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Emergency Department Visits for Bicycle-Related Traumatic Brain Injuries Among Children and Adults — United States, 2009–2018

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Bicycling leads to the highest number of sport and recreation–related emergency department (ED) visits for traumatic brain injuries (TBIs) in the United States (*1*). Because bicycling continues to grow in popularity,* primarily among U.S. adults, examining the strategies that mitigate the risk for TBI is important. CDC analyzed data from the National Electronic Injury Surveillance System-All Injury Program (NEISS-AIP) to determine the incidence of EDs for bicycle-related TBIs during 2009–2018. An estimated 596,972 ED visits for bicycle-related TBIs occurred in the United States during the study period. Rates of ED visits were highest among adult males (aged ≥18 years) and among children and adolescents aged 10–14 years during 2009–2018. Overall, the rate of ED visits for bicycle-related TBIs decreased by approximately one half (48.7%) among children and by 5.5% among adults. As the number of persons riding bicycles increases, expansion of comprehensive bicycling safety interventions for bicyclists and drivers by states and local communities, such as interventions to increase driver compliance with traffic laws and helmet use among riders, improvements in bicycling infrastructure, and customized interventions for males and other groups at high risk might help reduce bicycle-related injuries.

NEISS-AIP, operated by the U.S. Consumer Product Safety Commission, contains annual data on patients treated in hospital EDs drawn from a nationally representative, stratified probability sample of hospitals,† and weighted by the inverse probability of selection to provide national estimates. This analysis included data on bicycling-related TBIs that occurred among adults aged ≥18 years and children and adolescents (children) aged ≤17 years during 2009–2018. A case was classified as a TBI if the primary body part injured was the head and the principal diagnosis was concussion or internal organ injury. Rates of bicycle-related TBIs per 100,000 population per year were calculated by using U.S. Census Bureau population estimates as the denominator, stratified by sex and age

*https://www.npd.com/wps/portal/npd/us/news/press-releases/2020/cycling-industry-sales-growth-accelerates-in-april/
†https://www.cpsc.gov/s3fs-public/2001d010-6b6.pdf

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group. Rates and 95% confidence intervals were calculated by using SAS (version 9.4; SAS Institute), accounting for sample weights and the complex survey design. Temporal trends were evaluated by applying the Joinpoint Regression Program (version 4.7.0.0; National Cancer Institute) to the annual rates. Annual percentage change was estimated for each trend segment and considered significantly different from zero for p-values <0.05. Findings were cross-validated by applying SAS complex survey software to the record-level data. This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.[§]

During the 10-year study period, an estimated 596,972 ED visits involved bicycle-related TBIs (Table); most of the patients who incurred a TBI (83%) were treated and released from the ED. The rate per 100,000 population of ED visits for bicycle-related TBIs during this time decreased by 27.7%, from 18.8 in 2009 to 13.6 in 2018. The rate decrease among children aged ≤17 years (48.7%) was ninefold larger than that among adults (5.5%). From 2013 to 2018, a large overall decline occurred, resulting in an annual −9.8% decline (Figure 1).

Across all study years, the rate per 100,000 population of ED visits for TBIs among children aged ≤17 years (32.7) was approximately twice that of adults (14.6) (Table). The rate per 100,000 population of ED visits for bicycle-related TBIs among children aged 10–14 years (44.6) was higher than that among children aged 0–4 years (15.3) and adults aged ≥18 years (14.6). Because of the limited sample size of adults, stratification by age group was not possible. The rate per 100,000 population of ED visits for bicycle-related TBIs was higher for males than for females overall (28.8 and 9.2, respectively). The estimated annual percentage change differed by sex and age group (Table) (Figure 1) (Figure 2).

Discussion

During 2009–2018, an estimated 596,972 ED visits occurred for bicycle-related TBIs in the United States. The ninefold difference in the decrease in bicycle-related TBI rates among children compared with that among adults during the study period might be associated with changes in the prevalence of bicycling (i.e., more adults bicycling, fewer children bicycling, and more bicyclists using roadways to commute to work) and with the implementation of evidence-based policies and interventions by state and local communities, many of which focus on children. The progressive decline in rates of bicycle-related TBIs that began in 2013 might be associated with increased awareness among parents about TBI and emerging research on the potential for long-term sequelae among children (*2*). Future studies should examine the reasons behind these recent improvements to help guide prevention efforts.

This study found only slight declines in the rate of ED visits for bicycle-related TBIs among adults, which is in contrast to

[§] 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.

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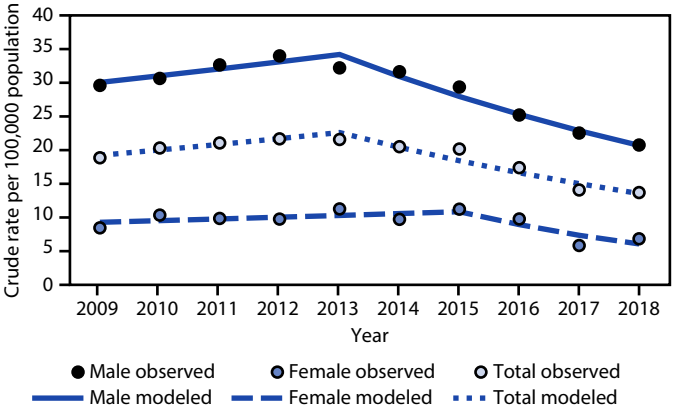
sharp declines in rates of bicycle-related injuries and deaths among children; however, bicycle-related deaths among adults have increased in recent years (*3*). In 2018, 857 adult bicyclists died from traffic-related crashes in the United States, the highest number in two decades (*3*). This discrepancy might indicate that bicycle safety interventions have had some effect on reducing some bicycle-related TBIs among adults, but more comprehensive strategies are needed to protect cyclists from death and the most severe types of injuries (*4*). Policies that recommend the use of bicycle helmets have achieved long-term sustained helmet use rates and a 20%–55% reduction in bicycle-related head injuries, including TBIs (*4*,*5*). However, bicycle helmets are not designed to prevent a concussion, which occurs after linear and rotational forces cause extreme brain movement inside the skull (*6*). To reduce injuries and deaths, a multipronged approach that includes programmatic, environmental, behavioral, and policy interventions not solely focused on bicycle helmets might be effective (*4*). Examples of promising strategies include building or improving roads with a focus on pedestrian and bicycling safety (e.g., adding physically protected bicycle lanes and intersections), increasing compliance with traffic laws (e.g., reducing distracted driving), and increasing active bicycle lighting (e.g., equipping bicycles with lights that a bicyclist can turn on) to increase visibility of cyclists in dark conditions.[¶]

During the study period, the rate of ED visits for bicycle-related TBIs among males of all ages was three times higher than that among females. A similar disparity was found in rates of bicycle-related deaths (*3*). Expanding bicycle safety policies and associated educational efforts that include customized messages for male children and adolescents and adult males

FIGURE 1. Trend in crude rates* of estimated bicycle-related traumatic brain injury emergency department visits, by sex† — National Electronic Injury Surveillance System-All Injury Program, United States, 2009–2018



Abbreviations: APC = annual percentage change; ED = emergency department.
* Crude rate per 100,000 population. Temporal trends were evaluated by applying the Joinpoint Regression Program to the annual rates. Findings were cross-validated by applying SAS complex survey software to the record-level data.
† APC estimates were considered significantly different from zero for p-values <0.05. The following APC values were statistically significant: male during 2009–2013 APC = 3.30% and during 2013–2018 APC = −9.61%; total APC = −9.80%, which represents a large decline in ED visits for bicycle-related traumatic brain injuries during 2013–2018.

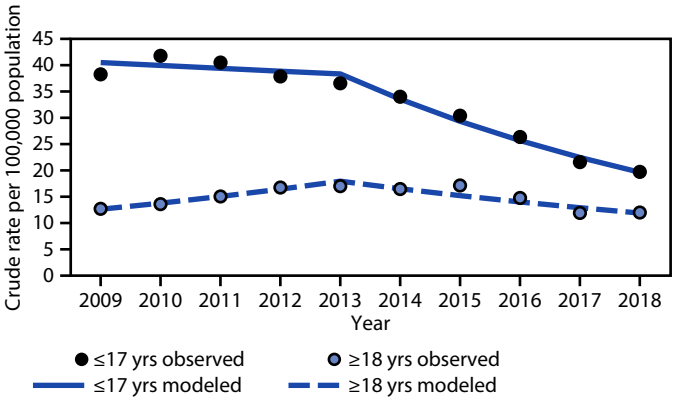
[¶] https://www.nhtsa.gov/sites/nhtsa.gov/files/documents/812478_countermeasures-that-work-a-highway-safety-countermeasures-guide-.pdf

TABLE. Estimated annual number and rate* of emergency department visits for all nonfatal bicycle-related traumatic brain injuries, by selected characteristics — National Electronic Injury Surveillance System–All Injury Program, United States, 2009–2018

Characteristic	2009		2018		2009–2018	
	No.† (%)	Rate (95% CI)	No.† (%)	Rate (95% CI)	No.† (%)	Rate (95% CI)
Age group, yrs						
0–17	28,343 (49.2)	38.2 (26.3–50.1)	14,403 (32.3)	19.6 (14.5–24.7)	**240,873 (40.3)**	**32.7 (25.2–40.1)**
0–4	2,797 (4.9)	13.8 (9.7–18.0)	986 (2.2)	—§	**30,614 (5.1)**	**15.3 (11.3–19.4)**
5–9	8,388 (14.6)	41.6 (25.0–58.1)	5,305 (11.9)	26.3 (17.1–35.5)	**71,763 (12.0)**	**35.2 (26.5–44.0)**
10–14	12,912 (22.4)	62.5 (43.2–81.8)	5,706 (12.8)	27.3 (18.5–36.2)	**92,316 (15.5)**	**44.6 (34.9–54.4)**
15–17	4,246 (7.4)	32.6 (15.7–49.4)	2,407 (5.4)	19.2 (11.2–27.3)	**46,180 (7.7)**	**36.4 (25.7–47.2)**
≥18	29,293 (50.8)	12.6 (5.9–19.3)	30,128 (67.7)	11.9 (6.7–17.0)	**355,869 (59.6)**	**14.6 (8.2–21.1)**
Sex						
Male	44,597 (77.4)	29.6 (18.5–40.6)	33,350 (74.9)	20.7 (13.3–28.1)	**448,719 (75.2)**	**28.8 (19.6–37.9)**
Female	13,038 (22.6)	8.4 (5.0–11.7)	11,181 (25.1)	6.7 (4.1–9.4)	**148,253 (24.8)**	**9.2 (5.9–12.5)**
Disposition						
Treated and released	48,534 (84.2)	15.8 (10.1–21.6)	36,356 (81.6)	11.1 (7.4–14.9)	**495,560 (83.0)**	**15.6 (10.7–20.6)**
Hospitalized/ Transferred	7,527 (13.1)	2.5 (1.1–3.8)	7,439 (16.7)	2.3 (1.2–3.4)	**83,231 (13.9)**	**2.6 (1.4–3.9)**
Other/Unknown	1,575 (2.7)	—§	736 (1.7)	—§	**18,181 (3.0)**	—§
Total†	**57,635 (100.0)**	**18.8 (11.8–25.7)**	**44,531 (100.0)**	**13.6 (8.8–18.4)**	**596,972 (100.0)**	**18.8 (12.7–24.9)**

Abbreviation: CI = confidence interval.
* Rate per 100,000 population.
† Numbers might not sum to totals because of rounding.
§ Estimates with coefficients of variation >30%, estimated annual number of <1,200, or an unweighted count of <20 are considered unstable, and resulting rates are not reported.

FIGURE 2. Trend in crude rates* of estimated bicycle-related traumatic brain injury emergency department visits, by age group† — National Electronic Injury Surveillance System-All Injury Program, United States, 2009–2018



Abbreviation: APC = annual percentage change.

* Crude rate per 100,000 population. Temporal trends were evaluated by applying the Joinpoint Regression Program to the annual rates. Findings were cross-validated by applying SAS complex survey software to the record-level data.

† APC estimates were considered significantly different from zero for p-values <0.05. The following APC values were statistically significant: children and adolescents aged ≤17 years during 2013–2018 APC = −12.57% and adults aged ≥18 years during 2009–2013 APC = 9.32% and 2013–2018 APC = −8.00%.

might be beneficial. Communities have had success using social marketing techniques to target bicycle injury prevention efforts to groups at risk (*7*). This might include targeted messages through media campaigns (e.g., use of social media platforms and signage in parks and public transit) about potential risk factors (e.g., distracted driving) and addressing known barriers (e.g., negative peer influence) to promote behavior change (*7*).

During the study period, most children and adults who visited an ED for a bicycle-related TBI were treated and released. Although many of these persons experienced a good recovery, some have experienced ongoing symptoms that have emotional, cognitive, behavioral, and academic sequelae (*8*). To reduce the risk for adverse outcomes, CDC has published guidelines for health care providers related to the care of children and adults with mild TBI.**

The findings in this report are subject to at least five limitations. First, rates of ED visits in this report likely underestimate actual rates of ED visits for bicycle-related TBIs. Many persons with TBI seek care in a primary care office or do not seek care at all (*9*). Second, because NEISS-AIP data included during the study period consisted of the principal diagnosis and primary body part recorded during the initial injury visit, some cases for which TBI was a secondary diagnosis might have been missed (such as skull fracture, which might indicate an underlying TBI). Third, this analysis did not examine differences by race/ethnicity or socioeconomic status, both of which are associated with limited bicycle safety infrastructures and an increased risk for bicycle-related injuries (*10*). Fourth, NEISS-AIP narrative descriptions do not provide detailed or consistent information about helmet use, injury circumstances (e.g., whether the injury occurred on a road or bicycle path), or about a person's level of exposure (e.g., how often a person rides a bicycle). Finally, the available data do not allow for assessment of whether any observed differences over time in the number of bicycle-related ED visits resulted from an actual change in incidence or other reasons, such as changes in care-seeking behaviors.

Bicycling provides an important opportunity for physical activity and is a popular commuting alternative that provides both health and environmental benefits.†† Such interventions as increased driver compliance with traffic laws and helmet use among riders, improvements in bicycling infrastructure, and customized interventions for males and other groups at high risk might help reduce bicycle-related injuries. Thus, expanding implementation of effective bicycle safety interventions can help ensure that children and adults are afforded the benefits of bicycling while staying safe from injuries, including TBIs.

Summary

What is already known about this topic?

Although most persons treated in an emergency department (ED) for a traumatic brain injury (TBI) have a good recovery, some might experience ongoing symptoms that have emotional, cognitive, behavioral, and academic sequelae.

What is added by this report?

During 2009–2018, an estimated 596,972 ED visits for bicycle-related TBIs occurred in the United States. The rate of ED visits for bicycle-related TBIs decreased by approximately one half among children and adolescents aged ≤17 years and by 5.5% among adults during this time. Rates were highest among adult males and children and adolescents aged 10–14 years.

What are the implications for public health practice?

Expanded implementation of comprehensive bicycling safety interventions (e.g., improving compliance with traffic laws, helmet use, and bicycling infrastructure) and targeted interventions might be beneficial.

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

†† https://www.thecommunityguide.org/findings/physical-activity-built-environment-approaches

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Prevalence of Inflammatory Bowel Disease Among Medicare Fee-For-Service Beneficiaries — United States, 2001–2018

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Inflammatory bowel disease (IBD), including Crohn's disease and ulcerative colitis, is characterized by chronic inflammation of the gastrointestinal tract. The number of affected persons worldwide has increased from 3.7 million in 1990 to 6.8 million in 2017 (*1*). The disease is more prevalent among non-Hispanic White persons than it is among persons in other racial/ethnic groups (*2*). As the prevalence increases with age group (*2*), it is important to understand the disease epidemiology among the older population. CDC analyzed 2018 Medicare data among beneficiaries aged ≥67 years to examine differences by demographic characteristics for both diseases and to assess trends of prevalence from 2001 through 2018 both overall and by race and ethnicity. In 2018, 0.40% and 0.64% of 25.1 million Medicare fee-for-service beneficiaries aged ≥67 years had received a diagnosis of either Crohn's disease or ulcerative colitis. Prevalence varied by age, sex, race and ethnicity, urban-rural residency, and state. During 2001–2018, the age-adjusted prevalence of both diseases increased (Crohn's disease annual percentage change [APC] = 3.4%, ulcerative colitis APC = 2.8%). The increase was higher among non-Hispanic Black persons (Crohn's disease APC = 5.0%, ulcerative colitis APC = 3.5%) than it was among non-Hispanic White, Hispanic, and Asian/Pacific Islander (A/PI) persons. Prevalence was consistently highest among non-Hispanic White persons for both diseases and lowest among A/PI persons for Crohn's disease. The study findings of increasing prevalence in all racial/ethnic groups among older adults, especially the higher rate of increase among certain racial/ethnic minority groups, underscore the importance for promoting health equity, guiding efforts to tailor disease management strategies for different populations, and continuing to monitor the temporal trends of the disease.

CDC examined data for U.S. adults aged ≥67 years who were continuously enrolled throughout a calendar year during 2001–2018 in Medicare parts A and B* and who were not enrolled in a health maintenance organization plan. This included 25.1 million beneficiaries in 2018 and ranged during 2001–2018 from 23.7 million persons in 2009 to 25.6 million in 2005. Study participants were identified by using *International Classification of Diseases, Clinical Modification* diagnosis codes from the ninth (ICD-9-CM) and, after October 1, 2015, the tenth (ICD-10-CM) revisions. Crohn's disease (ICD-9-CM: 555, ICD-10-CM: K50) and ulcerative colitis (ICD-9-CM: 556, ICD-10-CM: K51) were each identified by searching for any listed diagnosis code, including a 3-year look back, in Medicare part A data for at least one inpatient stay or in part B data for at least two claims with different dates. Beneficiaries with codes for both diseases were excluded (0.02% of all Medicare fee-for-service claims) to avoid possible disease misclassification. Variables included state of residence, age group (67–74, 75–84, and ≥85 years), sex, race/ethnicity (non-Hispanic White, non-Hispanic Black, Hispanic, non-Hispanic A/PI, and non-Hispanic American Indian/Alaska Native [AI/AN]), and urban-rural residency based on the National Center for Health Statistics 2013 classification scheme (large central metropolitan, large fringe metropolitan, medium metropolitan, small metropolitan, micropolitan, and noncore).† Prevalence estimates and 95% confidence intervals (CIs) were calculated overall and by demographic subgroups for 2018. Group differences were determined by z-test with the significance level set at 0.05. Prevalence estimates were age-adjusted§ when presented by state and for all trend analyses. For 2001–2018, annual prevalence was estimated overall and by race/ethnicity. Trends were assessed by using linear regression models weighted by inversed standard errors. An interaction term for race/ethnicity and year was included to assess the differences in trends between racial/ethnic groups. Analyses were performed by using SAS Enterprise Guide (version 7.1; SAS Institute).

In 2018, 0.40% and 0.64% of Medicare fee-for-service beneficiaries aged ≥67 years had received a diagnosis of either Crohn's disease or ulcerative colitis (Table). The prevalence of Crohn's disease was higher among younger beneficiaries, highest among non-Hispanic White persons, and lowest among non-Hispanic A/PI persons. The prevalence of ulcerative colitis was highest among beneficiaries aged 75–84 years and among non-Hispanic White persons. For both diseases, prevalence estimates were higher among women than they were among men. Estimates for both diseases were highest among persons in

* https://resdac.org/cms-data/files/medpar; https://resdac.org/cms-data/files/carrier-ffs; https://www.resdac.org/cms-data/files/op-ffs

† https://www.cdc.gov/nchs/data/series/sr_02/sr02_166.pdf

§ Direct age adjustment according to 2000 U.S. Census population (https://data.census.gov/cedsci/table?t=Age%20and%20Sex&y=2000&d=DEC%20Summary%20File%201&tid=DECENNIALSF12000.PCT012&hidePreview=false) based on three age groups (67–74, 75–84, and ≥85 years).

