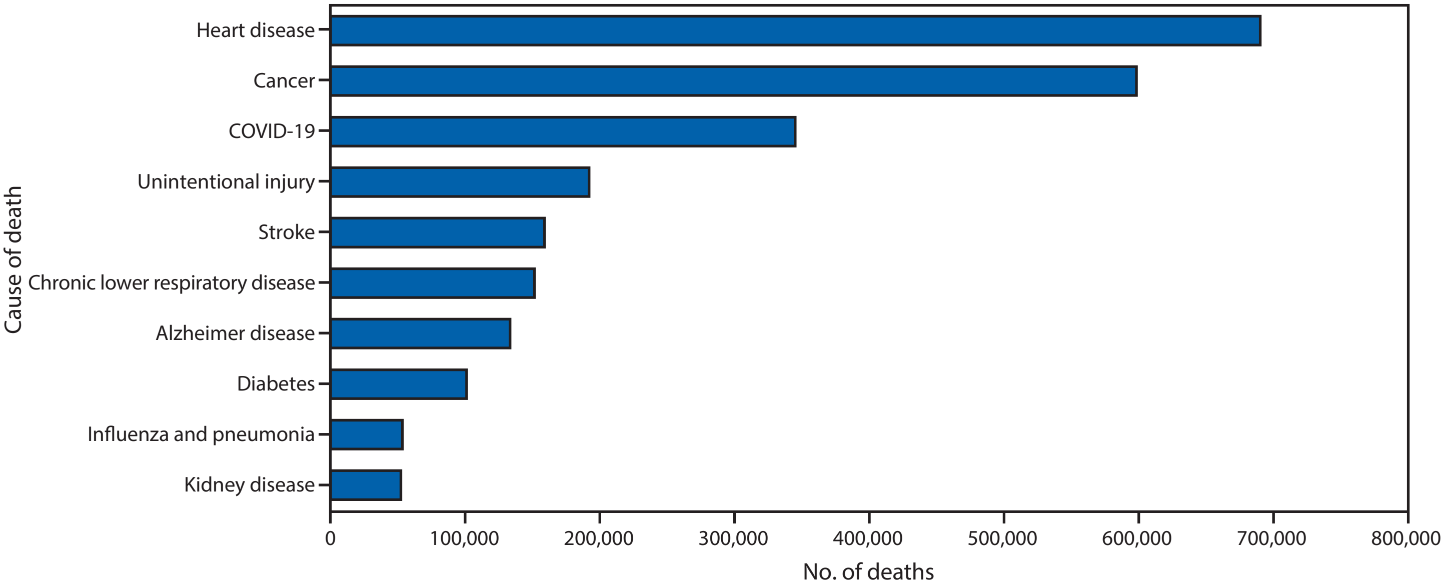
FIGURE 1. Provisional* number of COVID-19–related deaths† and other deaths, by week — National Vital Statistics System, United States, 2020



* National Vital Statistics System provisional data are incomplete. Data from December are less complete due to reporting lags. Deaths that occurred in the United States among residents of U.S. territories and foreign countries were excluded.

† Deaths with confirmed or presumed COVID-19 as an underlying or contributing cause of death, with *International Classification of Diseases, Tenth Revision* code U07.1.

FIGURE 2. Provisional* number of leading underlying causes of death† — National Vital Statistics System, United States, 2020



* National Vital Statistics System provisional data are incomplete. Data from December are less complete due to reporting lags. Deaths that occurred in the United States among residents of U.S. territories and foreign countries were excluded.

† Deaths for which COVID-19 was a contributing, but not the underlying, cause of death are not included in this figure.

All authors have completed and submitted the International Committee of Medical Journal Editors form for disclosure of potential conflicts of interest. No potential conflicts of interest were disclosed.

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Death Certificate–Based ICD-10 Diagnosis Codes for COVID-19 Mortality Surveillance — United States, January–December 2020

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On March 31, 2021, this report was posted as an MMWR *Early Release on the* MMWR *website (https://www.cdc.gov/mmwr).*

Approximately 375,000 deaths during 2020 were attributed to COVID-19 on death certificates reported to CDC (*1*). Concerns have been raised that some deaths are being improperly attributed to COVID-19 (*2*). Analysis of *International Classification of Diseases, Tenth Revision* (ICD-10) diagnoses on official death certificates might provide an expedient and efficient method to demonstrate whether reported COVID-19 deaths are being overestimated. CDC assessed documentation of diagnoses co-occurring with an ICD-10 code for COVID-19 (U07.1) on U.S. death certificates from 2020 that had been reported to CDC as of February 22, 2021. Among 378,048 death certificates listing U07.1, a total of 357,133 (94.5%) had at least one other ICD-10 code; 20,915 (5.5%) had only U07.1. Overall, 97.3% of 357,133 death certificates with at least one other diagnosis (91.9% of all 378,048 death certificates) were noted to have a co-occurring diagnosis that was a plausible chain-of-event condition (e.g., pneumonia or respiratory failure), a significant contributing condition (e.g., hypertension or diabetes), or both. Overall, 70%–80% of death certificates had both a chain-of-event condition and a significant contributing condition or a chain-of-event condition only; this was noted for adults aged 18–84 years, both males and females, persons of all races and ethnicities, those who died in inpatient and outpatient or emergency department settings, and those whose manner of death was listed as natural. These findings support the accuracy of COVID-19 mortality surveillance in the United States using official death certificates. High-quality documentation of co-occurring diagnoses on the death certificate is essential for a comprehensive and authoritative public record. Continued messaging and training (*3*) for professionals who complete death certificates remains important as the pandemic progresses. Accurate mortality surveillance is critical for understanding the impact of variants of SARS-CoV-2, the virus that causes COVID-19, and of COVID-19 vaccination and for guiding public health action.

Death certificates were processed using standard CDC protocols to convert all written text and diagnoses to ICD-10 codes (*4*). Individual data elements were extracted for analysis from death certificates that had the ICD-10 code for COVID-19 (U07.1) listed in Part I (the section for reporting chain of events leading directly to death, the immediate cause of death, and the underlying cause of death) or Part II (the section for reporting all other significant conditions that contributed to death) of the death certificate for deaths that occurred during the calendar year 2020 (Supplementary Figure, https://stacks.cdc.gov/view/cdc/104571) (*3*) and had been reported to CDC by February 22, 2021. First, the location of ICD-10 diagnoses in relation to the COVID-19 diagnosis was used to categorize the co-occurring diagnoses as being in the chain of events that directly caused the death (chain-of-event conditions) or a significant condition contributing to death (significant contributing conditions). Any co-occurring ICD-10 code that appeared on the same line or above U07.1 in Part I was considered to be a chain-of-event condition. Any ICD-10 code that appeared on a line below U07.1 in Part I or in Part II was considered to be a contributing condition. Second, the highest-frequency ICD-10 codes noted in ≥1% of all death certificates with COVID-19 listed in Part I and at least one diagnosis other than COVID-19 were reviewed for consistency and plausibility with conditions known to be associated with severe outcomes in patients with COVID-19 (*5*–*8*). Conditions consistent with those known to be associated with severe COVID-19 outcomes were coded as chain-of-event or significant contributing conditions regardless of their location on the death certificate. For example, a death certificate with an ICD-10 code for respiratory failure listed below U07.1 would be coded as a chain-of-event condition because respiratory failure caused by COVID-19 led directly to the death. Third, less frequently appearing ICD-10 codes that were determined to be consistent with those associated with severe COVID-19 outcomes were also coded as chain-of-event or significant contributing conditions. Finally, death certificates were categorized into five mutually exclusive categories according to the ICD-10 codes recorded on the death certificate 1) only the ICD-10 code for COVID-19; 2) at least one other co-occurring ICD-10 code for a chain-of-event condition; 3) at least one other co-occurring ICD-10 code for a significant contributing condition; 4) an ICD-10 code for both a chain-of-event and significant contributing condition; or 5) an ICD-10 code that could not be categorized as a plausible chain-of-event or significant contributing condition based on current knowledge. Results were stratified by age, sex, race/ethnicity, and setting of death reported on the death certificate. All analyses were conducted using SAS (version 9.4; SAS Institute) and Stata (version 15.0; StataCorp).

