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National, State-Level, and County-Level Prevalence Estimates of Adults Aged ≥18 Years Self-Reporting a Lifetime Diagnosis of Depression — United States, 2020

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Depression is a major contributor to mortality, morbidity, disability, and economic costs in the United States (*1*). Examining the geographic distribution of depression at the state and county levels can help guide state- and local-level efforts to prevent, treat, and manage depression. CDC analyzed 2020 Behavioral Risk Factor Surveillance System (BRFSS) data to estimate the national, state-level, and county-level prevalence of U.S. adults aged ≥18 years self-reporting a lifetime diagnosis of depression (referred to as depression). During 2020, the age-standardized prevalence of depression among adults was 18.5%. Among states, the age-standardized prevalence of depression ranged from 12.7% to 27.5% (median = 19.9%); most of the states with the highest prevalence were in the Appalachian* and southern Mississippi Valley† regions. Among 3,143 counties, the model-based age-standardized prevalence of depression ranged from 10.7% to 31.9% (median = 21.8%); most of the counties with the highest prevalence were in the Appalachian region, the southern Mississippi Valley region, and Missouri, Oklahoma, and Washington. These data can help decision-makers prioritize health planning and interventions in areas with the largest gaps or inequities, which could include implementation of evidence-based interventions and practices such as those recommended by The Guide to Community Preventive Services Task Force (CPSTF) and the Substance Abuse and Mental Health Services Administration (SAMHSA).

BRFSS is an ongoing, state-based, random-digit–dialed landline and cell phone survey of the U.S. adult population aged ≥18 years in all 50 states, the District of Columbia (DC), and participating U.S. territories.§ The combined (landline and cellular) median response rate for the 2020 BRFSS (excluding territories) was 47.6% and ranged among states from 34.5% to 67.2%.¶ A lifetime diagnosis of depression was defined as a

* The Appalachian region includes all of West Virginia and parts of Alabama, Georgia, Kentucky, Maryland, Mississippi, New York, North Carolina, Ohio, Pennsylvania, South Carolina, Tennessee, and Virginia (https://www.arc.gov/about-the-appalachian-region/); Alabama, Kentucky, Tennessee, and West Virginia were among the 10 states with the highest prevalence.

† The southern Mississippi Valley region includes parts of Arkansas, Louisiana, Mississippi, and Tennessee (https://www.usace.army.mil/Missions/Locations/); Arkansas, Louisiana, and Tennessee were among the 10 states with the highest prevalence.

§ https://www.cdc.gov/brfss/about/index.htm

¶ https://www.cdc.gov/brfss/annual_data/annual_2020.html

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"yes" response to the question, "Has a doctor, nurse, or other health professional ever told you that you had a depressive disorder, including depression, major depression, dysthymia, or minor depression?" Among the 2020 BRFSS respondents surveyed in all 50 U.S. states and DC, 392,746 (98.9%) responded to the depression question.

This report presents national, state-level, and county-level point estimates and 95% CIs for the prevalence of depression. National values were directly estimated from weighted BRFSS 2020 data for groups defined by age, sex, race or ethnicity, and education, and state-level estimates were directly estimated from weighted BRFSS 2020 data for each state and DC. Point estimates from survey data were estimated as weighted means and pairwise t-tests were used to determine differences (compared with a reference category) by age group, sex, race or ethnicity, and education level. Differences with $p<0.05$ were considered statistically significant. Because BRFSS is not designed to provide estimates at the county level, county-level estimates were obtained for all 3,143 U.S. counties using multilevel logistic regression and post-stratification.** The multilevel logistic regression model included depression as the binary dependent variable. The model's independent variables included each respondent's age group, sex, race and ethnicity, and education level from BRFSS 2020 data, county-level poverty data (<150% of the poverty level) from the 2016–2020 American Community Survey,†† and random effects for state and county. The model parameters were then applied to the U.S. Census Bureau Vintage 2020 county population data to generate model-based county-level estimates of depression prevalence.§§ A Monte Carlo simulation was used to generate 95% CIs for county-level estimates. These model-based county-level estimates were validated by comparing them with the weighted direct survey estimates from counties with sample size ≥500 (183) in BRFSS (Pearson correlation coefficient = 0.88). All national and state-level analyses were conducted using SAS-callable SUDAAN software (version 11; RTI International) to account for the BRFSS complex sample design and weighting, and county-level estimation was conducted using SAS software (version 9.4; SAS Institute). All prevalence estimates were age standardized to the 2000 U.S. Census Bureau population.¶¶ This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.***