TABLE. Prevalence of Crohn's disease and ulcerative colitis among 25.1 million Medicare fee-for-service beneficiaries,* by age group, sex, race/ethnicity, and urban-rural residency — United States, 2018

Characteristic	Crohn's disease,† % (95% CI)	Ulcerative colitis,§ % (95% CI)
No.	**99,665**	**161,494**
Crude rate	0.40 (0.40–0.40)	0.64 (0.64–0.65)
Age-adjusted¶	0.40 (0.40–0.40)	0.65 (0.64–0.65)
Age group, yrs		
67–74	0.42 (0.41–0.42)	0.60 (0.60–0.61)
75–84	0.41 (0.41–0.42)	0.70 (0.69–0.71)
≥85	0.32 (0.31–0.32)	0.65 (0.64–0.65)
Sex		
Male	0.36 (0.36–0.36)	0.61 (0.60–0.61)
Female	0.43 (0.43–0.43)	0.68 (0.67–0.68)
Race/Ethnicity		
White, non-Hispanic	0.43 (0.43–0.43)	0.69 (0.69–0.69)
Black, non-Hispanic	0.26 (0.25–0.27)	0.41 (0.40–0.42)
Hispanic	0.19 (0.18–0.20)	0.43 (0.42–0.44)
Asian/Pacific Islander, non-Hispanic	0.15 (0.14–0.15)	0.37 (0.36–0.38)
American Indian/Alaska Native, non-Hispanic	0.23 (0.20–0.26)	0.40 (0.36–0.43)
Urban-rural residency**		
Large central metropolitan	0.39 (0.38–0.39)	0.68 (0.67–0.69)
Large fringe metropolitan	0.46 (0.45–0.46)	0.76 (0.76–0.77)
Medium metropolitan	0.40 (0.40–0.41)	0.63 (0.62–0.63)
Small metropolitan	0.38 (0.37–0.39)	0.60 (0.59–0.61)
Micropolitan	0.36 (0.35–0.37)	0.54 (0.54–0.55)
Noncore	0.33 (0.32–0.34)	0.49 (0.48–0.50)

Abbreviation: CI = confidence interval.

* The estimated number of Medicare-eligible fee-for-service enrollees aged ≥67 years in 2017 was 25,069,000.

† *International Classification of Diseases, Tenth Revision, Clinical Modification* diagnosis code K50.

§ *International Classification of Diseases, Tenth Revision, Clinical Modification* diagnosis code K51.

¶ Age-adjusted to the 2000 U.S. Census population aged ≥67 years based on three age groups (67–74, 75–84, and ≥85 years). https://data.census.gov/cedsci/table?t=Age%20and%20Sex&y=2000&d=DEC%20Summary%20File%201&tid=DECENNIALSF12000.PCT012&hidePreview=false

** Based on the 2013 National Center for Health Statistics urban-rural classification scheme for counties. https://www.cdc.gov/nchs/data/series/sr_02/sr02_166.pdf

large fringe metropolitan counties, second lowest among those in micropolitan counties, and lowest among those in noncore counties. Age-adjusted state-level prevalence estimates ranged from 0.17% (Hawaii) to 0.62% (Rhode Island) for Crohn's disease and from 0.37% (Hawaii) to 0.91% (New Jersey) for ulcerative colitis. States with a higher prevalence of both diseases were generally concentrated in the Northeast (Figure 1).

During 2001–2018, the overall prevalence of Crohn's disease increased (APC = 3.4%, 95% CI = 3.2%–3.7%), as did the overall prevalence of ulcerative colitis (APC = 2.8%, 95% CI = 2.6%–3.0%) (Figure 2). The rate of increase was highest among non-Hispanic Black persons (APC = 5.0% for Crohn's disease and 3.5% for ulcerative colitis) than it was among non-Hispanic White, Hispanic, and A/PI persons (APC range = 2.7%–3.5% for Crohn's disease and 1.8%–2.9% for ulcerative colitis) (Figure 2). Prevalence estimates for both diseases were consistently highest among non-Hispanic White persons. The estimated prevalence of Crohn's disease was consistently lowest among non-Hispanic A/PI persons. The estimated prevalence of ulcerative colitis was consistently higher among Hispanic persons than it was among members of other racial and ethnic minority groups.

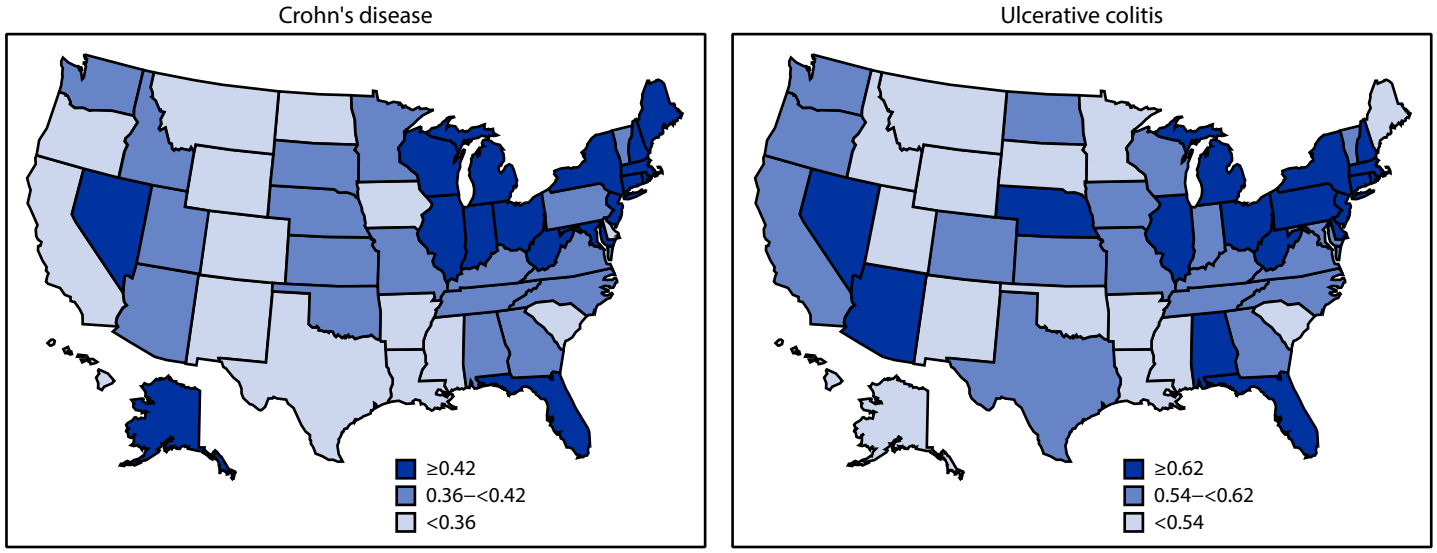
Discussion

During 2001–2018, the overall estimated prevalence of Crohn's disease and ulcerative colitis among Medicare fee-for-service beneficiaries increased. These trends are consistent with those observed worldwide (*1*). Prevalence of both diseases was consistently highest among non-Hispanic White persons. However, the annual percentage increase in prevalence of ulcerative colitis was highest among non-Hispanic Black persons, and the increase in prevalence for Crohn's disease was higher among non-Hispanic Black persons and among AI/AN persons than it was among non-Hispanic White persons. The potential rapid increase of disease prevalence in certain racial and ethnic minority groups indicates the need for tailored disease management strategies in these populations.

Racial/ethnic disparities have been noted in health care access, quality, and outcomes of patients with IBD (*3*). For example, hospitalization and mortality rates were higher among non-Hispanic Black patients than they were among non-Hispanic White patients. Non-Hispanic Black patients were more likely to have severe disease activity and were less likely to maintain medical therapy for IBD or to undergo surgery (*3*). Health literacy about IBD was also lower among non-Hispanic Black persons and Hispanic persons than it was among non-Hispanic White persons (*3*). These findings could help researchers understand racial/ethnic disparities in timing of diagnosis, health care access and use, and health literacy to promote health equity for IBD management in racial and ethnic minority groups.

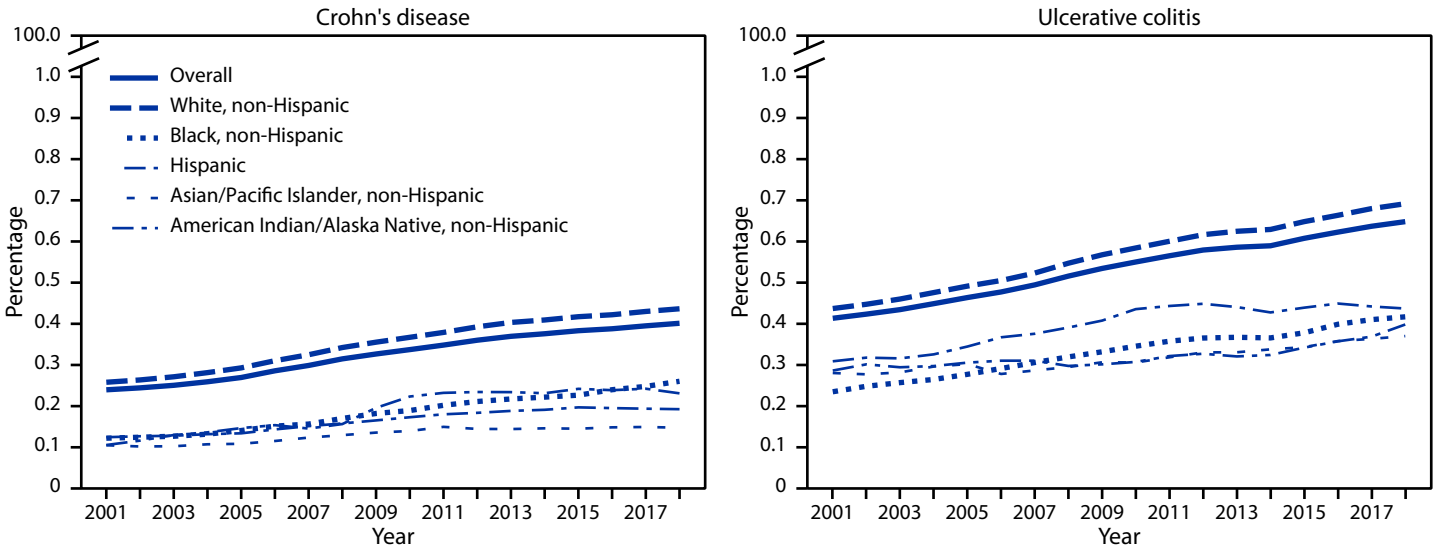
Although the incidence of IBD peaks at approximately age 15–29 years (*4*), 10%–15% of new diagnoses occur among adults aged ≥60 years (*5*). Because overall mortality among patients with IBD is similar to that among the general U.S. population (*6*), prevalence is expected to increase as the U.S. population ages. In addition, the evolving therapeutic paradigm and more advanced diagnostic tools to detect the disease might also contribute to the increasing prevalence trends (*1*). The rise in prevalence could impose substantial financial costs on the health care system (*1*). Patients with IBD are at risk for impaired quality of life (*7*) because of the complexity of this lifelong disease, the potential adverse effects of treatment, and

FIGURE 1. Age-adjusted prevalence*,† of Crohn's disease and ulcerative colitis among 25.1 million Medicare fee-for-service beneficiaries — United States, 2018



* Age-adjusted to the 2000 U.S. Census population aged ≥67 years based on three age groups (67–74, 75–84, and ≥85 years). https://data.census.gov/cedsci/table?t=Age%20and%20Sex&y=2000&d=DEC%20Summary%20File%201&tid=DECENNIALSF12000.PCT012&hidePreview=false
† State-level age-adjusted prevalence estimate (%) was categorized into tertiles.

FIGURE 2. Age-adjusted prevalence*,† of Crohn's disease and ulcerative colitis among Medicare fee-for-service beneficiaries — United States, 2001–2018§



Abbreviation: APC = annual percentage change.
* Age-adjusted to the 2000 U.S. Census population aged ≥67 years based on three age groups (67–74, 75–84, and ≥85 years). https://data.census.gov/cedsci/table?t=Age%20and%20Sex&y=2000&d=DEC%20Summary%20File%201&tid=DECENNIALSF12000.PCT012&hidePreview=false
† Trends in age-adjusted prevalence estimates were assessed in linear regressions weighted with the estimates-associated inversed standard errors. The estimated prevalence was natural logarithm transformed. For Crohn's disease, APC = 3.4% for overall, 3.5% for non-Hispanic White persons, 5.0% for non-Hispanic Black persons, 3.2% for Hispanic persons, 2.7% for Asian/Pacific Islander persons, and 5.3% for American Indian/Alaska Native persons. For ulcerative colitis, APC = 2.8% for overall, 2.9% for non-Hispanic White persons, 3.5% for non-Hispanic Black persons, 2.5% for Hispanic persons, 1.8% for Asian/Pacific Islander persons, and 1.5% for American Indian/Alaska Native persons. All were statistically significant ($p<0.001$).
§ The conversion from the *International Classification of Diseases, Ninth Revision* diagnosis codes to the *International Classification of Diseases, Tenth Revision* diagnosis codes occurred on October 1, 2015.

Summary

What is already known about this topic?

Inflammatory bowel disease (IBD) prevalence is higher among non-Hispanic White persons than it is among persons in other racial/ethnic groups.

What is added by this report?

In 2018, 0.40% and 0.64% of 25.1 million Medicare fee-for-service beneficiaries aged ≥67 years had received a diagnosis of Crohn's disease or ulcerative colitis. From 2001 to 2018, the age-adjusted prevalence of IBD increased among all racial/ethnic groups; the highest annual percentage increase was among non-Hispanic Black persons.

What are the implications for public health practice?

The study findings of increasing prevalence among older adults across all racial/ethnic groups, especially the higher rate of increase among certain racial and ethnic minority groups, underscore the importance for promoting health equity, guiding efforts to tailor disease management strategies for different populations, and continuing to monitor the temporal trends of the disease.

the fact that they tend to have more comorbidities than do patients without IBD (*2*), especially as they age.

The higher prevalence of IBD that was observed in women and in states in the Northeast region is consistent with a previous study (*8*). In addition, the current study found that the prevalence estimates of both diseases generally increased with a higher degree of urbanization. Living in urban areas, especially during early life, might be associated with risk for IBD through effects on the microbiome by factors such as pollution, diet, or lifestyle (*9*). The higher prevalence in large fringe metropolitan counties compared with large central metropolitan counties might be explained by the higher percentage of non-Hispanic White persons in large fringe metropolitan counties (*10*).

The findings in the report are subject to at least three limitations. First, Medicare data are collected for insurance reimbursement purposes. Therefore, certain socioeconomic measures, such as income and education, could not be assessed. Second, diagnosis codes related to Crohn's disease or ulcerative colitis might be subject to coding errors. Finally, the study population was limited to Medicare fee-for-service beneficiaries (67% of all Medicare beneficiaries), and the findings might not be generalizable to all older adults in the United States.

Despite the limitations, Medicare data are a useful resource to monitor prevalence of IBD over time, understand its prevalence among older adults, assess differences by demographic and geographic characteristics, and have rich information to study health care use. Understanding temporal trends, especially the rate of increase among certain racial and ethnic minority groups, is important for resource planning and efforts to reduce health disparities. For optimal disease management, older adults of all races and ethnicities who have IBD should have routine doctor visits, adhere to a medication regimen, receive recommended preventive care, and adopt a healthy lifestyle, such as eating a well-balanced diet and quitting smoking for those who currently smoke.¶

¶ https://www.cdc.gov/dotw/ibd/index.html

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Diagnostic Performance of an Antigen Test with RT-PCR for the Detection of SARS-CoV-2 in a Hospital Setting — Los Angeles County, California, June–August 2020

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Prompt and accurate detection of SARS-CoV-2, the virus that causes COVID-19, has been important during public health responses for containing the spread of COVID-19, including in hospital settings (*1*–*3*). In vitro diagnostic nucleic acid amplification tests (NAAT), such as real-time reverse transcription–polymerase chain reaction (RT-PCR) can be expensive, have relatively long turnaround times, and require experienced laboratory personnel.* Antigen detection tests can be rapidly and more easily performed and are less expensive. The performance† of antigen detection tests, compared with that of NAATs, is an area of interest for the rapid diagnosis of SARS-CoV-2 infection. The Quidel Sofia 2 SARS Antigen Fluorescent Immunoassay (FIA) (Quidel Corporation) received Food and Drug Administration Emergency Use Authorization for use in symptomatic patients within 5 days of symptom onset (*4*). The reported test positive percentage agreement§ between this test and an RT-PCR test result is 96.7% (95% confidence interval [CI] = 83.3%–99.4%), and the negative percentage agreement is 100.0% (95% CI = 97.9%–100.0%) in symptomatic patients.¶ However, performance in asymptomatic persons in a university setting has shown lower sensitivity (*5*); assessment of performance in a clinical setting is ongoing. Data collected during June 30–August 31, 2020, were analyzed to compare antigen test performance with that of RT-PCR in a hospital setting. Among 1,732 paired samples from asymptomatic patients, the antigen test sensitivity was 60.5%, and specificity was 99.5% when compared with RT-PCR. Among 307 symptomatic persons, sensitivity and specificity were 72.1% and 98.7%, respectively. Health care providers must remain aware of the lower sensitivity of this test among asymptomatic and symptomatic persons and consider confirmatory NAAT testing in high-prevalence settings because a false-negative result might lead to failures in infection control and prevention practices and cause delays in diagnosis, isolation, and treatment.

During a period of high community COVID-19 prevalence,** the Los Angeles County Department of Public Health collaborated with hospital A, a tertiary medical center serving a large urban population in central Los Angeles, to evaluate the performance of the Quidel Sofia 2 SARS Antigen FIA (antigen test) compared with that of the Fulgent COVID-19 RT-PCR (Fulgent Genetics) (RT-PCR test) for screening of all patients admitted to the hospital through the ED during June 30–August 31. Admitting orders included requests for both tests to enable prompt inpatient cohorting. Each admitted patient had two simultaneously collected samples for SARS-CoV2 testing by ED nursing staff members: an anterior nasal swab successively swabbing both nostrils with one swab and a nasopharyngeal swab. Nasopharyngeal swab specimens were processed and sent by courier to a Clinical Laboratory Improvement Amendments–certified laboratory for RT-PCR testing. Results were available 24–48 hours after specimen collection. Test cycle threshold (Ct) values for N1 and N2 nucleocapsid viral gene targets were reported. N1 and N2 targets with Ct values <40 were used to define a positive RT-PCR result, per manufacturer instructions.†† Because differences between N1 and N2 targets were negligible, for this analysis, N1 target Ct values were used. The anterior nasal swab specimens were processed for antigen testing using calibrated Sofia 2 analyzers in the ED.