Among 378,048 death certificates with the ICD-10 code U07.1, 94.5% (357,133) had at least one other ICD-10 code, whereas 5.5% (20,915) listed only U07.1 (Table 1); 330,198 (87%) listed COVID-19 in Part I. Death certificates with only U07.1 and no other diagnosis accounted for 2.9%–6.6% of death certificates for decedents across all age, sex, and racial/ethnic categories (Table 1). Having only COVID-19 listed on the death certificate was slightly more frequent for death certificates that listed "dead on arrival" (34; 10%) or "decedent's home" (2,006; 8.6%) as the place of death or "pending" (seven; 13.5%) as the manner of death.

Overall, 97.3% of 357,133 death certificates with at least one other diagnosis (91.9% of all 378,048 death certificates) were noted to have a co-occurring diagnosis that was a plausible chain-of-event condition (e.g., pneumonia, respiratory failure, adult respiratory distress syndrome, cardiac arrest, or sepsis), or significant contributing condition (e.g., hypertension, diabetes, dementia, or chronic obstructive pulmonary disease) (*5*), or both. The most frequent chain-of-event ICD-10 diagnosis codes on 330,198 death certificates that listed COVID-19 on Part I of the death certificate were J18.9 (pneumonia) (45%) and J96.0 (acute respiratory failure) (20%) (Table 2); the most frequent significant contributing condition ICD-10 codes were I10 (essential hypertension) (18%) and E14.9 (diabetes mellitus) (10%). Nearly 75% of all death certificates had a chain-of-event condition, alone or in combination with a significant contributing condition; this finding was noted for adults aged 18–84 years, males and females, persons of all races and ethnicities, those who died in inpatient and outpatient or emergency department settings, and those whose manner of death was listed as natural (Table 1).

Nearly 18% of death certificates had a co-occurring significant contributing condition only (Table 1). This finding was more frequent for death certificates indicating that the death occurred in the decedent's home (38.3%), a nursing home or long-term care facility (38.5%), or hospice facility (23.2%). A small proportion (9,638; 2.5%) of death certificates had co-occurring diagnosis codes that could not be plausibly categorized as either a chain-of-event or significant contributing condition. This finding was more frequent among decedents aged <18 years (64; 35.2%) and 18–29 years (145; 10.2%); these age groups represented only 0.4% (1,608) of all death certificates. This was recorded more frequently among decedents who died at home (1,259; 5.4%), were declared "dead on arrival" (15; 4.4%), or whose manner of death was self-inflicted (39; 63.9%), homicide (13; 43.8%), "could not determine" (18; 26.5%), or accidental (417; 20.0%).

Summary

What is already known about this topic?

During 2020, approximately 375,000 U.S. deaths were attributed to COVID-19.

What is added by this report?

Among 378,048 death certificates from 2020 listing COVID-19, 5.5% listed COVID-19 without codes for any other conditions. Among 357,133 death certificates with at least one other condition, 97% had a co-occurring diagnosis of a plausible chain-of-event condition (e.g., pneumonia or respiratory failure), or a significant contributing condition (e.g., hypertension or diabetes), or both.

What are the implications for public health practice?

These findings support the accuracy of COVID-19 mortality surveillance in the United States using official death certificates. High-quality documentation of death certificate diagnoses is essential for an authoritative public record.

Deaths reported from inpatient settings accounted for 240,770 (64%) of all death certificates; 86% of these had co-occurring diagnoses identified as chain-of-event and significant contributing conditions (104,250; 43%) or chain-of-event conditions only (103,475; 43%). A higher proportion of deaths reported from nursing homes or long-term care facilities (22% of all death certificates) listed contributing conditions only (39%) on the death certificate. Contributing conditions were also noted in a larger proportion of death certificates listing the decedent's home as the location of death (38%); these death certificates were less likely to have co-occurring chain-of-event diagnoses listed on the death certificate.

Discussion

Among death certificates from calendar year 2020 listing COVID-19 and at least one other co-occurring diagnosis, the documentation is consistent with these deaths being attributable to COVID-19. Specifically, in 97% of 357,133 death certificates with COVID-19 and at least one other diagnosis, the documented chain-of-event and significant contributing conditions were consistent with those reported in clinical and epidemiologic studies to occur among patients with severe COVID-19–associated outcomes (*5*,*9*). Only 5.5% of death certificates had COVID-19 without any other conditions listed. Attributability of death to COVID-19 could not be evaluated for these death certificates and represents an opportunity for improvement in documentation.

A small proportion (2.5%) of death certificates documented conditions that have not currently been described to be associated with COVID-19 critical illness or death. This was noted more often among those who died at home, declared dead on

TABLE 1. Distribution of death certificates with COVID-19 diagnosis* across five mutually exclusive categories defined by presence and classification of co-occurring diagnoses, by demographic characteristics, setting of death, and manner of death characteristics — National Center for Health Statistics, United States, January–December 2020