The age-standardized prevalence of depression among U.S. adults was 18.5% (crude = 18.4%) (Table 1). Age-specific

** The method for the small area estimate approach is used for the PLACES project conducted by CDC, which provides estimates for 29 chronic disease measures at county, place (incorporated and census-designated), census tract, and zip code tabulation area levels. The method does not include territories as part of the 3,143 counties. https://www.cdc.gov/places/methodology/index.html

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

§§ https://www.census.gov/programs-surveys/popest/technical-documentation/research/evaluation-estimates/2020-evaluation-estimates/2010s-county-detail.html

¶¶ https://www.cdc.gov/nchs/data/statnt/statnt20.pdf

*** 45 C.F.R. part 46.102(1)(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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TABLE 1. Prevalence estimates of adults aged ≥18 years self-reporting a lifetime diagnosis of depression,* by selected characteristics — Behavioral Risk Factor Surveillance System, United States, 2020

Characteristic	Sample size†	Unweighted no. with depression§	Weighted§ no. with depression (millions)	Prevalence§ % (95% CI)	Age-standardized prevalence¶ % (95% CI)
Overall	**392,746**	**74,830**	**47.0**	**18.4 (18.1–18.6)**	**18.5 (18.2–18.8)**
Age group, yrs					
18–24 (Ref)	24,850	5,688	6.6	21.5 (20.6–22.5)	NA
25–44	93,614	20,862	17.2	19.9 (19.5–20.4)**	NA
45–64	136,704	27,876	15.2	18.4 (17.9–18.9)**	NA
≥65	137,578	20,404	8.0	14.2 (13.7–14.6)**	NA
Sex					
Men (Ref)	179,937	24,587	16.3	13.1 (12.8–13.4)	13.3 (12.9–13.6)
Women	212,809	50,243	30.7	23.4 (22.9–23.8)**	24.0 (23.6–24.5)**
Race and ethnicity					
AI/AN, non-Hispanic	6,887	1,455	0.6	23.3 (21.1–25.7)**	23.4 (21.1–25.9)
Asian, non-Hispanic	9,414	792	1.1	7.6 (6.6–8.7)**	7.3 (6.3–8.5)**
Black or African American, non-Hispanic	30,158	4,823	4.9	16.1 (15.3–16.9)**	16.2 (15.4–17.0)**
NH/OPI, non-Hispanic	1,248	172	0.1	15.1 (11.8–19.1)**	14.6 (11.4–18.5)**
White, non-Hispanic (Ref)	295,741	58,598	32.2	20.6 (20.3–20.9)	21.9 (21.5–22.2)
Hispanic or Latino††	31,125	5,257	6.3	14.6 (13.8–15.5)**	14.6 (13.7–15.5)**
Multiracial, non-Hispanic	8,135	2,081	0.9	28.5 (26.3–30.8)**	27.9 (25.8–30.1)**
Other, non-Hispanic	3,545	720	0.3	19.3 (17.0–21.9)	19.6 (17.2–22.2)
Educational attainment					
Less than high school (Ref)	25,362	5,962	6.6	21.0 (20.0–22.1)	21.2 (20.1–22.3)
High school or equivalent	104,605	19,909	12.8	18.1 (17.6–18.6)**	18.5 (17.9–19.0)**
Technical college or some college	109,074	23,573	16.4	21.0 (20.4–21.5)	21.5 (20.9–22.0)
College degree or higher	151,949	25,182	11.1	14.9 (14.6–15.3)**	15.4 (15.0–15.8)**

Abbreviations: AI/AN = American Indian or Alaska Native; NA = not applicable; NH/OPI = Native Hawaiian or other Pacific Islander; Ref = referent group.

* Respondents were classified as having received a diagnosis of depression if they responded "yes" to the question, "Has a doctor, nurse, or other health professional ever told you that you had a depressive disorder, including depression, major depression, dysthymia, or minor depression?"

† Categories might not sum to sample total because of missing responses for some variables.

§ Weighted using the statistical weights provided in the Behavioral Risk Factor Surveillance System data set.