The RT-PCR test was used as the standard. Results were considered concordant if they were positive for both tests or negative for both, and discordant if one was positive and the other was negative. Persons were categorized as having COVID-19–compatible symptoms if they had a temperature ≥100.4°F (38°C) at triage, or reported respiratory distress, shortness of breath, cough, flu-like symptoms, nausea, vomiting, diarrhea, or headache. Signs and symptoms (ED chief complaints and vital signs) were categorized into those more commonly reported by COVID-19 patients (*6*) (i.e., fever, respiratory distress or shortness of breath, and cough) and those less commonly reported (i.e., flu-like symptoms, nausea or vomiting, diarrhea, and headache). Symptoms were retrospectively ascertained through medical record abstraction

* https://www.medrxiv.org/content/10.1101/2020.06.22.20136309v3

† Test performance includes sensitivity, specificity, positive predictive values, and negative predictive value.

§ The estimate for positive percentage agreement and negative percentage agreement is used in place of sensitivity in the absence of a reference standard test for comparison.

¶ https://www.quidel.com/sites/default/files/product/documents/EF1438905EN00.pdf

** http://dashboard.publichealth.lacounty.gov/covid19_surveillance_dashboard/

†† https://www.fda.gov/media/138150/download

using the ED triage assessment. Hospital service codes and vital signs were evaluated for patients without an ED chief complaint. Patients who went to a non-ED location (e.g., labor and delivery), might not have an ED chief complaint and were classified as asymptomatic for this analysis. Additional information regarding symptoms was obtained from the hospital's electronic medical records system for patients with discordant antigen and RT-PCR test results.

Data were managed and analyzed using SAS software (version 9.4; SAS Institute). Sensitivity, specificity, negative predictive value, and positive predictive value were calculated for antigen testing and compared with those of RT-PCR. N1 Ct values for antigen-positive and antigen-negative symptomatic and asymptomatic groups were compared using t-tests; p-values <0.05 were considered statistically significant. Signs and symptoms, demographic characteristics, and underlying medical conditions for the group of patients with discordant results were compared using chi-square or Fisher's exact tests. Odds ratios were calculated for each of the more common or less common symptoms and overall. This investigation was reviewed by the Los Angeles County Institutional Review Board and CDC and was conducted consistent with applicable federal law and CDC policy.[§§]

During June 30–August 31, hospital A tested 2,039 patients admitted through the ED with paired antigen and RT-PCR tests. Median patient age was 56 years (range = 16–107 years); 1,126 (55%) were female, and 913 (45%) were male. The mean test turnaround time for RT-PCR was 28.2 hours. Overall, 307 (15%) patients had COVID-19–compatible symptoms (Table 1). Among the 307 symptomatic patients, 120 (39%) had a positive test result by either test, including 52 (17%) by antigen and 68 (22%) by RT-PCR. Positive test result by both the antigen and the RT-PCR tests were reported for 49 (16%) patients. Mean N1 Ct values were significantly lower among patients with a positive antigen result (mean Ct = 21.3) than among patients with a negative antigen result (mean Ct = 28.5; p<0.001).

Among the 1,732 asymptomatic patients, 139 (8%) had a positive test result by either test (58 [3%] by antigen and 81 [5%] by RT-PCR). Mean N1 Ct values did not differ significantly between samples from patients who were symptomatic (mean Ct = 23.5) and those who were asymptomatic (mean Ct = 23.9). Among asymptomatic and symptomatic patients, the specificity of the antigen test was 99.5% and 98.7%, respectively, and the sensitivity was 60.5% and 72.1%, respectively. The diagnostic performance between the two groups did not differ significantly, with the exception of negative predictive value (p<0.001). Sensitivity of the discordant antigen test results from patients who were symptomatic and asymptomatic was assessed across a range of Ct values. Antigen test sensitivity increased in symptomatic and asymptomatic persons as N1 Ct values decreased (sensitivity 75% for Ct ≤30 and sensitivity 90.7% for Ct ≤25).

RT-PCR–positive and antigen-positive test results were compared with patients' signs and symptoms at the time of admission. Symptoms associated with a positive RT-PCR test result included fever, respiratory distress or shortness of breath, cough, and flu-like symptoms (Table 2). Shortness of breath was the most commonly reported symptom among persons with a positive RT-PCR test result (28%) and among both discordant groups (RT-PCR–positive/antigen-negative = 39%; RT-PCR–negative/antigen-positive = five of 12 patients) (Table 3). No COVID-19–compatible symptoms occurred in 27 (53%) patients with RT-PCR positive/antigen-negative test results and six of 12 patients with RT-PCR negative/antigen-positive test results. Some patients with RT-PCR–positive/antigen-negative test results had underlying medical conditions recorded in medical records (10% reporting having diabetes and 18% having hypertension) and were at higher risk for severe COVID-19–associated illness.[¶¶]

[§§] 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.

[¶¶] https://www.cdc.gov/coronavirus/2019-ncov/need-extra-precautions/people-with-medical-conditions.html

TABLE 1. Characteristics* of the Quidel Sofia 2 SARS Antigen Fluorescent Immunoassay test among symptomatic and asymptomatic persons admitted to a tertiary medical center through the emergency department (N = 2,039) — Los Angeles County, California, June 30–August 31, 2020

Test diagnostic characteristic	All patients (N = 2,039)	Symptomatic patients (n = 307)	Asymptomatic patients (n = 1,732)	p-value†
Positive RT-PCR test results, no. (%)	149 (7.3)	68 (22.2)	81 (4.7)	—
Positive antigen test results, no. (%)§	110 (5.4)	52 (16.9)	58 (3.4)	—
Sensitivity of antigen test, % (95% CI)	65.8 (57.6–73.3)	72.1 (61.4–82.7)	60.5 (49.9–71.1)	0.16
Specificity of antigen test, % (95% CI)	99.4 (98.9–99.7)	98.7 (97.3–100.0)	99.5 (99.1–99.8)	0.19
Positive predictive value of antigen test, % (95% CI)	89.1 (81.7–94.2)	94.2 (87.9–100.0)	83.0 (75.2–93.8)	0.13
Negative predictive value of antigen test, % (95% CI)	97.4 (96.5–98.0)	92.6 (89.3–95.8)	98.1 (97.4–98.7)	<0.001

Abbreviations: CI = confidence interval; RT-PCR = reverse transcription–polymerase chain reaction.

* Quidel Sofia 2 SARS Antigen Fluorescent Immunoassay test characteristics (sensitivity, specificity, positive predictive value, and negative predictive value) were based on comparison with the Fulgent COVID-19 RT-PCR test.

† Chi-square and Fisher's exact p-value comparing symptomatic patients with asymptomatic patients.

§ At hospital A, the Quidel Sofia 2 SARS Antigen Fluorescent Immunoassay was used for qualitative detection of nucleocapsid protein from SARS-CoV-2.

TABLE 2. Frequency and odds ratios for RT-PCR–positive results among patients admitted to hospital through a tertiary medical center emergency department, by chief complaint (N = 1,667)* — Los Angeles County, California, June 30–August 31, 2020

Patient's chief complaint	No. (%) RT-PCR–positive results (n = 138)	No. (%) RT-PCR–negative results (n = 1,529)	OR (95% CI) for RT-PCR–positive results†
More common COVID-19–like signs and symptoms			
Fever/Chills	11 (8.0)	31 (2.0)	4.2 (2.1–8.5)
Respiratory distress/Shortness of breath	39 (28.0)	150 (10.0)	4.1 (2.8–6.1)
Cough	6 (4.0)	8 (0.5)	9.9 (3.4–28.8)
Less common signs and symptoms			
Flu-like symptoms	10 (7.0)	5 (0.3)	27.1 (9.1–80.6)
Nausea/Vomiting	1 (0.7)	29 (2.0)	0.4 (0.1–3.2)
Diarrhea	1 (0.7)	5 (0.3)	2.5 (0.3–21.9)
Headache	0 (—)	11 (0.7)	0 (—)
Met case definition§	68 (49.0)	239 (16.0)	5.2 (3.7–7.5)

Abbreviations: CI = confidence interval; OR = odds ratio; RT-PCR = reverse transcription–polymerase chain reaction.
* 372 patients (11 RT-PCR–positive and 361 RT-PCR–negative) with missing emergency department chief complaint data were excluded.
† Among patients with and without symptoms.
§ Case was defined as symptomatic if patient had a chief complaint of more common or less common COVID-19–compatible signs and symptoms.

TABLE 3. Characteristics of patients admitted to hospital through a tertiary medical center emergency department with discordant SARS-CoV-2 antigen and RT-PCR test results* (N = 63)† — Los Angeles County, California, June 30–August 31, 2020

Discordant group characteristic	No. (%) RT-PCR–positive§/Antigen-negative (n = 51)	No. (%) RT-PCR–negative/Antigen-positive¶ (n = 12)	Total (N = 63)
Signs and symptoms at emergency department admission			
Fever/Chills	18 (35)	1 (8)	**19 (30)**
Cough	15 (29)	0 (0)	**15 (24)**
Shortness of breath	20 (39)	5 (42)	**25 (40)**
Fatigue	6 (12)	0 (—)	**6 (10)**
Muscle aches	9 (18)	0 (—)	**9 (14)**
Headache	0 (0)	1 (8)	**1 (2)**
Loss of taste or smell	1 (2)	1 (8)	**2 (3)**
Sore throat	3 (6)	0 (—)	**3 (5)**
Congestion	5 (9)	0 (—)	**5 (8)**
Nausea/Vomiting	7 (13)	1 (8)	**8 (13)**
Diarrhea	5 (10)	0 (—)	**5 (8)**
No symptoms**	27 (53)	6 (50)	—
Temperature >100.4°F (38°C)	5 (10)	5 (42)	**5 (8)**
Demographic characteristic			
Sex			
Female	25 (49)	8 (67)	**35 (56)**
Male	24 (47)	4 (33)	**28 (44)**
Race††			
Asian	7	5	**12**
White	6	—	**6**
Black	3	1	**4**
Other	32	6	**41**
Unknown	6	—	—
Age, yrs, mean (range)	59 (20–98)	67 (28–100)	**60 (21–100)**
Underlying medical condition			
Diabetes	5 (10)	1 (8)	**6 (10)**
Obesity	2 (4)	0 (—)	**2 (3)**
Hypertension	9 (18)	2 (17)	**11 (18)**
Heart disease	2 (4)	3 (25)	**5 (8)**

Abbreviation: RT-PCR = reverse transcription–polymerase chain reaction.
* False negative = antigen-negative and RT-PCR–positive; false positive = antigen-positive and RT-PCR–negative.
† 2,039 patients admitted through the emergency department were tested with paired SARS-CoV-2 antigen and RT-PCR tests.
§ The Fulgent COVID-19 by RT-PCR test, a real-time RT-PCR test intended for the qualitative detection of nucleic acid from SARS-CoV-2 in upper and lower respiratory specimens, was used.
¶ The Quidel Sofia 2 SARS Antigen Fluorescent Immunoassay was used for qualitative detection of the SARS-CoV-2 nucleocapsid protein.
** No symptoms identified through individual medical chart abstraction.
†† Ethnicity data were not collected for this analysis.

Summary

What is already known about this topic?

Prompt and accurate diagnosis of SARS-CoV-2 infection is critical to containing the spread of COVID-19 in a hospital setting.

What is added by this report?

The Quidel rapid antigen test had lower sensitivity in both asymptomatic (60.5%) and symptomatic (72.1%) patients but a high specificity (98.7% and 99.5% for symptomatic and asymptomatic patients, respectively) when compared with the reverse transcription–polymerase chain reaction (RT-PCR) test.

What are the implications for public health practice?

Antigen tests have lower sensitivity compared with RT-PCR; negative antigen test results in persons with symptoms should be confirmed with an RT-PCR test, because a false-negative result might lead to failures in infection control and prevention practices and cause delays in diagnosis, isolation, and treatment.

Discussion

In this analysis of RT-PCR and antigen testing of asymptomatic and symptomatic patients at the time of a tertiary hospital admission through the ED, the sensitivity of the Quidel Sofia 2 SARS Antigen FIA test was 66% (72% and 61% in symptomatic and asymptomatic patients, respectively) using the Fulgent COVID-19 RT-PCR test as the standard; specificity was high overall (>99%). The antigen test's sensitivity increased in specimens with lower Ct values, consistent with higher virus titers in the specimen. Proper interpretation of the antigen test results should consider the patient's signs, symptoms, and exposure history, the prevalence of COVID-19 in the community, and the test's performance characteristics.*** The lower sensitivity of antigen tests compared with RT-PCR testing supports the strategy of using a more sensitive NAAT test if there is high clinical suspicion for COVID-19. COVID-19–compatible symptoms in this study were associated with positive RT-PCR test results. A positive antigen test result with a high pretest probability, either because of symptoms, exposure to an active case, or residence in an area of high community prevalence, could enable early isolation and receipt of medical care. This analysis did not identify any statistical difference between N1 Ct values in the study samples collected from symptomatic and asymptomatic persons. Findings indicate that although sensitivity of the antigen test does increase with lower Ct values, sensitivity is still lower at Ct values <30 and even at Ct values <25 in symptomatic and asymptomatic persons.

The findings in this report are subject to at least four limitations. First, this community and tertiary medical center represent a convenience sample and are not representative of all U.S. community and medical center settings. Second, data regarding any COVID-19–compatible symptoms reported were not collected beyond the ED chief complaint for the concordant group; therefore, the number of symptomatic persons might be underestimated. Third, exposure history was not evaluated. Finally, RT-PCR is an imperfect standard for comparison because it detects the presence of viral RNA, which includes "dead" virus and might not be correlated with transmission.

Overall, this evaluation of the performance of a rapid antigen test among symptomatic and asymptomatic persons suggests cautious interpretation of rapid antigen test results given its lower sensitivity. A false-negative antigen test result in health care settings might lead to failures in infection control and prevention practices and cause delays in diagnosis, isolation, and treatment. Persons with COVID-19–compatible symptoms and negative Quidel Sofia 2 SARS Antigen FIA antigen test results should have an additional sample confirmed with a NAAT test. While awaiting confirmation, measures to prevent SARS-CoV-2 transmission are recommended, including the use of personal protective equipment, source control for the patient, adherence to infection prevention protocols, and avoidance of cohorting these patients with others who do not have confirmed or suspected COVID-19 infection.†††

*** https://www.cdc.gov/coronavirus/2019-ncov/lab/resources/antigen-tests-guidelines.html

††† https://www.cdc.gov/coronavirus/2019-ncov/hcp/using-ppe.html

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Community-Based Testing for SARS-CoV-2 — Chicago, Illinois, May–November 2020

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On May 13, 2020, Chicago established a free community-based testing (CBT) initiative for SARS-CoV-2, the virus that causes COVID-19, using reverse transcription–polymerase chain reaction (RT-PCR). The initiative focused on demographic groups and geographic areas that were underrepresented in testing by clinical providers and had experienced high COVID-19 incidence, including Hispanic persons and those who have been economically marginalized. To assess the CBT initiative, the Chicago Department of Public Health (CDPH) compared demographic characteristics, economic marginalization, and test positivity between persons tested at CBT sites and persons tested in all other testing settings in Chicago. During May 13–November 14, a total of 253,904 SARS-CoV-2 RT-PCR tests were conducted at CBT sites. Compared with those tested in all other testing settings in Chicago, persons tested at CBT sites were more likely to live in areas that are economically marginalized (38.6% versus 32.0%; p<0.001) and to be Hispanic (50.9% versus 20.7%; p<0.001). The cumulative percentage of positive test results at the CBT sites was higher than that at all other testing settings (11.1% versus 7.1%; p<0.001). These results demonstrate the ability of public health departments to establish community-based testing initiatives that reach communities with less access to testing in other settings and that experience disproportionately higher incidences of COVID-19.

Because of limited access to SARS-CoV-2 diagnostic testing in the early phase of widespread transmission in Chicago, CBT sites began operations on May 13, 2020. The City of Chicago's CBT initiative, with direction from CDPH and the Racial Equity Rapid Response Team,[†] located sites at community assets (e.g., schools and parks) in areas accessible to Black and Hispanic communities, and in areas with lower per-capita testing rates; testing was offered at no cost to persons tested. These areas were primarily in northwest and southwest Chicago. The CBT initiative focused specifically on Hispanic[§] persons, because this population had the highest daily incidence of COVID-19 of any racial/ethnic group in Chicago during May 13–November 14, 2020 (*1*). Demographic information was collected during online or on-site registration. No strict eligibility criteria were applied and anyone could seek testing; however, the initiative attempted to give priority to disproportionately affected communities and persons with symptoms, persons who had had close contact with someone with confirmed COVID-19, or persons who had taken part in activities that put them at higher risk for COVID-19. Initially, fixed CBT sites were established. Sites were administered by the Community Organized Relief Effort (CORE),[¶] which hired English- and Spanish-speaking staff members from local communities to supervise specimen collection, manage site operations, and engage with the community directly.

After overall COVID-19 incidence declined and transmission became increasingly localized, the number of fixed CBT sites were reduced from six to four on June 23, 2020, and a mobile testing strategy was begun. Mobile sites were deployed to zip codes with the highest 7-day average percentage of positive test results. Most mobile sites remained in place for 1–2 days, and many were redeployed more than once to the same location during the study period, if that location continued to have a high percentage of positive test results. CDPH and CORE promoted sites with messages in English and Spanish and partnered with community-based and faith-based organizations to identify and advertise CBT sites. Beginning September 23, 2020, persons seeking testing were asked to show a health insurance card or state identification at registration to allow Chicago to seek reimbursement from health insurance or the Health Resources and Services Administration (HRSA); showing either document was optional.[**] At all CBT sites, including fixed and mobile sites, oral swab specimens were self-collected under supervision and tested for SARS-CoV-2 by RT-PCR using the Curative SARS-CoV-2 assay.[††] CDPH provided test results, along with relevant guidance on COVID-19 isolation and quarantine of contacts or prevention of COVID-19, by email or by personal telephone call for persons without a valid email address or who declined email follow-up.

Demographic characteristics, economic marginalization, and percentage of positive test results were compared between

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[†] https://www.chicago.gov/city/en/depts/mayor/press_room/press_releases/2020/april/RERRTUpdate.html

[§] The registration form collected ethnicity as Latinx rather than Hispanic, but ethnicity is reported as Hispanic per U.S. Census guidelines. https://www.census.gov/topics/population/hispanic-origin.html

[¶] https://www.coreresponse.org/about-us

[**] Providing this information was voluntary. Chicago emphasized in public messages that testing remained at no cost to the person being tested and was accessible regardless of the ability to provide proof of health insurance, identification, proof of residence, or immigration status.