Characteristic	No. of death certificates	No. (row %)				
		COVID-19 only	COVID-19 and ≥1 chain-of-event condition only	COVID-19 and ≥1 significant contributing condition only	COVID-19 and ≥1 chain-of-event and ≥1 significant contributing condition	COVID-19 with no plausible chain-of-event or significant contributing condition
Total	**378,048**	**20,915 (5.5)**	**128,603 (34.0)**	**67,184 (17.8)**	**151,708 (40.1)**	**9,638 (2.5)**
Age group, yrs						
<18	182	8 (4.4)	70 (38.5)	18 (9.9)	22 (12.1)	64 (35.2)
18–29	1,426	77 (5.4)	636 (44.6)	167 (11.7)	401 (28.1)	145 (10.2)
30–39	4,161	275 (6.6)	1,712 (41.1)	550 (13.2)	1,371 (32.9)	253 (6.1)
40–49	11,053	660 (6.0)	4,551 (41.2)	1,408 (12.7)	3,982 (36.0)	452 (4.1)
50–64	55,719	2,911 (5.2)	22,788 (40.9)	6,693 (12.0)	21,666 (38.9)	1,661 (3.0)
65–74	80,705	3,841 (4.8)	30,439 (37.7)	10,756 (13.3)	33,820 (41.9)	1,849 (2.3)
75–84	104,294	5,277 (5.1)	34,784 (33.4)	17,858 (17.1)	44,179 (42.4)	2,196 (2.1)
≥85	120,508	7,866 (6.5)	33,623 (27.9)	29,734 (24.7)	46,267 (38.4)	3,018 (2.5)
Sex						
Female	172,615	10,007 (5.8)	55,207 (32.0)	35,525 (20.6)	67,186 (38.9)	4,690 (2.7)
Male	205,423	10,907 (5.3)	73,392 (35.7)	31,658 (15.4)	84,518 (41.1)	4,948 (2.4)
Race/Ethnicity						
Hispanic or Latino	70,011	3,680 (5.3)	28,035 (40.0)	7,875 (11.2)	29,016 (41.4)	1,405 (2.0)
American Indian or Alaska Native, non-Hispanic	4,460	266 (6.0)	1,652 (37.0)	501 (11.2)	1,920 (43.0)	121 (2.7)
Asian, non-Hispanic	13,339	676 (5.1)	5,352 (40.1)	1,687 (12.6)	5,331 (40.0)	293 (2.2)
Black, non-Hispanic	59,468	3,114 (5.2)	21,065 (35.4)	9,151 (15.4)	24,688 (41.5)	1,450 (2.4)
Native Hawaiian or Pacific Islander, non-Hispanic	679	20 (2.9)	224 (33.0)	73 (10.8)	350 (51.5)	12 (1.8)
White, non-Hispanic	227,387	12,961 (5.7)	71,227 (31.3)	47,531 (20.9)	89,379 (39.3)	6,289 (2.8)
Multiracial, non-Hispanic	1,123	43 (3.8)	379 (33.7)	165 (14.7)	512 (45.6)	24 (2.1)
Unknown	1,581	155 (9.8)	669 (42.3)	201 (12.7)	512 (32.4)	44 (2.8)
Setting of death						
Inpatient	240,770	10,084 (4.2)	103,475 (43.0)	18,719 (7.8)	104,250 (43.3)	4,242 (1.8)
Outpatient/Emergency department	12,851	830 (6.5)	4,287 (33.4)	2,411 (18.8)	4,971 (38.7)	352 (2.7)
Dead on arrival	339	34 (10.0)	98 (28.9)	70 (20.6)	122 (36.0)	15 (4.4)
Decedent's home	23,455	2,006 (8.6)	3,634 (15.5)	8,977 (38.3)	7,579 (32.3)	1,259 (5.4)
Hospice facility	10,458	412 (3.9)	2,722 (26.0)	2,430 (23.2)	4,612 (44.1)	282 (2.7)
Nursing home/Long-term care facility	82,843	6,986 (8.4)	13,183 (15.9)	31,904 (38.5)	27,597 (33.3)	3,173 (3.8)
Other	7,163	549 (7.7)	1,170 (16.3)	2,612 (36.5)	2,522 (35.2)	310 (4.3)
Unknown	169	14 (8.3)	34 (20.1)	61 (36.1)	55 (32.5)	5 (3.0)
Manner of death						
Accidental	2,080	0 (—)	233 (11.2)	890 (42.8)	540 (26.0)	417 (20.0)
Could not determine	68	1 (1.5)	16 (23.5)	14 (20.6)	19 (27.9)	18 (26.5)
Homicide	32	0 (—)	6 (18.8)	6 (18.8)	6 (18.8)	14 (43.8)
Natural	344,307	20,399 (5.9)	116,812 (33.9)	63,981 (18.6)	134,267 (39.0)	8,848 (2.6)
Pending investigation	52	7 (13.5)	7 (13.5)	9 (17.3)	28 (53.8)	1 (1.9)
Self-inflicted	61	0 (—)	8 (13.1)	10 (16.4)	4 (6.6)	39 (63.9)
Missing	31,448	508 (1.6)	11,521 (36.6)	2,274 (7.2)	16,844 (53.6)	301 (1.0)

* *International Classification of Diseases, Tenth Revision* code U07.1.

arrival, and whose manner of death was not natural. In particular, a higher percentage of decedents aged <18 years (35.2%) and 18–29 years (10.2%) did not have a chain-of-event or significant contributing condition listed on the death certificate, even though their death certificates did have at least one other diagnosis code along with COVID-19 in Part I or II. Although these age categories constituted a very small proportion of the entire decedent group, the information on the death certificate provides a starting point for identification of other conditions that might contribute to mortality in younger persons. Detailed evaluation of death certificates might provide insights into rare and lesser known conditions that are not yet understood to be associated with or contribute to death from COVID-19.

TABLE 2. Highest-frequency *International Classification of Diseases, Tenth Revision* (ICD-10) codes listed in death certificates with COVID-19 in Part I of death certificate and at least one diagnosis other than COVID-19 (330,198) — National Center for Health Statistics, United States, January–December 2020

Condition (ICD-10 code)	No. (% of 330,198[*])
Conditions listed as chain-of-event conditions on ≥1% of death certificates[†]	
Pneumonia, unspecified (J18.9)	148,530 (45.0)
Acute respiratory failure (J96.0)	66,609 (20.2)
Respiratory failure, unspecified (J96.9)	47,045 (14.2)
Cardiac arrest, unspecified (I46.9)	36,983 (11.2)
Adult respiratory distress syndrome (J80)	36,297 (11.0)
Sepsis, unspecified (A41.9)	20,117 (6.1)
Viral pneumonia, unspecified (J12.9)	12,421 (3.8)
Asphyxia (R09.0)	10,641 (3.2)
Respiratory arrest (R09.2)	7,009 (2.1)
Conditions listed as significant contributing conditions on ≥1% of death certificates[§]	
Essential (primary) hypertension (I10)	58,930 (17.8)
Unspecified diabetes mellitus without complications (E14.9)	34,038 (10.3)
Unspecified dementia (F03)	32,189 (9.7)
Chronic obstructive pulmonary disease, unspecified (J44.9)	24,678 (7.5)
Atherosclerotic heart disease (I25.1)	22,162 (6.7)
Type 2 diabetes mellitus without complications (E11.9)	21,038 (6.4)
Atrial fibrillation and flutter (I48)	19,784 (6.0)
Congestive heart failure (I50.0)	16,841 (5.1)
Tobacco use (F17.9)	16,424 (5.0)
Chronic kidney disease, unspecified (N18.9)	14,525 (4.4)
Alzheimer disease, unspecified (G30.9)	11,220 (3.4)
Hypertensive heart disease without (congestive) heart failure (I11.9)	9,881 (3.0)
Hyperlipidemia, unspecified (E78.5)	9,330 (2.8)
Other specified disorders of kidney and ureter (N28.8)	8,958 (2.7)
Obesity, unspecified (E66.9)	8,913 (2.7)
Chronic kidney disease, stage 5 (N18.5)	7,955 (2.4)
Stroke, not specified as hemorrhage or infarction (I64)	6,494 (2.0)
Heart failure, unspecified (I50.9)	6,436 (1.9)
Conditions listed on ≥0.5% of death certificates and not identified as known chain-of-event conditions or significant contributing conditions[¶]	
Other specified general symptoms and signs (R68.8)	1,124 (0.3)
Other lack of normal physiologic development, underweight (R62.8)	734 (0.2)
Dyspnea (R06.0)	363 (0.1)
Senility (R54)	331 (0.1)
Other and unspecified infectious disease (B99.9)	247 (0.1)
Gastrointestinal hemorrhage (K92.2)	213 (0.1)
Unspecified protein energy deficiency (E46)	204 (0.1)
Influenza due to unidentified influenza virus (J11.1)	174 (0.1)
Urinary tract infection (N39.0)	150 (0.0)
Malaise and fatigue (R53)	145 (0.0)
Unspecified fall (W19)	139 (0.0)
Multiple sclerosis (G35)	124 (0.0)

[*] A total of 330,198 death certificates had COVID-19 listed in Part I of death certificate and at least one other diagnosis listed on the death certificate.