¶ Except for age groups, estimates were age-standardized to the 2000 projected U.S. Census Bureau population aged ≥18 years using four groups (18–24, 25–44, 45–64, and ≥65 years). https://www.cdc.gov/nchs/data/statnt/statnt20.pdf

** Statistically significant (p<0.05) difference compared with the indicated Ref category.

†† Respondents who identified as Hispanic or Latino might be of any race.

prevalence of depression was highest among those aged 18–24 years (21.5%) and lowest among those aged ≥65 years (14.2%). The age-standardized prevalence of depression was higher among women (24.0%) compared with men (13.3%), higher among non-Hispanic White adults (21.9%) compared with non-Hispanic Black or African-American (16.2%), non-Hispanic Native Hawaiian or other Pacific Islander (14.6%), Hispanic or Latino (14.6%), and non-Hispanic Asian (7.3%) adults, and higher among adults who had attained less than a high school education (21.2%) compared with adults with a high school education or equivalent (18.5%) and college degree or higher (15.4%).

Among states, the age-standardized prevalence of depression ranged from 12.7% in Hawaii to 27.5% in West Virginia (median = 19.9%) (Table 2). The 10 states with the highest prevalence were (in descending order) West Virginia, Kentucky, Tennessee, Arkansas, Vermont, Alabama, Louisiana, Washington, Missouri, and Montana.

Among counties, the model-based age-standardized estimates ranged from 10.7% (Aleutians East Borough County, Alaska) to 31.9% (Logan County, West Virginia) (median = 21.8%) (Supplementary Table, https://stacks.cdc.gov/view/cdc/129404); most of the counties with the highest prevalence were in the Appalachian region, the southern Mississippi Valley region, and in Missouri, Oklahoma, and Washington (Figure). Estimates of depression also varied among counties within states. For example, even though all county prevalence estimates in West Virginia were in the highest quartile, estimates in the state by county ranged from 24.5% to 31.9%.

Discussion

During 2020, approximately one in five U.S. adults reported having ever received a diagnosis of depression by a health care provider, with prevalence of depression higher in women, younger adults, and adults with lower education levels. Previous reports that focused on measures of current depression (e.g., during the previous 2 weeks) rather than lifetime depression showed similar subgroup differences (*2–6*), including those observed before and throughout the COVID-19 pandemic (*4–6*).