[††] https://www.fda.gov/media/137089/download

persons tested at CBT sites and persons tested at any other setting in Chicago. Characteristics of Chicago residents tested at all other settings were extracted from the Illinois National Electronic Disease Surveillance System.[§§] Economic marginalization was assessed according to the Intercity Hardship Index (IHI) of the person's zip code of residence; IHI is a composite measure used to compare the economic condition of cities over time, based on unemployment, dependency, education, income level, crowded housing, and poverty (*2*). The IHI for each Chicago zip code was calculated and tertiles were derived. For this analysis, residents of zip codes with an IHI in the highest or lowest tertiles were defined as experiencing high or low levels of economic marginalization. Pairwise comparisons between groups were assessed using Pearson's chi-square test. P-values <0.05 were considered statistically significant. Analyses were conducted using SAS (version 9.4; SAS Institute). This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.[¶¶]

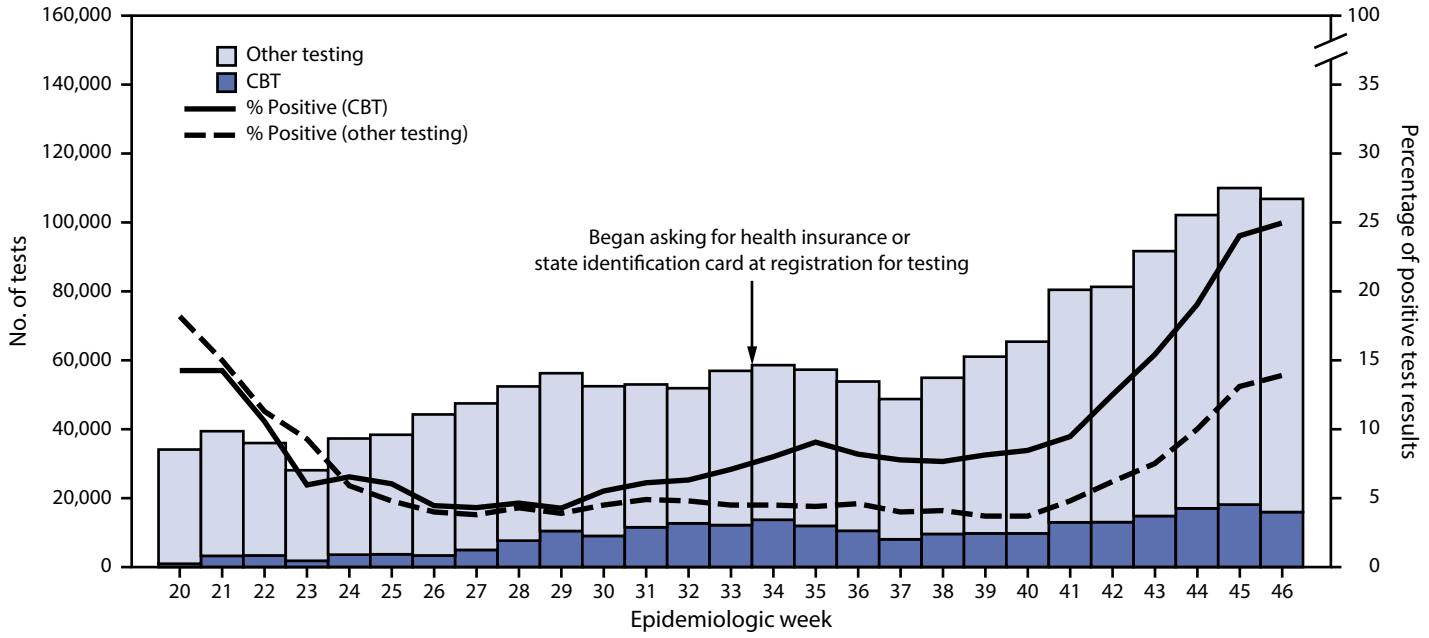
[§§] https://www.dph.illinois.gov/topics-services/diseases-and-conditions/infectious-diseases/infectious-disease-reporting

[¶¶] 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.

During May 13–November 14, approximately 1.6 million COVID-19 tests were conducted in Chicago, including 253,904 (16%) at CBT sites and 1,346,994 (84%) in all other testing settings. Overall, 11.1% of all SARS-CoV-2 test results at CBT sites were positive, with higher percentages of positive tests at CBT sites than in all other testing settings (11.1% versus 7.1%; p<0.001) (Figure). Differences between the percentage of positive test results at CBT sites and all other testing settings increased from epidemiologic week 29, after overall increases in citywide incidence and increases in mobile testing. Test positivity across mobile and fixed CBT sites was similar (11.1% versus 11.2%, respectively) (Table).

Compared with persons tested in all other settings, those tested at CBT sites were more likely to be aged <40 years (66.9% versus 51.7%; p<0.001) (Table). Race and ethnicity data were less likely to be missing for persons tested at CBT sites than for persons tested in all other settings (3.4% versus 45.2%; p<0.001). Among those with known race and ethnicity, persons tested at CBT sites were more likely than were those tested in all other settings to be Hispanic (50.9% versus 20.7%; p<0.001) and, based on zip code IHI, to have experienced high levels of economic marginalization (38.6% versus 32.0%; p<0.001). The proportion of persons tested at CBT sites who

FIGURE. Number of SARS-CoV-2 tests and percentage of positive test results, by test setting and epidemiologic week* — Chicago, Illinois, May 13–November 14, 2020†



Abbreviation: CBT = community-based testing.

* Epidemiologic week is a standardized measure of week, from Sunday through Saturday and ranging from 1 to 52 (sometimes 53), throughout the year; epidemiologic week 20 corresponds to the week beginning May 10, 2020.

† Chicago established a free CBT initiative for COVID-19, which focused on groups underrepresented in testing and with high levels of COVID-19, on May 13, 2020. Other testing includes Chicago residents tested in all other settings, as reported through the Illinois National Electronic Disease Surveillance System.

TABLE. Characteristics of persons receiving SARS-CoV-2 testing at community-based testing sites compared with those in all other settings — Chicago, Illinois, May 13–November 14, 2020

Characteristic	No. (%)				p-value¶
	Mobile CBT sites*	Fixed CBT sites†	Total CBT sites	All other settings§	
Total	**57,828**	**196,076**	**253,904**	**1,346,994**	—
Age group, yrs					
0–17	7,427 (12.8)	22,789 (11.6)	30,216 (11.9)	85,375 (6.3)	<0.001
18–29	17,154 (29.7)	62,419 (31.8)	79,572 (31.3)	340,965 (25.3)	
30–39	12,058 (20.9)	48,094 (24.6)	60,152 (23.7)	270,978 (20.1)	
40–49	8,011 (13.9)	27,222 (13.9)	35,233 (13.9)	181,798 (13.5)	
50–59	6,100 (10.6)	19,113 (9.8)	25,213 (9.9)	176,079 (13.1)	
60–69	4,513 (7.8)	10,970 (5.6)	15,483 (6.1)	150,340 (11.2)	
≥70	2,539 (4.4)	5,396 (2.8)	7,935 (3.1)	140,157 (10.4)	
Unknown	26 (0)	74 (0)	100 (0)	1,302 (0.1)	
Sex					
Female	32,799 (56.7)	108,623 (55.4)	141,422 (55.7)	716,631 (53.2)	<0.001
Male	24,655 (42.6)	85,693 (43.7)	110,348 (43.5)	581,671 (43.2)	
Other	374 (0.7)	1,760 (0.9)	2,134 (0.8)	—	
Unknown	—	—	—	48,692 (3.6)	
Race/Ethnicity					
Asian, NH	1,451 (2.5)	6,251 (3.2)	7,702 (3.0)	40,752 (3.0)	<0.001
Black, NH	9,979 (17.3)	29,276 (13.4)	36,255 (14.3)	222,823 (16.5)	
Hispanic	28,773 (49.8)	96,158 (49.0)	124,931 (49.2)	152,701 (11.3)	
Other, NH	3,267 (5.7)	10,693 (5.5)	13,960 (5.5)	50,025 (3.7)	
White, NH	12,747 (22.0)	49,644 (25.3)	62,391 (24.6)	271,510 (20.2)	
Unknown	1,611 (2.8)	7,054 (3.6)	8,665 (3.4)	609,183 (45.2)	
Test result					
Positive	6,391 (11.1)	21,915 (11.2)	28,306 (11.1)	96,036 (7.1)	<0.001
Negative	50,717 (87.7)	171,222 (87.3)	221,939 (87.4)	1,244,279 (92.4)	
Indeterminate	720 (1.2)	2,939 (1.5)	3,659 (1.4)	6,679 (0.5)	
Economic marginalization**					
Low	8,499 (14.7)	38,396 (19.6)	46,895 (18.5)	354,795 (26.3)	<0.001
Medium	17,790 (30.8)	64,817 (33.1)	82,607 (32.5)	505,253 (37.5)	
High	24,615 (42.6)	73,417 (37.4)	98,032 (38.6)	431,417 (32.0)	
Unknown	6,924 (12.0)	19,446 (9.9)	26,370 (10.4)	55,529 (4.1)	

Abbreviations: CBT = community-based testing; IHI = Intercity Hardship Index; NH = non-Hispanic.

* Selected weekly to specifically target zip codes with high or increasing incidence of COVID-19.

† Fixed locations that operate in communities with reduced access to SARS-CoV-2 testing.

§ Includes academic and community hospitals, congregate settings, federally qualified health centers, private providers, pharmacies, and all other testing sites.

¶ p-values are for a chi-square test for a global difference in a characteristic between all those tested at total CBT sites and those Chicago residents tested in all other settings as reported through the Illinois National Electronic Disease Surveillance System.

** Calculated based on the IHI of a person's zip code; residents of zip codes with an IHI in the highest tertile among all Chicago zip codes were defined as experiencing high levels of economic marginalization, and residents of zip codes with an IHI in the lowest tertile were defined as experiencing low levels of economic marginalization. https://data.cityofchicago.org/api/assets/A02C1C5F-8D89-466C-8492-B1FED3DA4C87

identified as Hispanic remained high even after health insurance information started to be collected (46.5% after September 23 versus 48.0% before). Persons tested at mobile sites were demographically similar to those tested at fixed sites; however, those tested at mobile sites were more likely than were those tested at fixed sites to live in a zip code experiencing economic marginalization (42.6% versus 37.4%; p<0.001).

Discussion

During May 13–November 14, 2020, approximately 1.6 million COVID-19 RT-PCR tests were conducted in Chicago, including approximately 250,000 (16%) through the city's CBT initiative. The CBT initiative effectively reached communities disproportionately affected by COVID-19, including Black and Hispanic communities and persons living in zip codes with high levels of economic marginalization (*3*,*4*). Mobile sites were particularly effective in reaching persons living in economically disadvantaged neighborhoods. The identification of persons with COVID-19 through the widespread availability of testing for persons with symptoms or those who have had close contact with persons known to have COVID-19 is critical, and consistent with CDC recommendations to contain the spread of COVID-19 (*5*). To advance health equity, such efforts are particularly important among populations disproportionately affected by COVID-19 and with less access to diagnostic testing through other means.

Although there were concerns that collecting health insurance information or identification might dissuade those in the highest risk groups, including undocumented persons, from using CBT sites, the proportion of Hispanic persons

seeking testing remained similar after sites started collecting this information. Seeking reimbursement through health insurance or HRSA might relieve the economic impact on public health departments and allow jurisdictions to sustain these operations while preserving equitable access. In Chicago, a community engagement team, including the city's Racial Equity Rapid Response Team, CDPH, CORE, and other partners, helped guide CBT efforts. This partnership between community-based organizations and government might represent a replicable model to mitigate inequities in access to other health services.

The findings in this report are subject to at least five limitations. First, large amounts of demographic data are missing, particularly the race and ethnicity of those who sought testing outside of CBT sites (45.2% missing). However, in a separate, unpublished CDPH study, missing race and ethnicity data were imputed using probabilistic methods based on individual persons' last name and U.S. Census tract of residence. This imputation did not materially change the general distribution of race and ethnicity in the sample.*** Second, the extent to which publicly funded CBT is additive by serving persons who would not have otherwise been tested, rather than partly replacing clinical testing, is not well understood. Third, although the proportion of persons identifying as Hispanic remained similar after collection of insurance information or identification began, these changes coincided with intensifying efforts to attract Hispanic communities through intentional messaging and enhanced Spanish-language media; these efforts might have offset possible declines that might have occurred in their absence. Fourth, although the proportion of positive test results was higher at CBT sites compared with that in all other settings, testing in other settings included high-volume testing of low prevalence groups (e.g., university students), whereas CBT deliberately located mobile testing sites in zip codes with high percentages of positive test results. Finally, dynamics of race, ethnicity, economic marginalization (*6*), and COVID-19 (*7*) in Chicago might not be generalizable to other jurisdictions.

This study demonstrates the capacity of public health agencies to establish community-based testing sites that reach communities disproportionately affected by COVID-19 and that have less access to testing in other settings. Collaboration between public health entities and community-based organizations is integral to promoting equitable access to affordable COVID-19 testing (*8*). The Advisory Committee on Immunization Practices has highlighted mitigating health inequities as an important ethical principle in distributing COVID-19 vaccines (*9*). Collaborative models developed through establishing community-based testing could be leveraged in this forthcoming effort.

*** https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3922477/pdf/hesr0049-0268.pdf

Summary

What is already known about this topic?

Chicago established a free community-based testing (CBT) initiative for COVID-19, focusing on groups underrepresented in testing and who experienced high levels of COVID-19.

What is added by this report?

During May 13–November 14, 2020, a total of 253,904 tests were conducted at CBT sites. Compared with persons in other testing settings, those tested at CBT sites were more likely to be Hispanic and to live in areas that are economically marginalized. The proportion of positive test results was larger at CBT sites.

What are the implications for public health practice?

CBT initiatives led by public health departments can reach communities with less access to testing in other settings and disproportionately higher COVID-19 rates.

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Rapid Emergence and Epidemiologic Characteristics of the SARS-CoV-2 B.1.526 Variant — New York City, New York, January 1–April 5, 2021

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On May 5, 2021, this report was posted as an MMWR *Early Release on the* MMWR *website (https://www.cdc.gov/mmwr).*

Recent studies have documented the emergence and rapid growth of B.1.526, a novel variant of interest (VOI) of SARS-CoV-2, the virus that causes COVID-19, in the New York City (NYC) area after its identification in NYC in November 2020 (*1*–*3*). Two predominant subclades within the B.1.526 lineage have been identified, one containing the E484K mutation in the receptor-binding domain (*1*,*2*), which attenuates in vitro neutralization by multiple SARS-CoV-2 antibodies and is present in variants of concern (VOCs) first identified in South Africa (B.1.351) (*4*) and Brazil (P.1).* The NYC Department of Health and Mental Hygiene (DOHMH) analyzed laboratory and epidemiologic data to characterize cases of B.1.526 infection, including illness severity, transmission to close contacts, rates of possible reinfection, and laboratory-diagnosed breakthrough infections among vaccinated persons. Preliminary data suggest that the B.1.526 variant does not lead to more severe disease and is not associated with increased risk for infection after vaccination (breakthrough infection) or reinfection. Because relatively few specimens were sequenced over the study period, the statistical power might have been insufficient to detect modest differences in rates of uncommon outcomes such as breakthrough infection or reinfection. Collection of timely viral genomic data for a larger proportion of citywide cases and rapid integration with population-based surveillance data would enable improved understanding of the impact of emerging SARS-CoV-2 variants and specific mutations to help guide public health intervention efforts.

SARS-CoV-2 specimens were sequenced at the Public Health Laboratory (PHL) or the Pandemic Response Laboratory (PRL). During January 1–April 5, 2021, PHL received specimens primarily from NYC residents at nine COVID Express laboratories. All nucleic acid amplification test (NAAT)-positive SARS-CoV-2 specimens with a cycle threshold (Ct) value <32 underwent whole genome sequencing (WGS) (Scott Hughes, PhD, NYC PHL, personal communication, April 2021). At PRL, specimens collected at approximately 190 outpatient facilities were randomly selected, and those with a Ct value ≤30 were sequenced (*5*,*6*). Characteristics of persons with sequenced viruses were compared with those of NYC residents with COVID-19 diagnoses during the same period to evaluate representativeness. Records of persons with sequenced viruses were matched to the DOHMH COVID-19 surveillance Citywide Immunization and Vital Registry databases.

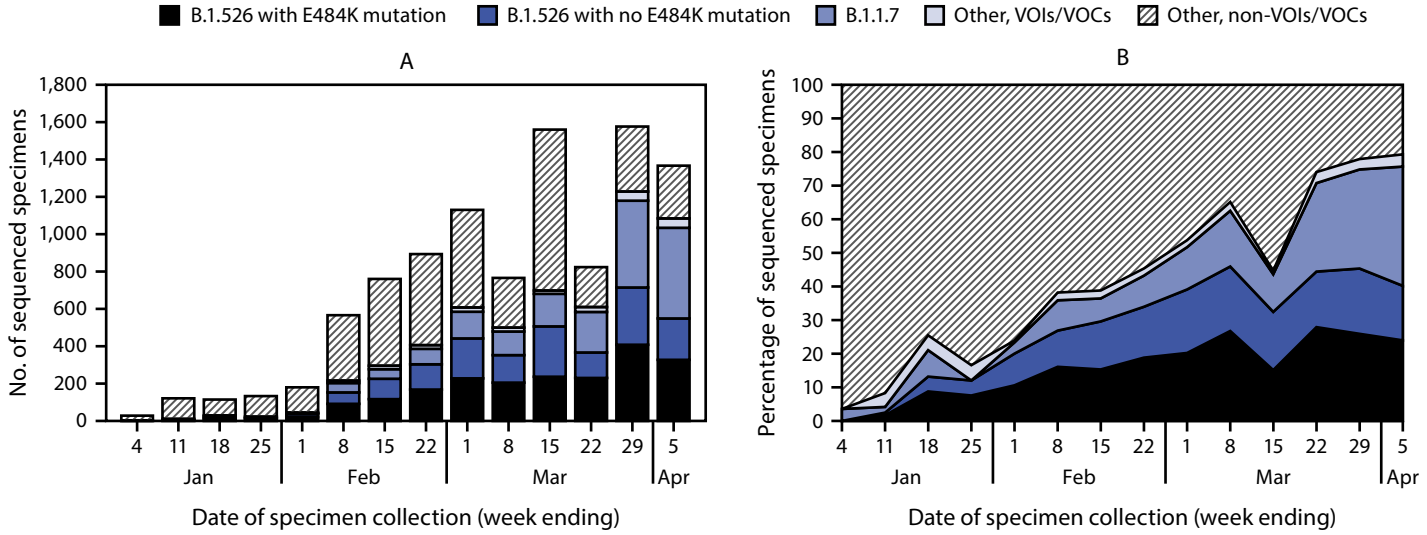
Persons infected with B.1.526 were compared with persons infected with variants that were not classified as VOIs or VOCs (i.e., non-VOI/VOC infections).† Persons infected with B.1.526 were also compared with those infected with B.1.1.7 because of the recent increase in B.1.1.7 cases in NYC and the documented increased transmissibility (*7*) and illness severity associated with this variant (*8*). To evaluate trends in socioeconomic status, neighborhood-level poverty was calculated as the percentage of residents in a ZIP code with household incomes <100% of the federal poverty level, per the American Community Survey 2014–2018. A case of possible reinfection was defined as an infection in a person with a sequenced specimen collected ≥90 days after a positive SARS-CoV-2 antigen or NAAT result. Breakthrough infections among partially vaccinated persons were defined as infections in persons with a sequenced specimen collected ≥14 days after the first vaccine dose and <14 days after the second dose (for mRNA vaccines). Breakthrough infections among fully vaccinated persons were defined as infections in persons with a sequenced specimen collected ≥14 days after either a second mRNA vaccine dose or a single dose viral vector vaccine. Comparisons across categorical characteristics were made using the chi-square or Fisher's exact test; continuous variables were compared using the Kruskal-Wallis test (SAS Enterprise Guide, version 7.1).

WGS was completed on 9,765 SARS-CoV-2 specimens, including 1,186 (12%) sequenced at PHL and 8,579 (88%) at PRL, representing 3.1% of NAAT-positive cases identified citywide during January 1–April 5, 2021. The number of specimens undergoing WGS at these laboratories increased over time (Figure), representing 7.7% of all NAAT-positive specimens by the week ending April 5. The B.1.1.7 variant was identified in 1,815 (19%) specimens. Among 3,679 (38%) B.1.526 variant viruses identified, 2,050 (56%) carried the E484K mutation. The proportion of B.1.526 viruses identified increased

* https://www.medrxiv.org/content/10.1101/2021.02.26.21252554v1

† https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html

FIGURE. Number of specimens undergoing whole genome sequencing* (A) and percentage of specimens with B1.526 variant with or without E484K mutation, B.1.1.7 variant, and other variants of concern or interest (B), by week of specimen collection — New York City, New York, January 1–April 5, 2021



Abbreviations: VOC = variant of concern; VOI = variant of interest.