[†] COVID-19 diagnosis listed in Part I of the death certificate; chain-of-event conditions listed on the same line or above the COVID-19 diagnosis in Part I of the death certificate.

[§] COVID-19 diagnosis listed in Part I of the death certificate; significant contributing conditions listed below the COVID-19 line in Part I or in Part II of the death certificate.

[¶] COVID-19 diagnosis listed in Part I of the death certificate; co-occurring conditions listed anywhere on the death certificate and not identified as known chain-of-event or significant contributing conditions.

The findings in this report are subject to at least two limitations. First, the accuracy of documentation of chain-of-event and significant contributing conditions on death certificates is known to be suboptimal (*10*); the effect of COVID-19 on completion of death certificates merits further study, with an emphasis on variation by time, jurisdiction in which the death occurred, age group, race, ethnicity, and setting of death. Second, CDC was unable to compare death certificate data with decedent's medical records or autopsy reports for end-of-life events and co-occurring diagnoses. Medical record review is needed to confirm findings from this study and elucidate more information for decedents with only COVID-19 listed on their death certificate or those that could not be plausibly categorized as attributable to COVID-19 based on death certificate data alone.

These findings support the accuracy of COVID-19 mortality surveillance in the United States using official death certificates. High-quality documentation of co-occurring diagnoses on the death certificate is essential for a comprehensive and authoritative public record. Continued messaging to and training of professionals who complete death certificates (*3*) remains important as the pandemic progresses. Accurate mortality surveillance is critical for understanding the impact of SARS-CoV-2 variants and of COVID-19 vaccinations and for guiding public health action.

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Community Transmission of SARS-CoV-2 Associated with a Local Bar Opening Event — Illinois, February 2021

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During February 2021, an opening event was held indoors at a rural Illinois bar that accommodates approximately 100 persons. The Illinois Department of Public Health (IDPH) and local health department staff members investigated a COVID-19 outbreak associated with this opening event. Overall, 46 COVID-19 cases were linked to the event, including cases in 26 patrons and three staff members who attended the opening event and 17 secondary cases. Four persons with cases had COVID-19–like symptoms on the same day they attended the event. Secondary cases included 12 cases in eight households with children, two on a school sports team, and three in a long-term care facility (LTCF). Transmission associated with the opening event resulted in one school closure affecting 650 children (9,100 lost person-days of school) and hospitalization of one LTCF resident with COVID-19. These findings demonstrate that opening up settings such as bars, where mask wearing and physical distancing are challenging, can increase the risk for community transmission of SARS-CoV-2, the virus that causes COVID-19. As community businesses begin to reopen, a multicomponent approach should be emphasized in settings such as bars to prevent transmission* (*1*). This includes enforcing consistent and correct mask use, maintaining ≥6 ft of physical distance between persons, reducing indoor bar occupancy, prioritizing outdoor seating, improving building ventilation, and promoting behaviors such as staying at home when ill, as well as implementing contact tracing in combination with isolation and quarantine when COVID-19 cases are diagnosed.

Investigation and Findings

On February 17, 2021, IDPH was notified through the state's outbreak reporting system of a possible COVID-19 outbreak (i.e., five or more cases linked to a common location) in persons who attended an opening event at a bar in a rural Illinois county. The event had occurred indoors, with no outside air flow, approximately 2 weeks earlier in a 2,800-sq-ft bar during normal operating hours (4:00 p.m. to 1:00 a.m.). Six employees staffed the bar. Although the total number of bar patrons who attended the event is unknown, the bar accommodates approximately 100 persons. Before the event, IDPH reported a 7-day average daily COVID-19 incidence of 41–42 cases per 100,000 persons in the county; 14 days after the event, the 7-day average daily incidence had more than doubled, to 86–87 cases per 100,000 persons (*2*). On February 12, through routine testing and contact tracing, local health department staff members identified a cluster of cases linked to the bar event, including a case in an asymptomatic attendee who received a confirmed COVID-19 diagnosis the day before the event.

A bar attendee case was defined as the onset of COVID-19–like symptoms or receipt of a positive SARS-CoV-2 test result within 14 days of the bar opening event in a bar patron or employee who reported attending the event and who had no previous identified epidemiologic link to a COVID-19 case outside that setting. A confirmed case was defined as receipt of a positive SARS-CoV-2 nucleic acid amplification test (NAAT) or antigen test result by a person who attended the event, and a probable case was defined as COVID-19–like symptoms in a person who attended the event but had no laboratory confirmation of infection.† A secondary case was defined as receipt of a positive SARS-CoV-2 NAAT or antigen test result by a close contact of a person with event-associated COVID-19.§

Local health department staff members, per standard practice, conducted case investigations within 48 hours of receipt of a positive SARS-CoV-2 test result in the county using a standardized questionnaire; demographic data, symptoms, and symptom onset date were entered into an electronic contact tracing platform. Through routine case investigation, local health department investigators identified a cluster of cases linked to the bar opening event through case reports indicating that persons attended the event or were close contacts of a person with an event-associated case during the 14 days before symptom onset or the testing date. All persons with a bar attendee case or secondary case of COVID-19 were interviewed by local health department staff members. This activity was reviewed by CDC

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

† https://www.cdc.gov/coronavirus/2019-ncov/symptoms-testing/symptoms.html

§ Close contact is defined as being within 6 ft of a person with laboratory-confirmed or probable SARS-CoV-2 infection for a cumulative total of ≥15 minutes in a 24-hour period. https://www.cdc.gov/coronavirus/2019-ncov/php/contact-tracing/contact-tracing-plan/appendix.html#contact and was conducted consistent with applicable federal law and CDC policy.¶

Bar patrons and employees. By February 16, 2021, 29 bar attendee cases had been identified among persons who reported attending the opening event (Figure), including 26 (89.7%) in bar patrons and three (10.3%) in employees; all identified cases were confirmed by NAAT or antigen testing, except one probable case in a person who had COVID-19–like symptoms but did not receive testing (Table). Three additional employees worked during the event, all of whom had received a positive test result during the preceding 90 days and had completed 10 days of isolation from symptom onset or test date. Among persons with bar attendee cases, 25 (86.2%) had symptomatic illnesses. Among persons with symptom onset after the start of the event, onset dates ranged from 1 to 7 days after the event. Four (13.8%) persons with bar attendee cases reported having symptoms on the day of the event and were not reported to be contacts of one another before the event. Event attendees reported inconsistent mask use and not maintaining ≥6 ft of physical distance, despite table spacing and signs encouraging physical distancing and mask use. Most persons with bar attendee cases were adults aged 18–44 years (75.9%), male (65.5%), and non-Hispanic White persons (79.3%). One of the 29 persons with a bar attendee case, a bar patron, had received a COVID-19 vaccination before the event (the first dose, 5 days before receipt of the positive SARS-CoV-2 test result). No other persons with bar attendee cases had received a COVID-19 vaccination.

Secondary community cases. After the bar opening event, at least 71 close contacts of persons with bar attendee COVID-19 were reported; among these, 37 (52.1%) received testing, 17 (45.9%) of whom received a positive test result within 14 days of the contact. Two persons with secondary COVID-19 cases were school-related contacts of persons with bar attendee COVID-19, three were LTCF contacts, and 12 were household contacts. Among the 17 persons with secondary cases of confirmed COVID-19, 13 were symptomatic, with symptom onset dates ranging from 3 to 11 days after the event. Median age was 28 years (range = 10–71 years), and nine persons were female.