* Whole genome sequencing of specimens (collection date during January 1–April 5, 2021) from New York City residents was performed at the Public Health Laboratory or the Pandemic Response Laboratory.

from 3% in mid-January to 34% by February 22 (Figure) and stabilized at 35%–45% weekly beginning March 8. The proportion of B.1.526 variants with the E484K mutation increased more quickly and as of April 5 represented 25% of all sequenced SARS-CoV-2 viruses, compared with 16% of B.1.526 variants without the E484K mutation. The proportion of B.1.1.7 viruses increased recently, reaching 36% by April 5. Other VOIs/VOCs were found among 253 specimens and were removed from additional analyses (B.1.427/B.1.429 variant in 166 specimens [viruses of B.1.427 or B.1.429 lineage, including those reported as B.1.427/B.1.429, without further differentiation]; P.1 variant in 50; B.1.525 variant in 20; B.1.351 variant in 12; and P.2 variant in 5).

The geographic distribution of persons with viruses sequenced at PHL or PRL was similar to that of persons with positive SARS-CoV-2 NAAT tests citywide; however, these persons were more frequently aged <45 years (67% versus 60% citywide), residents of neighborhoods with high poverty or very high poverty (45% versus 40%), or Black/African American (19% versus 16%) or Hispanic/Latino (35% versus 28%). A lower percentage of these persons were hospitalized (4% versus 9%) and died (0.5% versus 1.5%).

Among 3,679 persons infected with the B.1.526 variant, the median age was 35 years (Table 1). Compared with persons with non-VOI/VOC infections, those with B.1.526 infections were significantly more likely to live in the Bronx or in neighborhoods with high or very high poverty or to identify as Black/African American. Among persons with B.1.526 infections, 2,618 (71%) were symptomatic, 104 (4.3%) were hospitalized, and 11 (0.5%) died; these proportions are similar to or lower than those in persons with non-VOI/VOC infections (71%, 4.1%, and 0.7%, respectively). However, persons infected with the B.1.1.7 variant were more likely to be hospitalized (5.8%) than were persons with non-VOI/VOC infections (4.1%) ($p = 0.04$) (Table 2).

Possible reinfections were rare overall (0.5%), and the prevalence was similar among all persons with sequenced specimens (Table 1). No difference in rates of possible reinfection was found between persons infected with B.1.1.7 variants and those infected with B.1.526 variants with or without the E484K mutation (Supplementary Figure, https://stacks.cdc.gov/view/cdc/105634). The proportion of persons with a previous positive serology test result was 0.9% overall and similar among patients infected with all lineages (Table 1). Among persons infected with the B.1.526 variant carrying the E484K mutation, previous seropositivity was slightly more common (1.3%) than that among persons infected with the B.1.526 variant without the E484K mutation (0.7%), with the B.1.1.7 variant (0.7%), and with other non-VOI/VOC infections (0.9%); however, the difference was not significant ($p = 0.23$).

Among 32 fully vaccinated persons with sequenced viruses, eight (25%) were identified who were infected with the B.1.526 variant carrying the E484K mutation, three (9%) with the B.1.526 variant without the E484K mutation, seven (22%) with the B.1.1.7 variant, and 14 (44%) with non-VOI/VOC infections. No major differences between persons with B.1.526 and non-VOI/VOC infections were found in

TABLE 1. Number and percentage of SARS-CoV-2 variants* identified in specimens from New York City residents, by characteristics of residents — New York City, New York, January 1–April 5, 2021

Characteristic	Sequence result, no. (column %)			p-value† (B.1.526 vs. other)
	B.1.526	B.1.1.7	Other (non-VOI/VOC)	
Total§	**3,679**	**1,815**	**4,271**	—
B.1.526 with E484K mutation	2,050 (55.7)	NA	NA	NA
Median age, yrs (IQR)	35 (23–50)	34 (22–48)	35 (23–51)	0.13
Age group, yrs				
0–17	626 (17.0)	318 (17.5)	721 (16.9)	0.04
18–44	1,857 (50.5)	954 (52.6)	2,071 (48.5)	
45–64	954 (25.9)	437 (24.1)	1,133 (26.5)	
65–74	154 (4.2)	74 (4.1)	238 (5.6)	
≥75	87 (2.4)	32 (1.8)	108 (2.5)	
Sex				
Male	1,671 (45.4)	818 (45.1)	2,056 (48.1)	0.02
Female	2,003 (54.4)	996 (54.9)	2,211 (51.8)	
Race/Ethnicity¶				
Hispanic	1,325 (43.0)	556 (38.2)	1,495 (42.3)	<0.001
Asian or Pacific Islander	413 (13.4)	169 (11.6)	496 (14.0)	
Black/African American	753 (24.4)	352 (24.2)	722 (20.4)	
White	534 (17.3)	351 (24.1)	757 (21.4)	
Other	59 (1.9)	26 (1.8)	66 (1.9)	
Borough of residence				
Bronx	870 (23.6)	256 (14.1)	790 (18.5)	<0.001
Brooklyn	945 (25.7)	552 (30.4)	1,068 (25.0)	
Manhattan	529 (14.4)	214 (11.8)	658 (15.4)	
Queens	1,124 (30.6)	584 (32.2)	1,465 (34.3)	
Staten Island	211 (5.7)	209 (11.5)	290 (6.8)	
Neighborhood poverty**				
Low (<10%)	386 (10.5)	304 (16.7)	583 (13.7)	<0.001
Medium (10%–19.9%)	1,401 (38.1)	721 (39.7)	1,715 (40.2)	
High (20%–29.9%)	1,128 (30.7)	553 (30.5)	1,215 (28.4)	
Very high (≥30%)	682 (18.5)	203 (11.2)	675 (15.8)	
Clinical history				
Symptomatic††	2,618 (71.2)	1,247 (68.7)	3,010 (70.5)	0.51
Possible reinfection§§	19 (0.5)	8 (0.4)	17 (0.4)	0.43
Ever had a positive serology result before specimen collection	38 (1.0)	13 (0.7)	37 (0.9)	0.44
Vaccination history¶¶				
No recorded dose	3,609 (98.1)	1,777 (97.9)	4,205 (98.5)	0.34
Partially vaccinated	59 (1.6)	31 (1.7)	52 (1.2)	
Fully vaccinated	11 (0.3)	7 (0.4)	14 (0.3)	

Abbreviations: IQR = interquartile range; NA = not applicable; Pangolin = Phylogenetic Assignment of Named Global Outbreak Lineages; VOC = variant of concern; VOI = variant of interest.

* Classified by Pangolin (https://pangolin.cog-uk.io/) identification of lineage as B.1.526, B.1.1.7, or other lineages that were not VOCs or VOIs. Whole genome sequencing of specimens (collected during January 1–April 5, 2021) was performed at the Public Health Laboratory or the Pandemic Response Laboratory.

† p-values from chi-square test, Fisher's exact test, or Kruskal-Wallis test as indicated, comparing persons with B.1.526 to persons with other non-VOI/VOC sequences.

§ This total does not include other VOCs/VOIs (N = 253): B.1.427/B.1.429 variant (n = 166), P.1 variant (n = 50), B.1.525 variant (n = 20), B.1.351 variant (n = 12), and P.2 variant (n = 5).

¶ Denominators are among persons with known race/ethnicity; 1,691 persons had missing race/ethnicity (595 persons with variant B.1.526, 361 persons with variant B.1.1.7, and 735 persons with other VOCs/VOIs). All persons who identified as Hispanic/Latino, regardless of race, are classified as such.

** Neighborhood-level poverty was defined as the percentage of residents in a ZIP code tabulation area with household incomes of <100% of the federal poverty level, per the American Community Survey 2014–2018.

†† Having at least two of the following: fever, chills, rigors, myalgia, headache, sore throat, nausea or vomiting, diarrhea, fatigue, congestion, or runny nose; or any one of the following: cough, shortness of breath, difficulty breathing, new olfactory disorder, or new taste disorder. https://wwwn.cdc.gov/nndss/conditions/coronavirus-disease-2019-covid-19/case-definition/2020/08/05/

§§ An infection in a person with a sequenced specimen collected ≥90 days after collection of a specimen with a positive SARS-CoV-2 antigen or nucleic acid amplification test result.

¶¶ Partially vaccinated cases were defined as infections in persons with a sequenced specimen collected ≥14 days after the first vaccine dose and <14 days after the second dose (for mRNA vaccines). Fully vaccinated cases were defined as infections in persons with a sequenced specimen collected ≥14 days after a second mRNA vaccine dose or a single-dose viral vector vaccine.

TABLE 2. Number and percentage of SARS-CoV-2 variants* identified in specimens from New York City residents and number of hospitalizations, deaths, transmission to contacts, and clustering in buildings or households — New York City, New York, January 1–March 22, 2021†

Characteristic	Sequence result, no. (column %)			p-value§ (B.1.526 vs. other)
	B.1.526	B.1.1.7	Other (non-VOI/VOC)	
Total	**2,416**	**865**	**3,640**	—
Hospitalized within 14 days of specimen collection	104 (4.3)	50 (5.8)	151 (4.1)	0.77
Death within 60 days of specimen collection	11 (0.5)	4 (0.5)	27 (0.7)	0.17
Persons with COVID-19 with any known contacts¶	801/2,303 (34.8)	254/791 (32.1)	1,196/3,564 (33.6)	0.33
At least one contact had COVID-19**	359/801 (44.8)	99/254 (39.0)	520/1,196 (43.5)	0.55
Persons with COVID-19 with any known household contacts¶	735/2,303 (31.9)	240/791 (30.3)	1,102/3,654 (30.9)	0.42
At least one household contact had COVID-19**	327/735 (44.5)	97/240 (40.4)	464/1,102 (42.1)	0.31
COVID-19 cases associated with a building or household cluster††	1,482/2,199 (67.4)	474/769 (61.6)	2,241/3,386 (66.2)	0.35

Abbreviations: Pangolin = Phylogenetic Assignment of Named Global Outbreak Lineages; VOC = variant of concern; VOI = variant of interest.

* Classified by Pangolin (https://pangolin.cog-uk.io/) identification of lineage as B.1.526, B.1.1.7, or other non-VOC/VOI lineages. Whole genome sequencing of specimens (collected during January 1–April 5, 2021) was performed at the Public Health Laboratory or the Pandemic Response Laboratory.

† Persons with specimens collected March 23–April 5 were excluded from severity and transmission metrics because outcomes such as hospitalization, death, or transmission as well as diagnosis of contacts typically take weeks to occur and would not have been reported in time to be included.

§ p-values from chi-square test, Fisher's exact test, or Kruskal-Wallis test as indicated, comparing persons with B.1.526 sequences and persons with other non-VOI/VOC sequences.

¶ Contacts were reported by persons with COVID-19 and include those reported with a last name, first name, and date of birth.

** Among persons with known COVID-19; contacts are considered to be persons with known COVID-19 if they were infected with SARS-COV-2 and had a diagnosis date or an onset date within the 14 days after their exposure; the denominator is different because of the exclusion of residents of congregate settings.

†† A building cluster was defined as three or more confirmed cases with positive antigen test results within 21 days in the same building, and a household cluster was defined as two or more confirmed cases with positive antigen test results within 21 days in the same household, based on shared last name or unit number (or both); the denominator is different because only persons with COVID-19 with valid noncongregate residential addresses are included.

the secondary COVID-19 attack rate among household or community members identified as close contacts (Table 2).

Discussion

The B.1.526 SARS-CoV-2 lineage was identified in NYC in November 2020 (*1*), and its prevalence has increased sharply since mid-January 2021. By April 5, the B.1.526 variant accounted for 40% of all viruses sequenced by two major laboratories from a relatively representative sample of NYC COVID-19 cases. Approximately one half of the B.1.526 variants identified were found to have the E484K mutation, which has been shown to attenuate antibody neutralization in vitro (*3*). Although the proportional increase in B.1.526 infections suggests that this variant might be more transmissible than other SARS-CoV-2 variants, the secondary attack rate was not higher. Compared with persons infected with non-VOI/VOC viruses, B.1.526 appears to be slightly more prevalent in populations that have experienced disproportionate levels of COVID-19–associated morbidity and mortality (*9*) and that have lower vaccination rates than higher income NYC populations (*10*).

These preliminary data suggest that the SARS-CoV-2 B.1.526 variant does not cause more severe disease. In NYC, evidence does not indicate a higher reinfection rate among persons infected with B.1.526 viruses carrying the E484K mutation compared with those with infections without the mutation, although this might reflect incomplete case ascertainment during early 2020 because of limited testing capacity. Whereas a slightly larger proportion of persons infected with the B.1.526 variant carrying the E484K mutation had a previous positive antibody test than those infected with B.1.526 without the mutation, the difference is not significant, and data are insufficient to conclude that there is an increased risk for reinfection. Laboratory studies of B.1.526 variants carrying the E484K mutation showed that vaccine-induced antibodies against this virus had decreased neutralizing activity and that certain monoclonal antibodies had impaired activity§ (*3*). Additional evaluations in human populations are required to assess immune evasion of B.1.526.

The findings in this report are subject to at least four limitations. First, the majority of documented B.1.526 infections are recent, and because of lags in the confirmation of hospitalizations and deaths and incomplete ascertainment of previous infection or vaccination, drawing conclusions regarding severity of infection, risk for reinfection, vaccine breakthrough, or secondary attack rate is challenging. Second, infections in persons with sequenced viruses represent a small proportion of diagnosed cases; the lower rate of hospitalizations and deaths in this population might limit the ability to detect a difference in severe outcomes associated with the B.1.526 variant. However, the lack of evidence for increased severity of the B.1.526 variant contrasts with the significantly higher hospitalization rate that was observed among persons with B.1.1.7 infections using these methods, which is consistent with evidence that this variant has increased virulence (*8*). Third, persons with sequenced viruses might differ from those with nonsequenced viruses. Finally, the population with the

§ https://www.biorxiv.org/content/10.1101/2021.03.24.436620v1

Summary

What is already known about this topic?

B.1.526 emerged in November 2020 as a SARS-CoV-2 variant of interest in New York City (NYC). The presence of the E484K mutation is concerning because it has been shown to attenuate antibody neutralization in vitro.

What is added by this report?

The NYC Department of Health and Mental Hygiene analyzed laboratory and epidemiologic data to characterize cases of B.1.526 infection and the associated potential for breakthrough infection and reinfection. Preliminary evidence suggests that, to date, B.1.526 does not lead to more severe disease or increased risk for infection after vaccination.

What are the implications for public health practice?

Rapid integration of whole genome sequencing and population-based surveillance data is critical to characterizing new SARS-CoV-2 variants.

highest prevalence of B.1.526 infection in NYC has lower vaccination rates, limiting the ability to discern an increased risk for vaccine breakthrough (*10*).

Although the SARS-CoV-2 B.1.526 variant emerged rapidly in NYC, early evidence suggests that this variant, even with the E484K mutation, does not lead to more severe disease and is not associated with increased risk for breakthrough infection or reinfection compared with other sequenced SARS-CoV-2 viruses. The number of persons with reinfection or breakthrough infection whose specimens underwent WGS is low, limiting the statistical power to detect modest increases in immune escape that could have a substantial impact on public health. Improved capacity for genomic surveillance, establishment of automated and efficient exchange of WGS data, and integration with population-based clinical and epidemiologic data would enable the rapid characterization of emerging SARS-CoV-2 variants, which could guide public health policies related to reopening, prevention strategies, identifying areas for vaccination, and guiding future vaccine development.

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Identification of and Surveillance for the SARS-CoV-2 Variants B.1.427 and B.1.429 — Colorado, January–March 2021

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The B.1.427 and B.1.429 variants of SARS-CoV-2, the virus that causes COVID-19, were first described in Southern California on January 20, 2021 (*1*); on March 16 they were designated variants of concern* (*2*). Data on these variants are limited, but initial reports suggest that, compared with other lineages, they might be more infectious (*1*,*2*), cause more severe illness (*2*), and be less susceptible to neutralizing monoclonal antibody products such as bamlanivimab, an investigational treatment for mild-to-moderate COVID-19 (*1*–*3*). On January 24, the Colorado Department of Public Health and Environment (CDPHE) identified the first Colorado case of COVID-19 attributed to these variants. B.1.427 and B.1.429 were considered a single variant described as CAL.20C or B.1.427/B.1.429 in the 20C clade (*1*,*3*); in this report "B.1.427/B.1.429" refers to B.1.427 or B.1.429 lineage, including those reported as B.1.427/B.1.429 without further differentiation.

In Colorado, most routine SARS-CoV-2 whole genome sequencing (WGS) is performed by the CDPHE laboratory, generally on a convenience sample of available specimens. Whereas reverse transcription–polymerase chain reaction (RT-PCR) S-gene target failure, which suggests the presence of the SARS-CoV-2 B.1.1.7 variant, is used to prioritize specimens for sequencing (*4*), no such indicator exists for B.1.427/B.1.429 and other variants of concern. To improve convenience sampling to identify and track emerging variants, CDPHE established a 30-site statewide sentinel surveillance system. Sites submit a random sample of up to 30 SARS-CoV-2 RT-PCR–positive specimens from inpatients and outpatients to CDPHE for sequencing each week. COVID-19 B.1.427/B.1.429 variant cases were identified through tiled amplicon WGS.[†,§] Assembly of sequencing data into whole genomes was performed using CDPHE's publicly available Illumina and Nanopore data workflows.[¶] Phylogenetic Assignment of Named Global Outbreak Lineages (Pangolin)[**] (*5*) and Nextstrain's Nextclade tools (*6*) were used to assign lineage designations to each assembled genome. CDPHE conducted enhanced case investigation and contact tracing, including reinterview of previously interviewed persons, upstream contact tracing, increased testing of asymptomatic contacts, resource coordination to assist persons with successful isolation or quarantine, and involvement of CDPHE's Cultural Navigation program, which ensures culturally informed communication with immigrants, refugees, and other groups that are disproportionally affected by COVID-19.[††]

By March 31, CDPHE reported 327 COVID-19 B.1.427/B.1.429 cases with specimen collection dates during January 4–March 20, including 90 (28%) B.1.427, 218 (67%) B.1.429, and 19 (6%) not differentiated by the reporting commercial laboratory. B.1.427/B.1.429 case sequences were identified a median of 14.5 days after specimen collection (range = 7–38 days). Median patient age was 39 years (range = <1–95 years); 186 (57%) patients were male. Cases were identified in 31 (48%) of Colorado's 64 counties. Enhanced interviewing of all patients with variant cases was attempted through February; 60 (83%) such interviews were completed. Among these, nine (15%) persons reported travel outside Colorado (three to California, two to Nevada, and one each to Georgia, Minnesota, Utah, and the District of Columbia); none reported international travel. Through March, among 211 patients with symptom information available, 193 (91%) were symptomatic. Forty-six (14%) hospitalizations and eight (2%) deaths were reported; not all ill persons had recovered at time of data analysis. Based on available data, seven (2%) vaccine breakthrough cases[§§] were identified. Although Colorado variant data were derived from a convenience sample, when compared with national estimates of 85% symptomatic illness and 5% hospitalization rates among patients with positive SARS-CoV-2 test results,[¶¶] these data suggest that B.1.427/B.1.429 might more frequently cause discernible and severe illness than do nationally circulating lineages overall.

* A variant for which there is evidence of increased transmissibility, more severe disease, reduction in neutralization by vaccine- or infection-induced antibodies, reduced effectiveness of treatments or vaccines, or diagnostic detection failures.

† https://artic.network/ncov-2019

§ https://www.protocols.io/view/sars-cov-2-sequencing-on-illumina-miseq-using-arti-bffyjjpw

¶ https://github.com/CDPHE

** https://pangolin.cog-uk.io/

†† https://sites.google.com/state.co.us/refugeecoe/resources/cultural-navigation-2-0

§§ https://www.cdc.gov/vaccines/covid-19/health-departments/breakthrough-cases.html

¶¶ https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/burden.html

CDPHE tracked a steady increase in the proportion of sequenced specimens that were B.1.427/B.1.429, from 3%–4% in late January to 20%–22% in early March; during this time, national genomic surveillance data were insufficient to provide variant prevalence estimates for Colorado. Although sequencing performed for surveillance or research should not be used for individual clinical decision-making, these statewide population-level data provided general treatment decision support to clinicians for patients with positive SARS-CoV-2 test results in Colorado. Because of the increasing proportion of Colorado B.1.427/B.1.429 variant cases and their association with resistance to bamlanivimab, CDPHE issued a Health Alert Network advisory on March 22 recommending against monotherapy with bamlanivimab. On April 16, the Food and Drug Administration revoked the Emergency Use Authorization for monotherapy with this product.*** Establishing a state public health laboratory–based sequencing program and sentinel surveillance system in Colorado and merging laboratory and epidemiologic data has improved SARS-CoV-2 variant situational awareness and efforts to control the spread of variants, and also has provided data to guide Colorado clinicians and contributed timely data to inform important national clinical policy decisions. Given delays in sequencing results and increasing proportions of variant cases, all COVID-19 cases should be considered potential variant cases upon initial report.

*** https://www.fda.gov/news-events/press-announcements/coronavirus-covid-19-update-fda-revokes-emergency-use-authorization-monoclonal-antibody-bamlanivimab

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Modeling of Future COVID-19 Cases, Hospitalizations, and Deaths, by Vaccination Rates and Nonpharmaceutical Intervention Scenarios — United States, April–September 2021

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After a period of rapidly declining U.S. COVID-19 incidence during January–March 2021, increases occurred in several jurisdictions (*1*,*2*) despite the rapid rollout of a large-scale vaccination program. This increase coincided with the spread of more transmissible variants of SARS-CoV-2, the virus that causes COVID-19, including B.1.1.7 (*1*,*3*) and relaxation of COVID-19 prevention strategies such as those for businesses, large-scale gatherings, and educational activities. To provide long-term projections of potential trends in COVID-19 cases, hospitalizations, and deaths, COVID-19 Scenario Modeling Hub teams used a multiple-model approach comprising six models to assess the potential course of COVID-19 in the United States across four scenarios with different vaccination coverage rates and effectiveness estimates and strength and implementation of nonpharmaceutical interventions (NPIs) (public health policies, such as physical distancing and masking) over a 6-month period (April–September 2021) using data available through March 27, 2021 (*4*). Among the four scenarios, an accelerated decline in NPI adherence (which encapsulates NPI mandates and population behavior) was shown to undermine vaccination-related gains over the subsequent 2–3 months and, in combination with increased transmissibility of new variants, could lead to surges in cases, hospitalizations, and deaths. A sharp decline in cases was projected by July 2021, with a faster decline in the high-vaccination scenarios. High vaccination rates and compliance with public health prevention measures are essential to control the COVID-19 pandemic and to prevent surges in hospitalizations and deaths in the coming months.

Following previous short-term disease forecasting efforts, the COVID-19 Scenario Modeling Hub (*4*) convened six modeling teams in an open call to provide long-term, 6-month (April–September 2021) COVID-19 projections in the United States using data available through March 27, 2021 (*2*,*5*). Teams each developed a model to project weekly reported cases, hospitalizations, and deaths, both nationally and by jurisdiction (50 states and the District of Columbia), for each scenario, using data from the Johns Hopkins Center for Systems Science and Engineering Coronavirus Resource Center and federal databases (*2*,*5*). Four scenarios were considered in each model: high vaccination with moderate NPI use, high vaccination with low NPI use, low vaccination with moderate NPI use, and low vaccination with low NPI use (*4*) (Table) Vaccination scenarios took into account vaccine effectiveness (VE), weekly state-specific data on COVID-19 vaccination rates, and age- and risk-specific vaccine prioritization (e.g., older adults and health care workers); VE estimates were based on protection against clinical disease in randomized clinical trials[§]; parameters for effectiveness against infection and transmission were determined by each modeling team (*4*). For each NPI scenario, teams estimated a level of NPI adherence in March 2021 and then implemented a linear decrease of that level beginning in April to be 50% or 80% lower in September 2021. All scenarios included the spread of the B.1.1.7 variant, with the assumption that it was 50% more transmissible than were previously circulating SARS-CoV-2 variants (*3*,*4*). Individual modeling teams provided probabilistic projections for each future week, characterizing uncertainty with quantiles. These were combined into an ensemble for each scenario, outcome, week, and location by using the

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[§] https://www.cdc.gov/mmwr/volumes/69/wr/mm695152e1.htm?s_cid=mm695152e1_w; https://www.cdc.gov/mmwr/volumes/69/wr/mm6950e2.htm?s_cid=mm6950e2_w; https://www.cdc.gov/mmwr/volumes/70/wr/mm7009e4.htm?s_cid=mm7009e4_w

TABLE. COVID-19 projection scenarios* — United States, March 27–September 25, 2021

Vaccination and NPIs	Moderate NPI use; moderate reduction in NPI	Low NPI use; high reduction in NPI
High vaccination (high VE, administration, and vaccine coverage)		
Moderna/Pfizer (2 doses)	75%/95% VE against symptoms† 50M 1st doses administered monthly during Apr–Sep 2021§	75%/95% VE against symptoms† 50M 1st doses administered monthly during Apr–Sep 2021§
Johnson & Johnson (1 dose)	70% VE against symptoms† 10–20M doses administered monthly (Apr: 10M, May: 15M, Jun–Sep: 20M)§	70% VE against symptoms† 10–20M doses administered monthly (Apr: 10M, May: 15M, June–Sep: 20M)§
Vaccination coverage per group¶	Maximum = 90%	Maximum = 90%
NPIs	Estimated NPI levels in Mar 2021 are gradually reduced by 50% during Apr–Sep 2021	Estimated NPI levels in Mar 2021 are gradually reduced by 80% during Apr–Sep 2021
Low vaccination (low VE, administration, and vaccine coverage)		
Moderna/Pfizer (2 doses)	50%/85% VE against symptoms† 45M 1st doses administered monthly during Apr–Sep 2021§	50%/85% VE against symptoms† 45M 1st doses administered monthly during Apr–Sep 2021§
Johnson & Johnson (1 dose)	60% VE against symptoms† 5M doses administered monthly during Apr–Sep 2021§	60% VE against symptoms† 5M doses administered monthly during Apr–Sep 2021§
Vaccination coverage per group¶	Maximum = 75%	Maximum = 75%
NPIs	Estimated NPI levels in Mar 2021 are gradually reduced by 50% during Apr–Sep 2021	Estimated NPI levels in Mar 2021 are gradually reduced by 80% during Apr–Sep 2021

Abbreviations: M = million; NPI = nonpharmaceutical interventions; VE = vaccine effectiveness.

* Scenarios were defined to control for uncertainty in two specific factors: vaccination and adherence to NPIs with high/moderate and low levels for each. All scenarios included the B.1.1.7 variant and assumed that it was 50% more transmissible than previously circulating SARS-CoV-2 variants. All other transmission and outcome assumptions were decided by the six modeling teams.

† VE is defined as vaccine effectiveness against symptomatic disease 2 weeks after administration, based on clinical trials. For 2-dose vaccines, the first VE represents protection 2 weeks after the 1st dose. Assumptions about effectiveness and affects on other outcomes (e.g., infection, hospitalization, and death) were left to the discretion of individual teams. Five teams assumed that VE against infection was the same as VE against symptomatic disease, and one team assumed lower VE against infection; details on model structure and assumptions are available at MIDAS Network COVID-19 Scenario Modeling Hub. Accessed April 19, 2021. https://github.com/midas-network/covid19-scenario-modeling-hub

§ Vaccine doses reflect published manufacturing capacity estimates in the high vaccination scenarios and a continuation of the pace of vaccination observed at the end of March 2021 in the low vaccination scenarios.

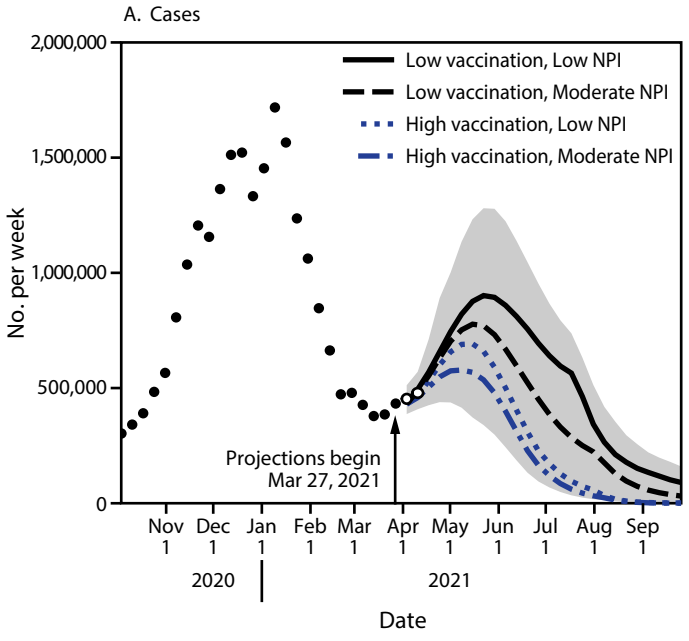
¶ If the maximum level of vaccination specified (e.g., 75% or 90%) was reached in a population group during the projection period, models assume that no more vaccination occurs in that group. Past reported vaccine coverage up to March 27, 2021, can exceed these levels.

median across teams for each quantile (*4*,*6*). The individual models differed substantially in structure and design (*4*), but all accounted for age groups, enabling prioritization of vaccination based on federal and state guidelines.

In all four scenarios, COVID-19 cases were projected to increase through May 2021 at the national level because of increased prevalence of the B.1.1.7 variant and decreased NPI mandates and compliance (Figure 1). A sharp decline in cases was projected by July 2021, with a faster decline in the high-vaccination scenarios. Increases in hospitalizations and deaths (Figure 1), although more moderate, were also projected. A peak of 7,000–11,100 weekly deaths nationwide was projected in May (range = 5,382–15,677, which includes the central 50% of the projected distributions for all scenarios in the ensemble). The larger increases in cases relative to hospitalizations and deaths were attributable to higher vaccination coverage among groups with higher risk for severe COVID-19.

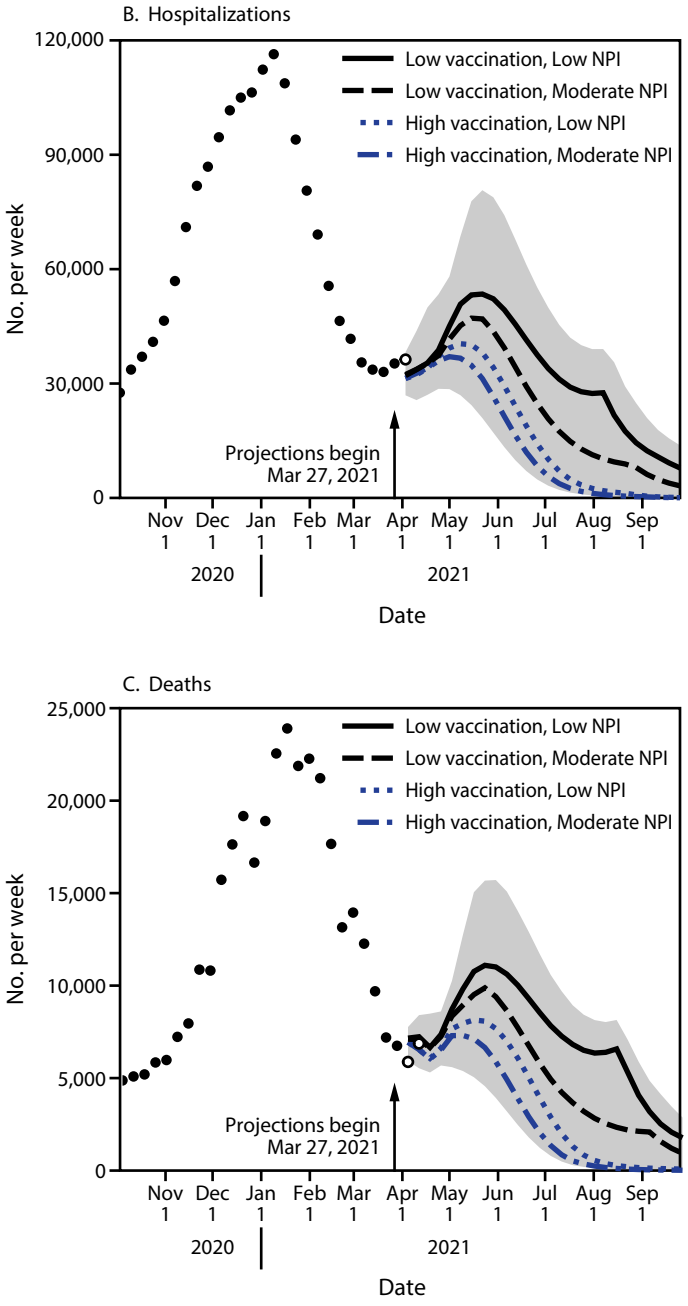
Moderate NPI use reduced cases and deaths in both the high and low vaccination scenarios, compared with low NPI use. The effect of maintaining moderate levels of NPI adherence was larger in the low vaccination scenarios, illustrating the counterbalance between and complementary effects of the two strategies (Figure 2). When low vaccination coverage was combined with

FIGURE 1. Weekly projections of reported numbers of cases (A), hospitalizations (B), and deaths (C)* under four scenarios representing different levels of vaccination and nonpharmaceutical intervention adherence — United States, March 27–September 25, 2021



See footnotes on the next page.

FIGURE 1. (*Continued*) Weekly projections of reported numbers of cases (A), hospitalizations (B), and deaths (C)* under four scenarios representing different levels of vaccination and nonpharmaceutical intervention adherence — United States, March 27–September 25, 2021



Abbreviation: NPI = nonpharmaceutical intervention.

* Historical data are shown as filled points, curves represent ensemble projections based on six models, and the grey area represents the maximum and minimum of the 50% projection intervals among all four scenarios. Vertical arrows represent the last date of observations used in the projections. Observations available after projections were made are shown as open points. Projection intervals are based on the 25th percentile of the more optimistic scenario (high vaccination and moderate NPI use) and the 75th percentile of the more pessimistic scenario (low vaccination and low NPI use). Ensemble projection curves represent the median of six median model projections, so they might not always appear smooth; the discontinuity in low vaccination scenario ensembles arises as two models project a late summer resurgence.

Summary

What is already known about this topic?

Increases in COVID-19 cases in March and early April occurred despite a large-scale vaccination program. Increases coincided with the spread of SARS-CoV-2 variants and relaxation of nonpharmaceutical interventions (NPIs).

What is added by this report?

Data from six models indicate that with high vaccination coverage and moderate NPI adherence, hospitalizations and deaths will likely remain low nationally, with a sharp decline in cases projected by July 2021. Lower NPI adherence could lead to substantial increases in severe COVID-19 outcomes, even with improved vaccination coverage.

What are the implications for public health practice?

High vaccination coverage and compliance with NPIs are essential to control COVID-19 and prevent surges in hospitalizations and deaths in the coming months.

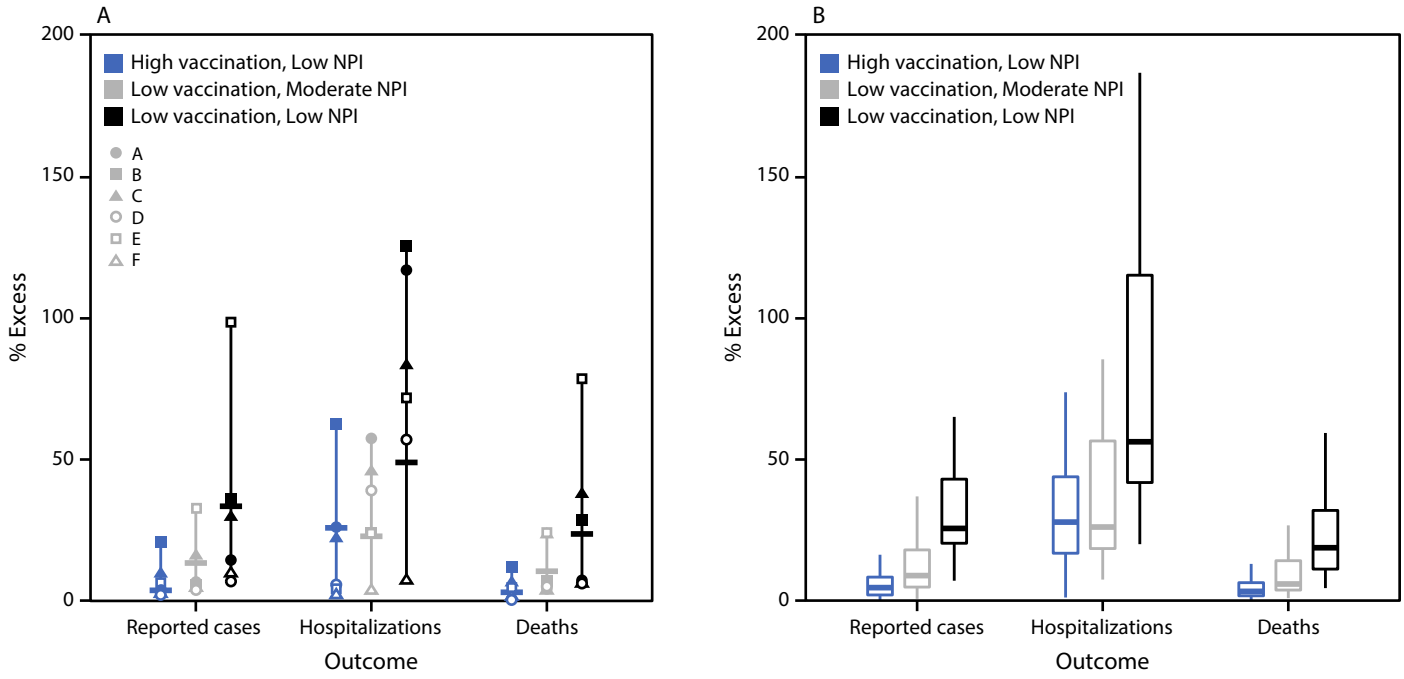
low NPI adherence, cumulative cases, hospitalizations, and deaths were substantially higher compared with other scenarios. The largest differences among scenarios was in the cumulative excess percentage of hospitalizations. Differences in deaths were lower because many of the groups at highest risk were already vaccinated at the beginning of the projection window. Differences in cases were relatively small because in all scenarios a substantial number of new cases occurred.