One bar attendee with COVID-19 reported the onset of a runny nose 2 days after the event and reported 26 close contacts at school during indoor sports practice and in-person school instruction. Two student athletes who were close contacts of this person subsequently received COVID-19 diagnoses 8 and 13 days after the event. Local health department officials were notified by a school official that the school district would close for 2 weeks beginning February 18 because 13 staff members were in isolation, in quarantine, or absent because their own child was quarantined.

One bar attendee who worked at an LTCF as a certified nursing assistant was asymptomatic and received a positive test result during routine COVID-19 testing at the facility 4 days after the event. After receipt of the positive test result, all LTCF residents and staff members in the facility were tested; three secondary cases (one in a staff member and two in residents) in persons who were close contacts of the bar attendee with COVID-19 were identified in the facility 5–9 days after the event. One resident with a secondary case was hospitalized on February 20, within 14 days of the positive test result, and was discharged the same day. None of the four persons in the LTCF with bar attendee or secondary COVID-19 had received a COVID-19 vaccination; all LTCF staff members and residents had been previously offered the vaccine.

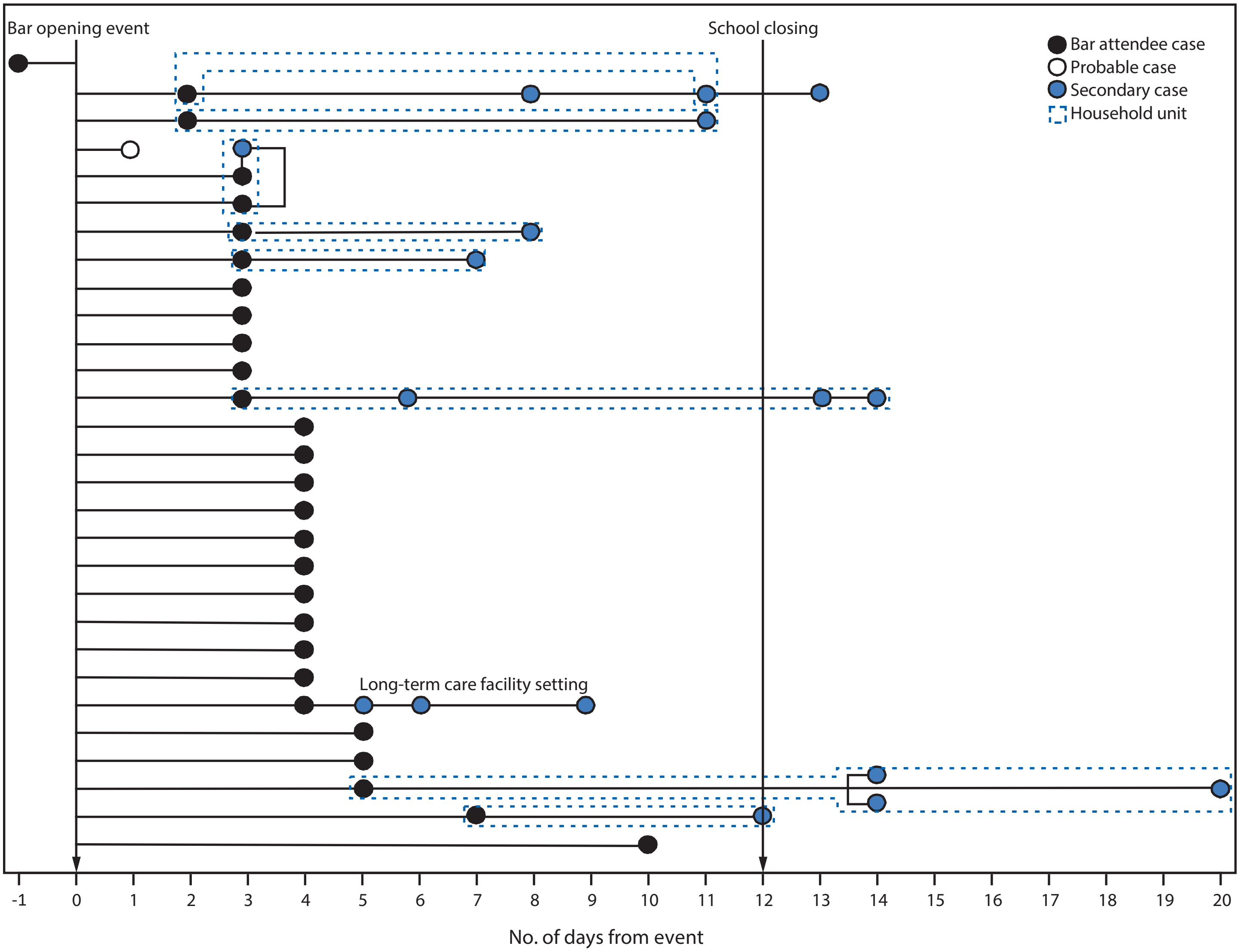
By February 26, 12 household contacts in eight different households had received positive SARS-CoV-2 test results, including five school-aged children. Local health department staff members interviewed household contacts to assess exposures. Secondary household cases were linked to nine (31.0%) of 29 bar attendee cases. Eleven persons were symptomatic, and cases were confirmed by NAAT or antigen testing. No household contacts with COVID-19 were hospitalized.

Discussion

An event held to celebrate a bar opening led to an outbreak among bar patrons and employees and was the likely source of subsequent COVID-19 transmission among household members, LTCF residents and staff members, and school athletes, leading to 46 cases, hospitalization of an LTCF resident, and a school closure affecting 650 children. Attendees included one person with an asymptomatic infection who received a COVID-19 diagnosis the day before the event and four symptomatic persons who subsequently received a COVID-19 diagnosis after the event. Asymptomatic persons are estimated to account for approximately 40%–45% of infections (*3*); the high percentage (82.6%) of symptomatic persons who were linked to the bar opening event suggests that the total number of cases in this outbreak was higher than reported and highlights the need for increased testing and reporting through contact tracing, in combination with isolation and quarantine, to promptly reduce transmission. As community businesses begin to reopen, these findings underscore the importance of businesses and individuals adhering to public health prevention and mitigation guidelines to reduce additional community transmission, including isolation after receipt of a COVID-19 diagnosis and while experiencing COVID-19–like symptoms, even as vaccination efforts expand.

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

FIGURE. Bar attendee* (N = 29) and secondary† (N = 17) confirmed§ and probable¶ COVID-19 cases associated with a local bar opening event, by timing of specimen collection relative to event — Illinois, February 2021



Abbreviation: NAAT = nucleic acid amplification test.

* Onset of COVID-19–like symptoms or receipt of a positive SARS-CoV-2 test result within 14 days of the bar opening event in a bar patron or employee who reported attending the event and who had no previous identified epidemiologic link to a COVID-19 case outside that setting.

† Positive SARS-CoV-2 NAAT or antigen test result received by a close contact of a person with an event-associated case.

§ Positive SARS-CoV-2 NAAT or antigen test result.

¶ COVID-19–like symptoms in a person with an epidemiologic link to the bar opening event but no laboratory confirmation of infection.