Whereas the benefits of increased control measures varied substantially between models, the largest excess percentages in estimated effects for each model were consistently found in scenarios with the lowest NPI use and vaccination levels (Figure 2). Considerable range in state-specific projections was observed (Figure 2), suggesting that some states could reach levels of disease similar to those observed in late 2020 in scenarios with lower use of NPIs.

Discussion

In this modeling study using data through March 27, 2021, COVID-19 cases were projected to increase nationally in April and peak in May 2021 in four assessed scenarios of vaccination coverage and NPI adherence. A moderate resurgence in deaths and hospitalizations was also projected during this period. Nationally, reported cases, hospitalization, and deaths are now decreasing or stable. However, transmission remains widespread and increased cases, hospitalizations, and deaths continue to be reported in some jurisdictions and, as this study indicates, the potential for future increases persists. Within each modeled scenario, substantial variation existed in the projected trajectory within individual states, potentially driven by the differences in the levels of population immunity, introduction and expansion of new variants, effectiveness of existing NPIs, and

FIGURE 2. Excess percentage of reported cases, hospitalizations, and deaths projected to occur under scenarios with reduced vaccination coverage, nonpharmaceutical intervention adherence, or both, compared with the more optimistic scenario (high vaccination and moderate nonpharmaceutical intervention adherence),* nationally (A)† and by state (B)§ — United States, March 27–September 25, 2021



Abbreviation: NPI = nonpharmaceutical intervention.

* Cumulative estimates for the projection period March 27–September 25, 2021, are compared with the more optimistic scenario (high vaccination and moderate NPI).

† National estimates represent the range of projections generated by the six contributing teams (symbols = individual models, dash = ensemble median). Individual models have been developed by six academic teams and are named JHU_IDD-CovidSP (A); JHUAPL-Bucky (B); Karlen-pypm (C); MOBS_NEU-GLEAM_COVID (D); USC-SIkJalpha (E); and UVA-adaptive (F). Details on model structure and assumptions are available at MIDAS Network COVID-19 Scenario Modeling Hub. Accessed April 19, 2021. https://github.com/midas-network/covid19-scenario-modeling-hub

§ Box plots represent the distribution of ensemble estimates in the 50 U.S. states and the District of Columbia. Boxes represent the interquartile range and the horizontal lines within each box represent the median. The whiskers extend to the most extreme data point that is no further from the box than 1.5 times the interquartile range.

vaccine acceptance and coverage. Even moderate reductions in NPI adherence were shown to undermine vaccination-related gains during the subsequent 2–3 months; decreased NPI adherence, in combination with increased transmissibility of some new variants, was projected to lead to surges in hospitalizations and deaths. Based on these findings, public health messaging to encourage vaccination and use of effective NPIs is essential to control the COVID-19 pandemic and prevent increases in COVID-19–related hospitalizations and deaths in the coming months.

All contributing models attributed increased SARS-CoV-2 transmission in many parts of the United States to the relaxation of mitigation strategies and the increasing prevalence of more transmissible variants, although the relative contribution of each factor varied among models. The emergence of new variants has been associated with resurgence in cases, hospitalizations, and deaths in Europe, South Africa, Brazil, and India, requiring new restrictions to prevent local outbreaks. In the United States, B.1.1.7 and other variants of domestic and international origin were projected to drive continued increases in case counts in the coming months (*3*) and could negate recent gains in controlling SARS-CoV-2 transmission. This is consistent with the findings in this study, which indicate that local conditions and rapid establishment of emerging variants place many states at risk for high incidences of COVID-19 cases in the spring, potentially requiring implementation of increased control measures to limit SARS-CoV-2 spread.

This is the first multiple model effort to project long-term trajectories of COVID-19 in real-time in the United States under different epidemiologic scenarios. Model differences identified critical areas of uncertainty, including vaccine acceptance, adherence to recommended NPIs, prevalence of the B.1.1.7 variant, duration of immunity, and state-level NPI policies (*4*). These models can be updated in response to changing conditions through new scenarios, updated fitting or structural changes of individual models, and the addition of new models. In contrast to the results generated by the COVID-19 Forecasting Hub (*6*), the projections in this study are intended to bound plausible outbreak trajectories and should not be considered forecasts of the most likely outcome.

These projections could be used for planning purposes (e.g., to estimate needs for COVID-19 treatments and hospital beds) and to guide public health efforts (e.g., to balance vaccination efforts with implementation of NPIs).

The findings in this report are subject to at least four limitations. First, considerable uncertainty is inherent when modeling the trajectory of COVID-19 over longer time frames (*7*,*8*). Whereas this analysis identifies a range of realistic uncertainty through well-defined scenarios and by combining multiple models, unforeseen events (e.g., a temporary pause in the use of a vaccine) could cause deviations that might not be reflected by the modeled scenarios (e.g., low and high vaccination). Second, only the B.1.1.7 variant was included in the scenarios given its increasing prevalence in the United States at the time modeling groups were convened and its increased transmissibility. The effect of B.1.1.7, as modeled, can be considered a proxy for more transmissible variants in general, but other emerging variants might have different effects. Third, the estimates are limited to six models based on existing data, and the models might not fully encompass the range of plausible trajectories. A larger number of models would better represent uncertainty in the epidemiology of COVID-19 (*8*). Finally, one approach to combining individual models and model-specific uncertainty into a single ensemble projection for each scenario was used (*9*). Different approaches to combining individual models into an ensemble changed the magnitude, but not the direction, of the expected impacts. Regardless of the approach used to generate the ensembles, they do not convey all potentially divergent trajectories that individual models project.

The rapid rollout of vaccination is having a positive impact on the COVID-19 pandemic in the United States and reported disease nationally during April has been on the lower end of the scenario projections to date. However, multiple jurisdictions have seen a resurgence of COVID-19 cases and others likely will if NPI adherence declines too rapidly. Increases in deaths and hospitalizations could be more moderate because of prioritization of vaccination groups at high risk for COVID-19 but are still expected, particularly in locations with pronounced increases in transmission earlier during the vaccine rollout. These modeled scenarios show that ongoing efforts to continue to increase vaccination coverage and maintain physical distancing, masking, isolation, and quarantine are warranted. As the COVID-19 pandemic evolves and more data become available regarding factors affecting outbreak dynamics, future projections from the COVID-19 Scenario Modeling Hub can provide new and improved insights for public health response (*10*).

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Demographic and Social Factors Associated with COVID-19 Vaccination Initiation Among Adults Aged ≥65 Years — United States, December 14, 2020–April 10, 2021

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Compared with other age groups, older adults (defined here as persons aged ≥65 years) are at higher risk for COVID-19–associated morbidity and mortality and have therefore been prioritized for COVID-19 vaccination (*1*,*2*). Ensuring access to vaccines for older adults has been a focus of federal, state, and local response efforts, and CDC has been monitoring vaccination coverage to identify and address disparities among subpopulations of older adults (*2*). Vaccine administration data submitted to CDC were analyzed to determine the prevalence of COVID-19 vaccination initiation among adults aged ≥65 years by demographic characteristics and overall. Characteristics of counties with low vaccination initiation rates were quantified using indicators of social vulnerability data from the 2019 American Community Survey.* During December 14, 2020–April 10, 2021, nationwide, a total of 42,736,710 (79.1%) older adults had initiated vaccination. The initiation rate was higher among men than among women and varied by state. On average, counties with low vaccination initiation rates (<50% of older adults having received at least 1 vaccine dose), compared with those with high rates (≥75%), had higher percentages of older adults without a computer, living in poverty, without Internet access, and living alone. CDC, state, and local jurisdictions in partnerships with communities should continue to identify and implement strategies to improve access to COVID-19 vaccination for older adults, such as assistance with scheduling vaccination appointments and transportation to vaccination sites, or vaccination at home if needed for persons who are homebound.† Monitoring demographic and social factors affecting COVID-19 vaccine access for older adults and prioritizing efforts to ensure equitable access to COVID-19 vaccine are needed to ensure high coverage among this group.

COVID-19 vaccine administration data are reported to CDC by multiple entities using immunization information systems, the Vaccine Administration Management System, pharmacy systems, or direct submission of electronic health records.§ Vaccination initiation rates were estimated as the percentage of older adult residents who received at least 1 dose of COVID-19 vaccine during December 14, 2020–April 10, 2021, and whose data were reported to CDC by April 16, 2021.¶ Vaccination initiation rates by age group (65–74 or ≥75 years) and sex, nationally and by state,** were estimated by dividing demographic data reported for each vaccine recipient by population estimates for adults aged ≥65 years from the U.S. Census Bureau 2019 Population Estimates Program.†† Analyses of vaccination initiation rates by race/ethnicity of the vaccine recipient were conducted at the national level only (because of a high level of missing data by state and low sample size for some race/ethnicity groups) and are presented as the percentage of total adults aged ≥65 years with known race/ethnicity information in each race/ethnicity category.

* https://www.census.gov/programs-surveys/acs

† https://www.cdc.gov/vaccines/covid-19/clinical-considerations/homebound-persons.html; https://www.cdc.gov/vaccines/covid-19/clinical-considerations/older-adults-and-disability/access.html

§ https://www.cdc.gov/vaccines/covid-19/vaccination-provider-support.html; https://www.cdc.gov/vaccines/covid-19/reporting/vams/index.html

¶ Providers are required to report administration records to the state immunization information system within 72 hours; 5 additional days of observation were included to account for delays in reporting and transmission of records to CDC. Data include all COVID-19 vaccine manufacturers, including the Janssen (Johnson & Johnson) vaccine, which only requires a single dose.

** Exclusions from the state-level dataset include 1) recipients for whom state of residence was unknown (48,524); 2) recipients aged ≥65 years for whom specific age (36,153) or sex (318,018) was unknown; and 3) residents of eight U.S. territories and freely associated states and armed forces overseas (409,206) for which population denominator data were not available.

†† Exclusions from the county-level dataset include 1) recipients for whom county of residence was unknown (2,406,423) or was known yet reported with an invalid state of residence (70,955); 2) recipients for whom state of residence was unknown (28,313); 3) residents of eight U.S. territories, freely associated states, and armed forces overseas (405,139) for which population denominator data were not available, and after excluding based on the above criteria; 4) residents of Delaware and the District of Columbia because each has three or fewer counties (218,240); and 5) residents of Georgia, Hawaii, South Dakota, and West Virginia because of unknown county of residence in >20% of records (776,207).

For county-level analyses, five frequent indicators of social vulnerability (*3*,*4*) for older adults were gathered from the U.S. Census Bureau American Community Survey 5-year estimates from 2019: the percentage of older adult county residents 1) without a computer (e.g., desktop or laptop computer [excludes mobile phones]); 2) with a computer but without Internet access; 3) living alone; 4) having an annual income below the federal poverty level; and 5) identifying as a person with race/ethnicity other than non-Hispanic White (White) alone. A generalized estimating equation for each of these social vulnerability indicators was used with a normal distribution and identity link function to quantify and compare the average percentage of older adults with social vulnerabilities in each county to the county vaccination initiation rate, divided into initiation categories of <50%, 50% to <75%, and ≥75%.[§§] SAS software (version 9.4; SAS Institute) was used to conduct analyses. This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.[¶¶]

During December 14, 2020–April 10, 2021, a total of 42,736,710 older adult residents of 50 states and the District of Columbia received at least 1 dose of COVID-19 vaccine (Table). The rate of vaccination initiation was 79.1% overall and, by jurisdiction, ranged from 68.9% (Alabama) to 99.9% (New Hampshire). Nationally, the rate of vaccination initiation was 1.3 percentage points higher among persons aged 65–74 years (79.6%) than among persons aged ≥75 years (78.3%). Among persons aged 65–74 years, vaccination initiation rates ranged from 66.8% (Alabama) to 99.9% (New Hampshire), and among persons aged ≥75 years, ranged from 69.1% (Mississippi) to 99.9% (New Hampshire) (Figure 1). Nationally, the vaccination initiation rate was 2.1 percentage points higher among men (79.6%) than among women (77.5%).[***]

Among recipients of at least 1 dose of COVID-19 vaccine, race/ethnicity was missing in 17,903,625 (41.9%) records. Among the 24,833,085 recipients with reported race/ethnicity, 17,561,065 (70.7%) were White; 1,885,433 (7.6%) were non-Hispanic Black; 1,548,776 (6.2%) were non-Hispanic multiracial; 1,657,517 (6.7%) were Hispanic; 880,040 (3.5%) were non-Hispanic Asian; 190,856 (0.8%) were non-Hispanic American Indian or Alaskan Native; 42,747 (0.2%) were Native Hawaiian or Other Pacific Islander; and 1,066,651 (4.3%) identified as "all other races/ethnicities."

Counties with <50% vaccination initiation rates had significantly higher average percentages of older adults with social vulnerabilities than did counties with vaccination initiation rates ≥75%, with the exception of the race/ethnicity other than White indicator (Figure 2). In counties with <50% vaccination initiation rates, an average of 24.6% (95% confidence interval [CI] = 22.3%–26.9%) of older adults did not have a computer, compared with 19.1% (95% CI = 17.8%–20.4%) in counties with ≥75% vaccination initiation rates. Similarly, the average percentage of older adults without Internet access was 9.9% (95% CI = 8.9%–10.9%) in counties with <50% vaccination initiation rates, compared with 7.4% (95% CI = 7.0%–7.8%) in counties with ≥75% vaccination initiation rates. The average percentage of older adults living in poverty was 10.3% (95% CI = 9.2%–11.4%) in counties with <50% vaccination initiation rates, compared with 7.6% (95% CI = 7.0%–8.2%) in counties with ≥75% vaccination initiation rates. The average percentage of older adults living alone was 14.3% (95% CI = 13.8%–14.9%) in counties with <50% vaccination initiation rates, compared with 12.2% (95% CI = 11.8%–12.6%) in counties with ≥75% vaccination initiation rates. The average percentage of older adults indicating race/ethnicity other than White was similar in counties with <50% vaccination initiation rates (8.0%; 95% CI = 4.9%–11.1%) and ≥75% vaccination initiation rates (9.3%; 95% CI = 6.4%–12.1%).

Discussion

Among adults aged ≥65 years in the United States, 79.1% had initiated COVID-19 vaccination as of April 10, 2021. Despite COVID-19 vaccine becoming available on December 14, 2020, and many states including older adults among the first groups eligible for vaccination, as many as 11.3 million older adults remained unvaccinated as of April 10, 2021.[†††] Further, vaccination initiation was lower among certain demographic groups (e.g., women) and states, and on average, counties with lower vaccination initiation rates had higher percentages of older adults with social vulnerabilities.

As of April 10, 2021, vaccination initiation rates among older adults nationwide were higher among men and persons aged 65–74 years than among women and persons aged ≥75 years. In comparison, according to reports of recent estimates, no differences by sex have been observed in initiation of vaccination with influenza and shingles vaccine, both of which are also recommended for older adults.[§§§] Vaccination acceptance by age group and sex will be followed to determine whether these differences persist as vaccine availability expands.

[§§] https://www.census.gov/data/datasets/time-series/demo/popest/2010s-counties-total.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.

[***] Among recipients aged ≥65 years, sex was missing in 318,018 of records.

[†††] The U.S. Census Bureau estimates the population of older adults to be 54,058,263. With 42,736,710 older adults receiving ≥1 COVID-19 vaccine dose, an estimated 11,321,553 older adults remained unvaccinated as of April 10, 2021.

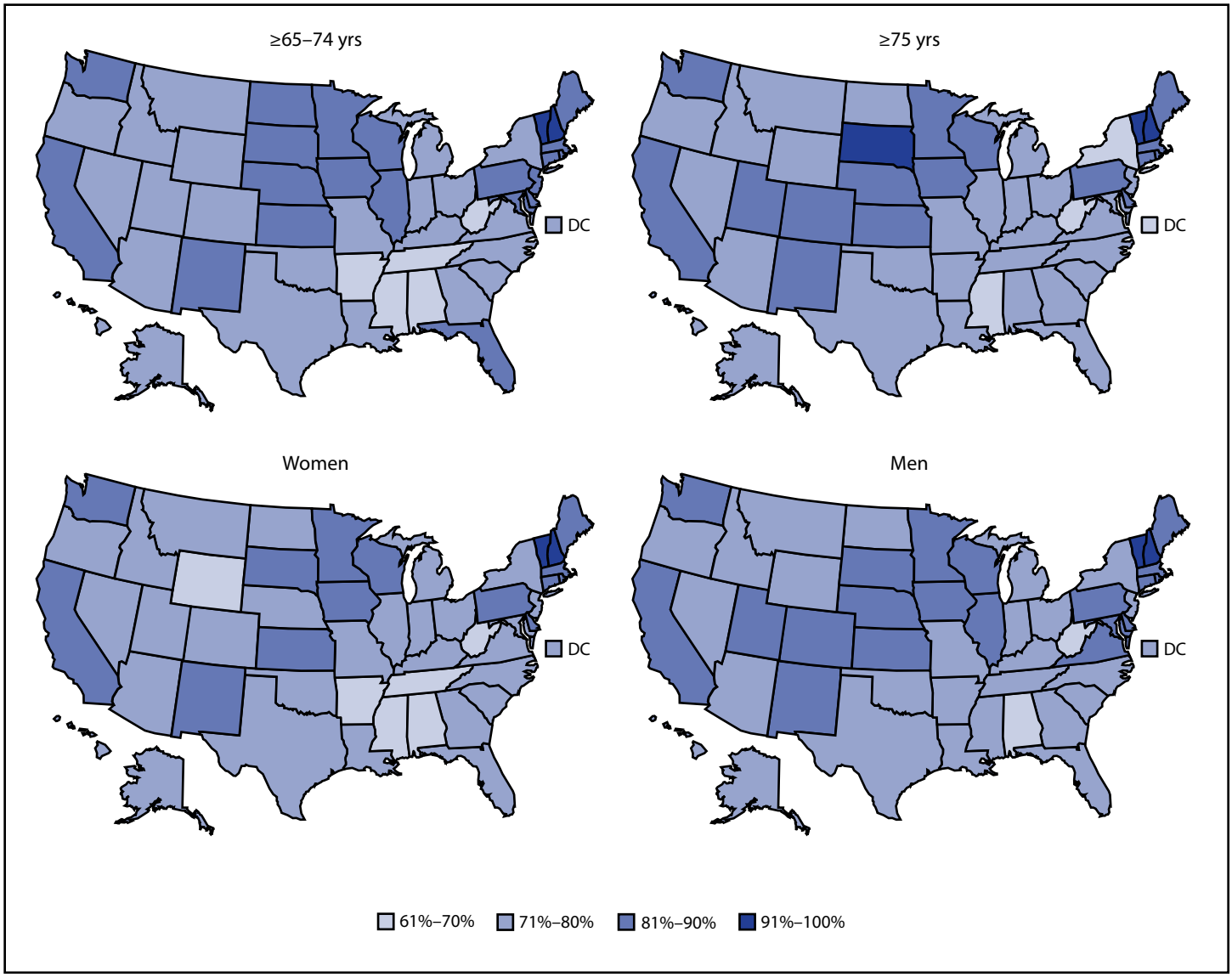
[§§§] https://www.cdc.gov/nchs/products/databriefs/db370.htm; https://www.cdc.gov/flu/fluvaxview/coverage-1920estimates.htm

TABLE. COVID-19 vaccination initiation rate among adults aged ≥65 years, by state, age group, and sex* — United States, December 14, 2020–April 10, 2021