Similar gatherings that involve eating or drinking, such as on-premises dining at restaurants, weddings, and night clubs, have been associated with increased risk for acquiring COVID-19 and have the potential to become super-spreading events for SARS-CoV-2 infection (*4*–*8*). This investigation further demonstrates that inconsistent mask use and inadequate physical distancing in an indoor environment can increase transmission risk** (*9*,*10*). According to CDC's COVID-19 guidelines for restaurants and bars, reducing patron capacity, ensuring adequate room air ventilation, prioritizing outdoor seating, and promoting behaviors such as staying at home when ill, washing hands often, wearing masks, and maintaining physical distance are important strategies to reduce the spread of SARS-CoV-2 infection (*1*).

The findings in this report are subject to at least four limitations. First, interviews were voluntary, and many community members were reluctant to disclose contacts or additional details about themselves, including their occupation. Therefore, the number of cases described in this report is likely

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** https://www.medrxiv.org/content/10.1101/2020.04.04.20053058v1

TABLE. Number and percentage of COVID-19 cases (N = 46) associated with a local bar opening event, by demographic and clinical characteristics — Illinois, February 2021

Characteristic	No. (%)				
		Secondary cases			
	Bar attendee cases (N = 29)	Total (N = 17)	Household contacts (n = 12)	Long-term care facility contacts (n = 3)	School-related contacts (n = 2)
Classification					
Bar employee	3 (10.3)	NA	NA	NA	NA
Bar patron	26 (89.7)	NA	NA	NA	NA
Adult household contact	NA	7 (41.2)	7 (58.3)	NA	NA
School-aged child (aged 10–16 yrs) contact	NA	7 (41.2)	5 (41.7)	NA	2 (100)
LTCF staff member contact	NA	1 (5.9)	NA	1 (33.3)	NA
LTCF resident contact	NA	2 (11.8)	NA	2 (66.7)	NA
Case status					
Symptomatic confirmed*	24 (82.8)	13 (76.5)	11 (91.7)	1 (33.3)	1 (50.0)
Symptomatic probable†	1 (3.4)	0 (—)	0 (—)	0 (—)	0 (—)
Asymptomatic confirmed§	4 (13.8)	4 (23.5)	1 (8.3)	2 (66.7)	1 (50.0)
Hospitalized¶	0 (—)	1 (5.9)	0 (—)	1 (33.3)	0 (—)
Age group, yrs					
<18	0 (—)	7 (41.2)	5 (41.7)	0 (—)	2 (100)
18–44	22 (75.9)	4 (23.5)	3 (25.0)	1 (33.3)	0 (—)
45–54	5 (17.2)	1 (5.9)	1 (8.3)	0 (—)	0 (—)
55–64	2 (6.9)	3 (17.6)	3 (25.0)	0 (—)	0 (—)
≥65	0 (—)	2 (11.8)	0 (—)	2 (66.7)	0 (—)
Sex					
Male	19 (65.5)	8 (47.1)	5 (41.7)	1 (33.3)	2 (100)
Female	10 (34.5)	9 (52.9)	7 (58.3)	2 (66.7)	0 (—)
Race/Ethnicity**					
Hispanic/Latino	0 (—)	0 (—)	0 (—)	0 (—)	0 (—)
White, non-Hispanic	23 (79.3)	16 (94.1)	12 (100)	2 (66.7)	2 (100)
Black, non-Hispanic	0 (—)	0 (—)	0 (—)	0 (—)	0 (—)
Multiracial/Other race	0 (—)	0 (—)	0 (—)	0 (—)	0 (—)
Unknown	6 (20.7)	1 (5.9)	0 (—)	1 (33.3)	0 (—)

Abbreviations: LTCF = long-term care facility; NA = not applicable; NAAT = nucleic acid amplification test.

* Positive NAAT or antigen test result received by a symptomatic person.

† COVID-19–like symptoms in a person with an epidemiologic link to the bar opening event but no laboratory confirmation of infection.

§ Positive NAAT or antigen test result received by an asymptomatic person.

¶ Hospitalized within 14 days of the positive SARS-CoV-2 test result.

** Persons for whom ethnicity was missing or ethnicity was reported but race was missing were categorized as having unknown race/ethnicity.

lower than the actual number of bar attendee and secondary cases associated with the event. Second, it is unlikely that all asymptomatic cases were counted, and not all contacts were tested; therefore, some infected contacts might have been missed. Third, information on individual-level behaviors such as wearing masks and physical distancing was not collected from persons with cases. Finally, specimens were not available for whole genome sequencing; thus, the relationship among strains was not documented, and whether the increase in county-level incidence might be attributed to variants that spread more easily than the original SARS-CoV-2 strain cannot be determined.

Bars can play a role in community spread of COVID-19 because of limited mask use while eating or drinking and lack of consistent physical distancing. These findings show that SARS-CoV-2 transmission originating in a business such as a bar not only affects the patrons and employees of the bar but can also affect an entire community. As community businesses begin to reopen, considering additional prevention measures is important, such as limiting building occupancy levels and improving ventilation, especially in locations where consistent and correct mask wearing and physical distancing are difficult to enforce. Businesses can work with local health officials to promote behaviors and maintain environments that reduce the risk for SARS-CoV-2 transmission and develop strategies for reopening safely to prevent outbreaks in the community, such as modifying layouts and operating procedures (*1*).

Acknowledgments

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Summary

What is already known about this topic?

Gatherings in settings where mask wearing and physical distancing do not occur are known to increase the spread of COVID-19.

What is added by this report?

Forty-six cases of COVID-19 were linked to an indoor bar opening event that occurred during February 2021 in a rural Illinois county. Event patrons were linked to secondary cases among household, long-term care facility, and school contacts, resulting in one hospitalization and one school closure affecting 650 students.

What are the implications for public health practice?

Opening up settings such as bars, where mask wearing and physical distancing are challenging, can affect the community. As community businesses reopen, prevention measures should be emphasized, including limiting building occupancy, improving ventilation, prioritizing outdoor seating, enforcing correct mask wearing and physical distancing, staying home when ill, and encouraging COVID-19 vaccination to reduce transmission on site and within the community.

All authors have completed and submitted the International Committee of Medical Journal Editors form for disclosure of potential conflicts of interest. No potential conflicts of interest were disclosed.

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Notes from the Field

COVID-19 Case Investigation and Contact Tracing Program — Spirit Lake Tribe, North Dakota, September–November 2020

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In late September 2020, the incidence of confirmed COVID-19* in North Dakota began increasing rapidly, from approximately 300 new cases per day to approximately 2,260 cases on November 13, 2020 (*1*). On October 20, the North Dakota Department of Health reported that contact tracing notification efforts were delayed. Because of the delay, COVID-19 patients were asked to notify their own contacts about potential exposure and encourage them to seek testing for SARS-CoV-2, the virus that causes COVID-19 (*2*). The Spirit Lake sovereign nation in east central North Dakota is home to approximately 7,500 members of the Spirit Lake Tribe. In response to increasing incidence of COVID-19 on the Spirit Lake Reservation, CDC assisted the Spirit Lake Tribe in building a tribally managed program for comprehensive COVID-19 case investigations, case notification, contact tracing, contact testing, and contact management to ensure timely implementation of these critical epidemic control measures.

Through the Spirit Lake Tribe case investigation and contact tracing program, the tribe's COVID-19 Incident Command System staff members conducted case investigations and contact tracing, provided COVID-19 education, followed up with patients regularly by telephone, and monitored daily symptoms of close contacts. Members of the Spirit Lake community served as contact tracers. Symptom monitoring was facilitated through CDC's Text Illness Monitoring system (version TIM^2), using a free, two-way text-messaging platform to query enrolled contacts about daily COVID-19 symptoms. The system also alerted Spirit Lake Tribal Health authorities when participants reported symptoms or did not to respond (*3*). This report describes case investigation and contact tracing for the Spirit Lake Tribe during September 29, 2020 (when the case and contact tracing launched) through November 20, 2020 (when the CDC field response ended) and lessons learned from program implementation. This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.†

During September 29–November 20, data were retrieved by COVID-19 response team members from Spirit Lake Tribal Health's COVID-19 case and contact database, including patient demographics; links between COVID-19 patients and close contacts; test results; and symptom onset, isolation, and quarantine dates. Symptom data from Spirit Lake's TIM^2 monitoring system were analyzed to assess COVID-19 symptoms reported by close contacts of COVID-19 patients during October 22, (when TIM^2 use began for contact management) through November 30 (when the last close contact unit§ enrolled by November 20 completed quarantine).

During September 29–November 20, a total of 317 persons with confirmed COVID-19 and 667 close contacts among the Spirit Lake Tribe were reported; 129 (19.3%) of these close contacts received a subsequent COVID-19 diagnosis (Table). The average interval between specimen collection to receipt of a positive SARS-CoV-2 test result was 2.25 days (median = 3 days, range = 0–9 days). Overall, 254 (80.1%) of 317 patients with confirmed COVID-19 and 420 (78.1%) of 538 close contacts who did not receive a COVID-19 diagnosis were contacted by program staff members and instructed to isolate or quarantine within 24 hours of receipt of test results or identification of cases.¶ The proportion of confirmed new COVID-19 cases arising from known contacts was 41% (weekly range = 24%–59%).

During October 22–November 30, a total of 44 close contact units were enrolled in TIM^2, which logged 366 responses during 524 quarantine days (70% daily response rate). Among these 44 enrolled close contact units, 17 (39%) reported one or more persons with symptoms, 16 (94%) of whom were contacted within 24 hours and instructed to quarantine to prevent further transmission. A total of 20 persons from eight close contact units received a COVID-19 diagnosis. During the assessment period, the incidence of COVID-19 in the Spirit Lake Tribe plateaued at approximately 520–600 cases per 100,000 persons per week; during the same period, a 1.5-fold increase in incidence occurred in North Dakota, from 455 to 1,137 cases per 100,000 per week (*1*,*4*).

Implementation of a COVID-19 case investigation and contact tracing program for the Spirit Lake Tribe highlighted several important lessons. First, the program required daily, continuous staffing to effect timely COVID-19 mitigation. Second, obtaining information from and maintaining contact

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* The COVID-19 case definition followed CDC guidelines from September 2020. https://wwwn.cdc.gov/nndss/conditions/coronavirus-disease-2019-covid-19/case-definition/2020/08/05/

† 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.

§ Individual persons or family units sharing a phone number.

¶ Patients were instructed to isolate in accordance with CDC guidance at the time (https://www.cdc.gov/coronavirus/2019-ncov/hcp/duration-isolation.html), and close contacts were instructed to quarantine in accordance with CDC guidance at the time, which was 14 days after last exposure to a COVID-19 patient.

TABLE. Number of patients with confirmed COVID-19 and close contacts who did or did not receive a COVID-19 diagnosis — Spirit Lake Tribe, North Dakota, September 29–November 20, 2020*

Dates[†]	No. of patients with confirmed COVID-19 (% of cases from close contacts)[§]	Close contacts		
		No. who received a COVID-19 diagnosis (%)[§]	No. who did not receive a COVID-19 diagnosis[¶]	Total no.
September 29–October 2**	35 (20)	7 (10)	61	**68**
October 3–9	39 (59)	23 (23)	75	**98**
October 10–16	39 (41)	16 (18)	74	**90**
October 17–23[††]	40 (50)	20 (25)	60	**80**
October 24–30	40 (38)	15 (15)	88	**103**
October 31–November 6	42 (36)	15 (26)	43	**58**
November 7–13	37 (24)	9 (9)	88	**97**
November 14–20	45 (53)	24 (33)	49	**73**
Total	**317 (41)**	**129 (19)**	**538**	**667**

* These numbers might not include all patients or close contacts associated with the Spirit Lake Tribe because of limited sharing of health information among overlapping state, local, and tribal jurisdictions.

[†] The date used for confirmed COVID-19 patients was the date of receipt of a positive SARS-CoV-2 test result; for close contacts the date used was the date of identification as a close contact by a confirmed COVID-19 patient.

[§] Close contacts who received a COVID-19 diagnosis were included in the total number of patients with confirmed COVID-19 on the date that they received their positive test result. The percentage of cases among close contacts was calculated as the number of close contacts who received a COVID-19 diagnosis divided by the number of confirmed COVID-19 cases.

[¶] Included close contacts who received a negative SARS-CoV-2 test result, those who did not receive testing after exposure, and SARS-CoV-2 infections not reported to Spirit Lake Tribal Health and Spirit Lake Health Center.

** This week only contains 4 days to align with the assessed period (September 29–November).

[††] During this and all subsequent weeks, close contacts of confirmed COVID-19 patients were given the option to enroll in CDC's Text Illness Monitoring system (version TIM[2]) for daily symptom monitoring.

with COVID-19 patients and their close contacts was challenging. Using Spirit Lake community members as investigators and contact tracers aided in outreach because of their knowledge of alternate methods to reach patients or contacts (in-home or family contacts) when locating information was incomplete. These community members also helped to improve response rates about COVID-19 exposures because they were trusted by the community and were able to provide culturally appropriate advice about the need to isolate or quarantine. Third, shared rooms and living spaces among multigenerational families or within whole households with cases or exposures in this community often hindered within-home quarantine and isolation and adherence to these measures. To address this challenge, program staff members distributed critical supplies (e.g., groceries, over-the-counter medications, thermometers, personal protective equipment, and cleaning supplies) and health literacy information (about daily temperature logs, isolation and quarantine procedures, and mask use) to each household. Finally, approximately 100 (10%) persons identified through the case investigation and contact tracing program experienced homelessness or unstable housing during this period, necessitating the provision of temporary shelter and meals at a motel for these persons during isolation and quarantine.

Despite these challenges, this tribally managed COVID-19 case investigation and contact tracing program effectively reached Spirit Lake tribal members to provide isolation, quarantine, symptom monitoring, and support services and contributed to timely case and contact management. This program might help guide similar programs in other tribes and the public health community.