Jurisdiction	No. of persons with at least 1 COVID-19 vaccine dose (% vaccination initiation)				
	Total men and women aged ≥65 years	Age group, yrs		Sex	
		65–74	≥75	Men	Women
National total	**42,736,710 (79.1)**	**25,051,017 (79.6)**	**17,685,693 (78.3)**	**19,166,329 (79.6)**	**23,252,363 (77.5)**
Alabama	585,732 (68.9)	334,760 (66.8)	250,972 (72.0)	260,221 (70.1)	324,554 (67.8)
Alaska	70,003 (76.4)	47,306 (77.2)	22,697 (74.9)	34,965 (76.9)	34,306 (74.4)
Arizona	991,737 (75.8)	568,864 (75.7)	422,873 (75.9)	460,031 (76.4)	528,908 (74.9)
Arkansas	372,077 (71.0)	210,948 (69.7)	161,129 (72.9)	165,732 (71.0)	200,562 (69.1)
California	4,939,416 (84.6)	2,934,905 (86.7)	2,004,511 (81.8)	2,228,999 (85.7)	2,690,716 (83.2)
Colorado	677,637 (80.4)	415,844 (79.6)	261,793 (81.7)	312,828 (80.9)	363,544 (79.8)
Connecticut	549,241 (87.1)	308,545 (87.5)	240,696 (86.8)	242,538 (87.9)	305,959 (86.4)
Delaware	159,934 (84.7)	96,468 (85.5)	63,466 (83.5)	71,975 (85.1)	87,258 (83.6)
District of Columbia	65,115 (74.6)	39,254 (78.2)	25,861 (69.7)	27,615 (77.3)	37,141 (72.0)
Florida	3,632,615 (80.8)	2,037,253 (82.6)	1,595,362 (78.5)	1,657,775 (81.7)	1,957,688 (79.3)
Georgia	1,114,150 (73.4)	679,273 (73.4)	434,877 (73.6)	483,369 (73.1)	608,901 (71.2)
Hawaii	208,887 (77.8)	115,405 (75.9)	93,482 (80.3)	96,534 (79.4)	110,985 (75.6)
Idaho	216,332 (74.4)	127,441 (72.5)	88,891 (77.4)	101,554 (73.7)	112,489 (73.6)
Illinois	1,641,523 (80.3)	955,599 (81.3)	685,924 (79.1)	726,643 (81.2)	908,243 (79.1)
Indiana	822,469 (75.8)	481,217 (75.6)	341,252 (76.0)	370,554 (77.1)	450,399 (74.4)
Iowa	458,859 (83.0)	260,017 (83.5)	198,842 (82.3)	204,719 (82.3)	248,043 (81.5)
Kansas	408,580 (85.9)	234,751 (86.2)	173,829 (85.5)	183,897 (86.0)	223,731 (85.5)
Kentucky	583,439 (77.7)	349,547 (78.0)	233,892 (77.3)	262,481 (78.8)	318,951 (76.4)
Louisiana	539,780 (72.8)	323,992 (73.2)	215,788 (72.3)	241,328 (74.1)	297,074 (71.5)
Maine	252,223 (88.4)	150,338 (88.9)	101,885 (87.7)	116,099 (89.3)	135,291 (87.1)
Maryland	771,161 (80.4)	452,878 (80.6)	318,283 (80.0)	337,410 (81.3)	429,662 (78.9)
Massachusetts	1,025,207 (87.7)	588,874 (87.5)	436,333 (88.0)	445,646 (87.6)	570,880 (86.4)
Michigan	1,333,607 (75.5)	787,506 (75.9)	546,101 (75.0)	606,985 (76.7)	725,509 (74.5)
Minnesota	784,098 (85.2)	452,519 (85.2)	331,579 (85.2)	357,349 (85.2)	419,766 (83.8)
Mississippi	337,396 (69.3)	200,815 (69.5)	136,581 (69.1)	149,898 (70.7)	186,511 (67.9)
Missouri	777,239 (73.2)	446,746 (73.2)	330,493 (73.1)	349,730 (74.4)	426,141 (72.0)
Montana	156,168 (75.6)	92,439 (74.2)	63,729 (77.9)	74,335 (75.1)	80,694 (75.1)
Nebraska	255,621 (81.8)	146,664 (82.0)	108,957 (81.6)	115,091 (81.7)	137,046 (79.9)
Nevada	366,508 (73.9)	221,813 (73.1)	144,695 (75.1)	173,614 (74.3)	192,185 (73.2)
New Hampshire	275,371 (99.9)	168,361 (99.9)	107,010 (99.9)	124,620 (99.9)	144,939 (99.9)
New Jersey	1,178,070 (79.8)	678,214 (81.4)	499,856 (77.8)	513,465 (80.5)	659,877 (78.8)
New Mexico	311,667 (82.5)	183,263 (81.6)	128,404 (83.9)	142,292 (82.6)	168,281 (81.9)
New York	2,424,208 (73.5)	1,416,044 (76.1)	1,008,164 (70.2)	1,063,736 (74.8)	1,329,168 (71.0)
North Carolina	1,308,317 (74.7)	785,219 (75.0)	523,098 (74.2)	580,067 (75.7)	717,019 (72.8)
North Dakota	95,434 (79.6)	53,736 (80.6)	41,698 (78.4)	43,160 (78.0)	49,043 (76.0)
Ohio	1,561,494 (76.3)	907,395 (76.3)	654,099 (76.3)	686,703 (76.1)	849,450 (74.2)
Oklahoma	494,734 (77.9)	288,388 (78.4)	206,346 (77.3)	223,789 (78.8)	270,043 (76.9)
Oregon	588,122 (76.8)	349,384 (75.2)	238,738 (79.2)	269,639 (76.8)	316,839 (76.4)
Pennsylvania	2,084,215 (87.1)	1,208,999 (89.3)	875,216 (84.2)	900,086 (85.6)	1,131,953 (84.4)
Rhode Island	164,945 (88.2)	95,963 (90.4)	68,982 (85.3)	72,707 (89.3)	91,967 (87.0)
South Carolina	726,525 (77.5)	432,172 (75.7)	294,353 (80.3)	327,860 (78.7)	397,494 (76.4)
South Dakota	131,960 (86.9)	74,675 (83.7)	57,285 (91.4)	59,261 (83.9)	69,307 (85.3)
Tennessee	806,104 (70.5)	465,412 (68.3)	340,692 (73.7)	362,397 (71.6)	441,628 (69.3)
Texas	2,801,138 (75.0)	1,694,786 (75.5)	1,106,352 (74.3)	1,250,589 (74.9)	1,519,330 (73.6)
Utah	297,419 (81.3)	176,259 (80.3)	121,160 (82.8)	137,974 (80.9)	155,667 (79.7)
Vermont	116,107 (92.9)	69,807 (92.8)	46,300 (92.9)	54,190 (94.1)	61,845 (91.7)
Virginia	1,089,519 (80.2)	642,006 (80.0)	447,513 (80.4)	489,594 (81.2)	597,041 (79.0)
Washington	1,002,812 (82.9)	604,837 (82.2)	397,975 (83.9)	458,165 (83.0)	537,814 (81.8)
West Virginia	253,825 (69.2)	148,838 (68.5)	104,987 (70.1)	117,940 (70.5)	134,669 (67.5)
Wisconsin	857,203 (84.3)	502,468 (84.5)	354,735 (84.0)	393,780 (84.6)	459,800 (83.3)
Wyoming	70,767 (71.4)	42,810 (70.7)	27,957 (72.4)	34,400 (72.0)	36,052 (70.1)

* Information on sex was missing for 318,018 (0.74%) vaccine recipients.

FIGURE 1. State COVID-19 vaccination initiation rate of adults aged ≥65 years, by age group and sex — United States, December 14, 2020–April 10, 2021

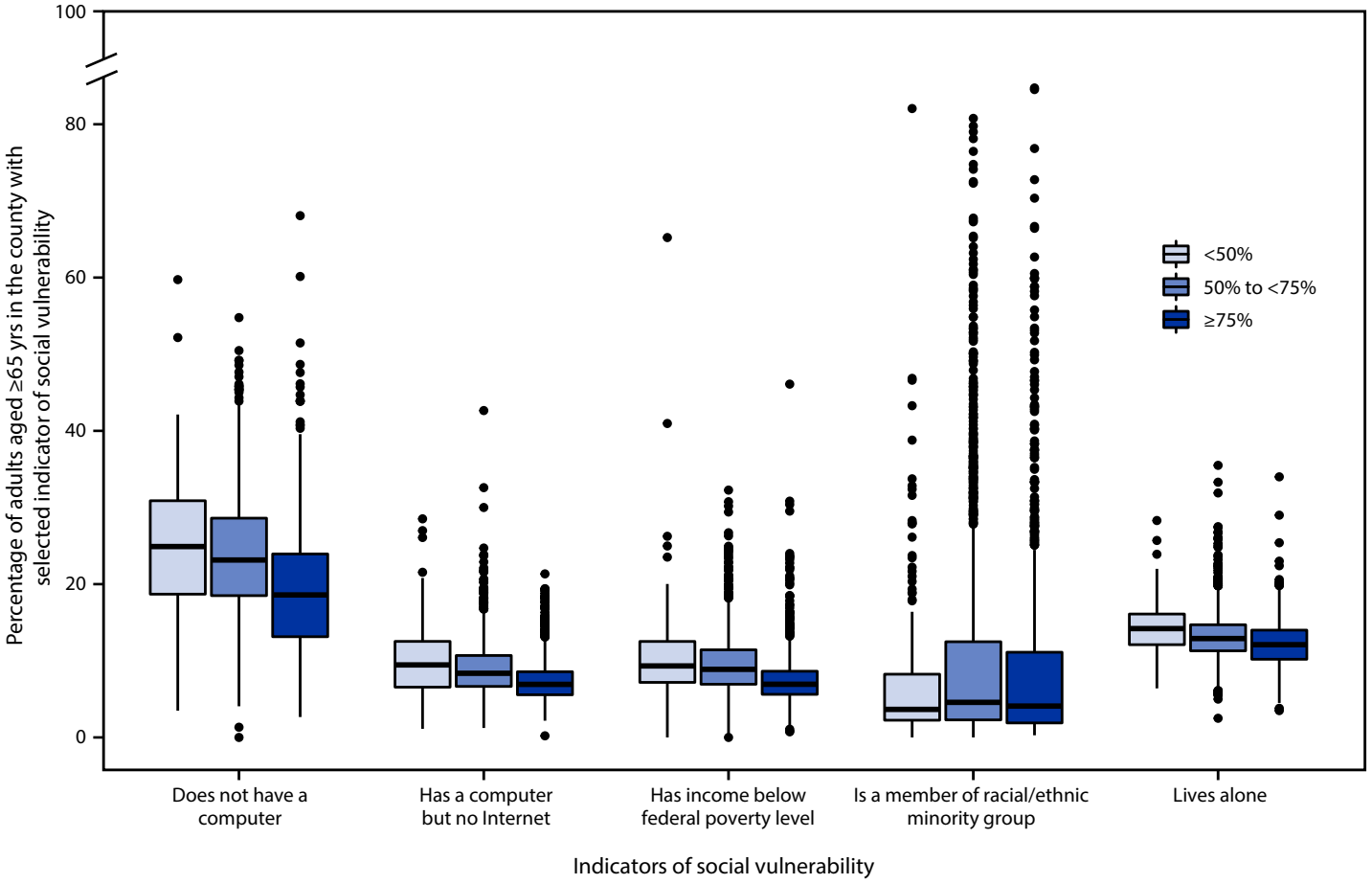


Abbreviation: DC = District of Columbia.

Initiation overall and by demographic subpopulation varied by state, indicating that national-level analyses might obscure more local trends. New Hampshire and Vermont had the two highest overall vaccination initiation rates among older adults. New Hampshire established early partnerships with pharmacies, first responders, and the National Guard, in addition to creating a centralized state website for vaccination sign-up. In Vermont, state health authorities established a partnership to coordinate vaccine distribution and administration with the Association of Hospitals and Health Systems, which represents Vermont's 14 nonprofit hospitals. At the county level, the upper Midwest (e.g., Iowa, Minnesota, and Wisconsin) reported high vaccination initiation rates as well, relative to other regions.

In addition to differences in vaccination initiation rates by age group and sex identified at the state level, counties with <50% initiation rates, on average, included higher percentages of older adults experiencing social vulnerabilities than did counties with ≥75% initiation. The identification of higher prevalence of older adults with social vulnerabilities in counties with low relative vaccination initiation rates is consistent with previous disparities identified among older adults who had received the shingles vaccine and among all adults who

FIGURE 2. County residents aged ≥65 years with selected indicators of social vulnerability, by vaccination initiation percentage — United States, December 14, 2020–April 10, 2021*



Abbreviation: IQR = interquartile range.

* This figure presents boxplots with the distributions of each indicator of social vulnerability for each of the categories of vaccination initiation among the population aged ≥65 years. The horizontal line in each box indicates the median; the top and bottom edges of each box indicate the 75th and 25th percentile values, respectively; the top and bottom of each vertical line show the maximum (75th percentile value + 1.5 × IQR) and minimum (25th percentile value - 1.5 × IQR); the dots represent outliers for each distribution.

had received the COVID-19 vaccine.[¶¶¶] Given the increased risk for COVID-19–related morbidity and mortality among older adults, addressing COVID-19 vaccine access barriers for socially vulnerable communities of older adults is critical. Among older adults, issues such as loneliness or absence of regular companionship (*5*), lack of computer or Internet literacy (*6*), and limited transportation options might be addressed through specialized outreach and vaccine distribution programs, as jurisdictions such as Miami, Florida, and Fulton County, Georgia, have demonstrated (*7*,*8*). In some states, such as Texas and Pennsylvania, state health departments and vaccination providers have formed partnerships with interest groups and community-based organizations to create programs designed to guide older adults through the vaccination sign-up process and transport them to vaccination sites (*9*,*10*).

The findings in this report are subject to at least five limitations. First, persons who were vaccinated through the Pharmacy Partnership for Long-Term Care Program[****] were not analyzed separately. These persons, whose vaccinations were arranged and administered by pharmacy partners at their residential facilities, might not face access barriers similar to those experienced by persons in other residential settings. However, an estimated 95% of Medicare beneficiaries (who constitute an estimated 96% of older adults) reside in the community rather than long-term care facilities.[††††] Second, associations between

[¶¶¶] https://www.cdc.gov/mmwr/volumes/70/wr/mm7012e1.htm?s_cid=mm7012e1_w; https://www.cdc.gov/nchs/products/databriefs/db370.htm

[****] https://www.cdc.gov/vaccines/covid-19/long-term-care/pharmacy-partnerships.html

[††††] https://www.agingstats.gov/docs/LatestReport/OA20_EmbargoCopy.pdf

Summary

What is already known about this topic?

Older adults have experienced higher risk for COVID-19–associated morbidity and mortality and therefore have been prioritized for COVID-19 vaccination.

What is added by this report?

After the first 3.5 months of the U.S. COVID-19 vaccination program, 79.1% of adults aged ≥65 years had received ≥1 dose, with higher vaccination initiation among men. Counties with lower vaccination initiation rates had higher percentages of older adults with social vulnerabilities.

What are the implications for public health practice?

Monitoring demographic and social factors affecting COVID-19 vaccine access for older adults and prioritizing efforts to ensure equitable access to COVID-19 vaccine are needed to ensure high coverage among this group.

county social vulnerability and vaccination initiation rates are ecological and reported for population-based indicators rather than individual-level vulnerability. Third, vulnerabilities and vaccination initiation rates might vary within counties because state and local jurisdictions might prioritize vaccination efforts for communities of older adults in smaller geographic units (e.g., ZIP codes). Fourth, older adult health and health care access are associated with numerous additional indicators for which recent data at the county level are not available. These additional indicators, such as living in multigenerational households or limitations accessing public transportation, might be associated with unexplained variance in the models. Finally, given that vaccine administration data are reported to CDC by multiple entities using various data systems, the possibility of underreporting, and thus, underestimation of vaccination coverage cannot be ruled out.

As COVID-19 vaccine supply expands along with the individual eligibility criteria, state and local jurisdictions can continue to ensure that older adults have equitable access to COVID-19 vaccines, including assistance with scheduling vaccination appointments and transportation to vaccination sites, or vaccination at home if needed for persons who are homebound. Assistance to ensure that persons receiving a vaccine that requires 2 doses to complete the series might be needed as well. Public health officials should continue to monitor vaccination initiation rates in the context of socioeconomic and demographic vulnerability to promote vaccine administration among this population at high risk for severe illness and death from COVID-19.

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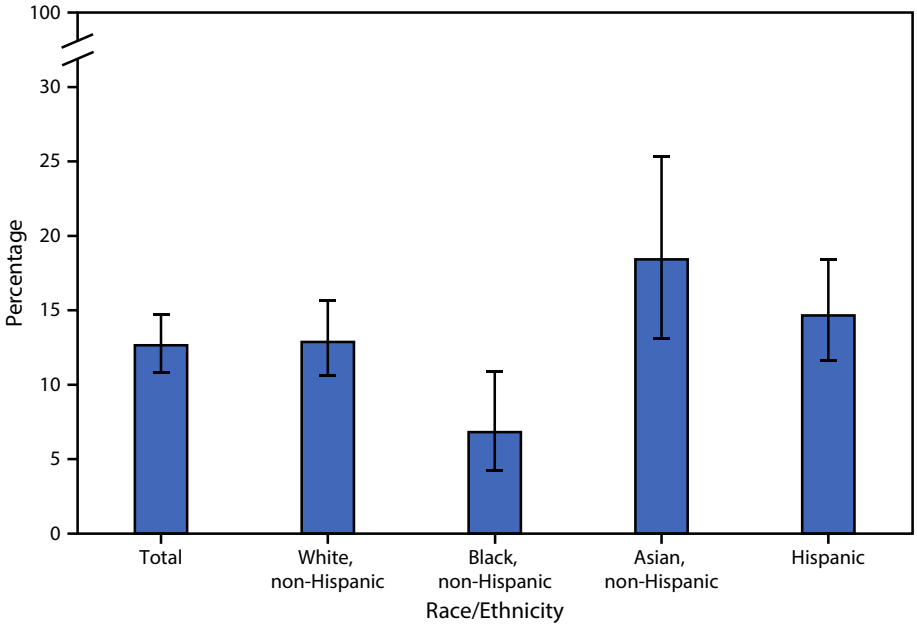
QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Percentage* of Adults Aged ≥50 Years with Osteoporosis,† by Race and Hispanic Origin§ — United States, 2017–2018



* 95% confidence intervals indicated with error bars.
† Osteoporosis is defined as a bone mineral density of 2.5 standard deviations or more below the mean value for a young woman at either the femur neck or the lumbar spine, or both locations, as measured by dual energy x-ray absorptiometry.
§ Estimates for persons reporting more than one race are not shown separately but are included in the total.

During 2017–2018, the age-adjusted prevalence of osteoporosis among adults aged ≥50 years was 12.6%. A lower percentage of non-Hispanic Black adults (6.8%) had osteoporosis compared with non-Hispanic White adults (12.9%), non-Hispanic Asian adults (18.4%), and Hispanic adults (14.7%). The observed differences among non-Hispanic White, non-Hispanic Asian, and Hispanic adults did not reach statistical significance.

Sources: Sarafrazi N, Wambogo EA, Shepherd JA. Osteoporosis or low bone mass in older adults: United States, 2017–2018. National Center for Health Statistics (NCHS) data brief, no. 405. https://www.cdc.gov/nchs/products/databriefs/db405.htm; NCHS, National Health and Nutrition Examination Survey (NHNES) data, NHNES 2017–2018. https://www.cdc.gov/nchs/nhanes.htm

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