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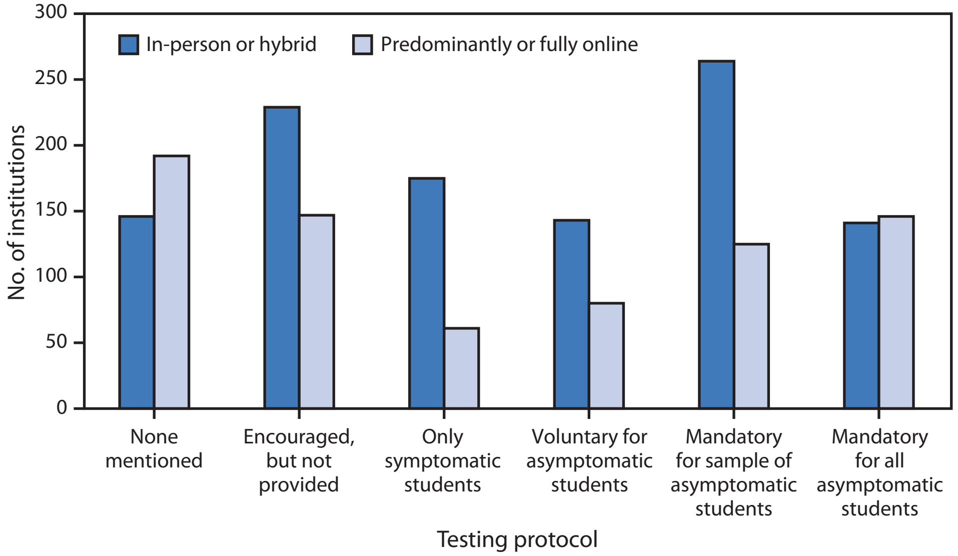
COVID-19 Stats

College and University* COVID-19 Student Testing Protocols,† by Mode of Instruction§ (N = 1,849) — United States, Spring 2021¶



* Includes 1,849 4-year, bachelor's degree-granting public and private, nonprofit colleges and universities with first-time, full-time undergraduate students as denoted in the National Center for Educational Statistics Integrated Postsecondary Education Data System (IPEDS); does not include 166 4-year institutions in IPEDS missing mode of instruction data, without clear modes of instruction, with specialized forms of instruction that do not clearly fit into a mode of instruction classification, or with no instruction of any kind for spring 2021.

† Institutions conducting mandatory testing for samples of asymptomatic students required periodic testing for various subgroups. The testing "encouraged, but not provided" category includes institutions requiring prearrival testing only, without provision of testing by the institutions themselves (symptomatic or asymptomatic).

§ Includes whether an institution's classes were predominantly or fully online (online), primarily or fully in-person (in-person), or some mix of the two (hybrid). Institutions were classified as "predominantly online" if the majority of classes were offered online, and hybrid when classes were offered with both in-person and online components. Mode of instruction refers to how classes were taught, not whether students were living on campus; 621 institutions conducting classes online allowed a limited number of students to live on campus.

¶ Data as of March 17, 2021. For institutions that did not announce a specific mode of instruction for spring 2021, the one for fall 2020 was assumed.

As of March 17, 2021, a total of 899 (49%) of 1,849 public and private, nonprofit 4-year U.S. colleges and universities provided some type of COVID-19 testing for asymptomatic students, including 548 (30%) institutions conducting classes in-person or in a hybrid format. Among institutions providing testing for asymptomatic students, 389 (43%) had protocols that required periodic testing for various subgroups (e.g., athletes, fraternity and sorority activity participants, and a random sample of students); 287 (32%) mandated that all students receive testing (ranging from every other day to once every other week), which did not vary by public or private, nonprofit status or by mode of instruction. Among institutions, 18% (338 of 1,849) did not mention a COVID-19 testing protocol on their websites, including146 with in-person or hybrid instruction. Although asymptomatic transmission is estimated to account for approximately one half of SARS-CoV-2 transmission, a majority (950; 51%) of institutions did not publish a testing protocol for screening asymptomatic students in spring 2021.

Source: Data from college and university websites collected by the College Crisis Initiative, Davidson College. https://www.collegecrisis.org

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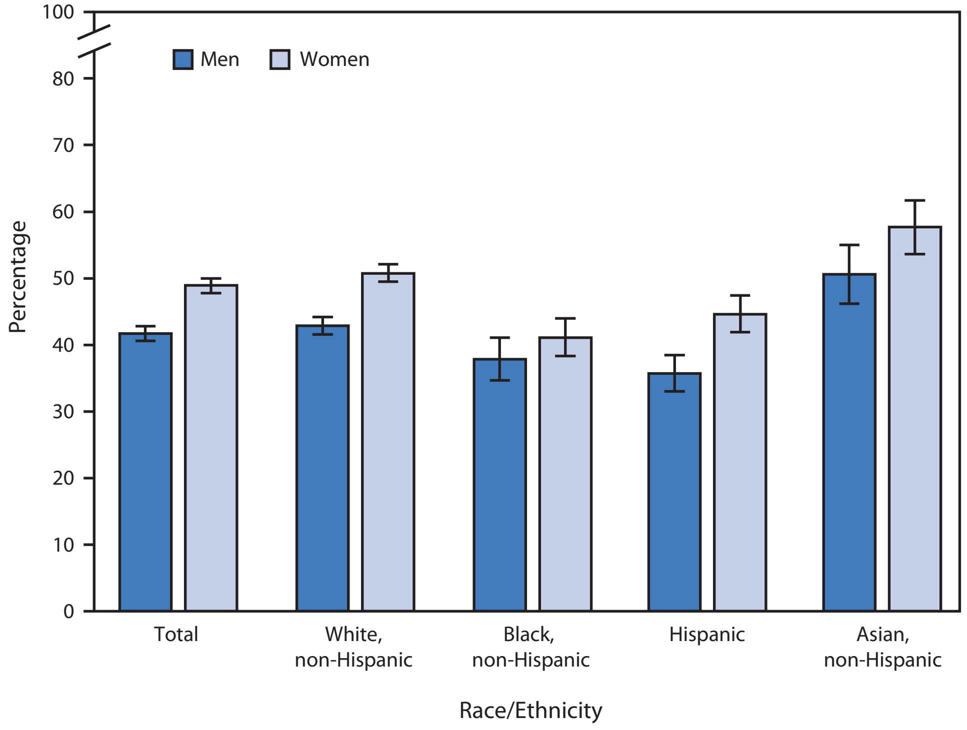
QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Age-Adjusted Percentage* of Adults Aged ≥18 Years Who Had an Influenza Vaccination in the Past 12 Months,† by Sex and Race/Ethnicity§ — National Health Interview Survey, United States, 2019¶



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* Age-adjusted percentages are based on the 2000 U.S. Census standard population, with 95% confidence intervals indicated by error bars.

† Based on an affirmative response to the question, "There are two types of flu vaccinations. One is a shot and the other is a spray, mist, or drop in the nose. During the past 12 months, have you had a flu vaccination?" Annual calendar-year estimates of vaccinations differ from seasonal influenza vaccination totals, which reflect vaccinations obtained during the influenza season.

§ Adults categorized as non-Hispanic White, non-Hispanic Black, and non-Hispanic Asian reported only one race; respondents had the option to select more than one racial group. Hispanic respondents might be of any race or combination of races. Total includes non-Hispanic adults of multiple or other races who are not shown separately.

¶ Estimates are based on household interviews of a sample of the civilian, noninstitutionalized U.S. population.

In 2019, women aged ≥18 years were more likely than were men (48.9% versus 41.7%) to have had an influenza vaccination in the past 12 months. This pattern was found for non-Hispanic White adults (50.8% versus 42.9%), Hispanic adults (44.6% versus 35.7%), and non-Hispanic Asian adults (57.7% versus 50.7%), but there was no statistically significant difference by sex among non-Hispanic Black adults (41.1% versus 37.9%). For both men and women, non-Hispanic Black and Hispanic adults were less likely to have had an influenza vaccination in the past 12 months than were non-Hispanic White and non-Hispanic Asian adults.

Source: National Center for Health Statistics, National Health Interview Survey, 2019. https://www.cdc.gov/nchs/nhis.htm

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