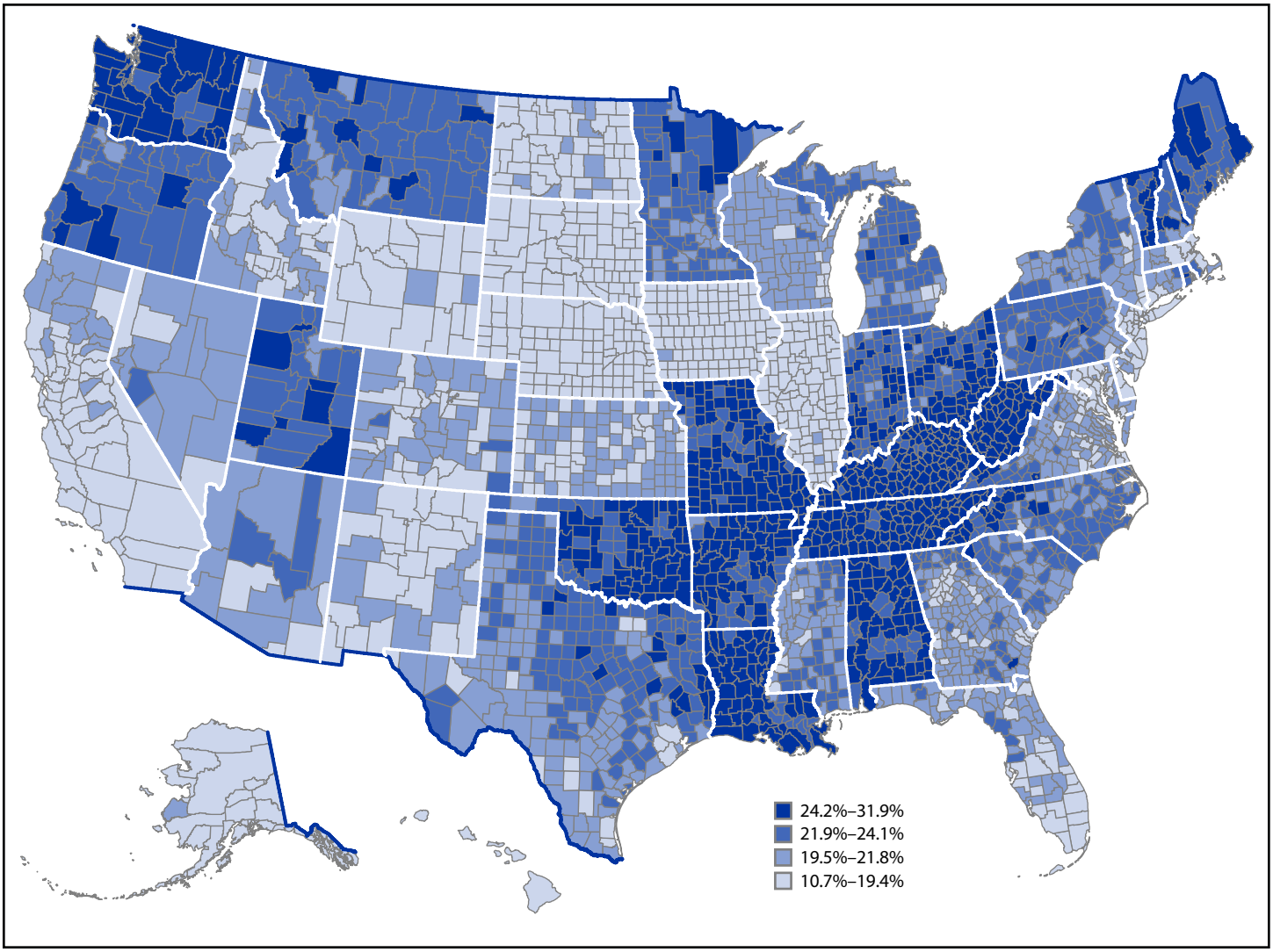
TABLE 2. State estimates of adults aged ≥18 years self-reporting a lifetime diagnosis of depression* — Behavioral Risk Factor Surveillance System, United States, 2020

Jurisdiction	Sample size	Unweighted no. with depression	Weighted† no. with depression (thousands)	Prevalence† % (95% CI)	Age-standardized prevalence§ % (95% CI)
Alabama	5,316	1,252	899	23.5 (22.1–25.0)	23.8 (22.2–25.4)
Alaska	3,649	566	87	15.9 (14.1–17.9)	15.7 (13.9–17.6)
Arizona	10,224	1,867	992	17.4 (16.4–18.4)	17.5 (16.4–18.6)
Arkansas	5,216	1,116	544	23.5 (21.9–25.2)	24.2 (22.4–26.1)
California	4,776	758	4,324	14.1 (12.8–15.5)	13.9 (12.7–15.3)
Colorado	10,131	1,836	842	18.5 (17.6–19.4)	18.5 (17.6–19.4)
Connecticut	8,929	1,649	500	17.7 (16.5–19.0)	18.4 (17.0–19.8)
Delaware	4,010	654	121	15.6 (14.1–17.1)	15.8 (14.3–17.6)
District of Columbia	3,410	621	114	19.8 (18.0–21.7)	19.9 (18.1–21.8)
Florida	11,746	2,038	2,570	14.7 (13.4–16.0)	14.9 (13.5–16.4)
Georgia	9,040	1,618	1,413	17.2 (16.0–18.5)	17.3 (16.0–18.6)
Hawaii	7,735	1,098	141	12.7 (11.8–13.7)	12.7 (11.8–13.8)
Idaho	5,947	1,058	258	18.9 (17.5–20.3)	19.0 (17.6–20.5)
Illinois	3,659	509	1,435	14.7 (13.2–16.4)	15.0 (13.4–16.7)
Indiana	8,435	1,753	1,137	21.9 (20.8–23.0)	22.2 (21.1–23.4)
Iowa	9,606	1,541	422	17.4 (16.5–18.4)	18.1 (17.1–19.1)
Kansas	10,475	1,820	424	19.2 (18.2–20.2)	19.6 (18.5–20.7)
Kentucky	3,918	918	838	24.2 (22.5–26.0)	25.0 (23.2–26.9)
Louisiana	4,722	1,089	829	23.5 (21.9–25.2)	23.8 (22.1–25.6)
Maine	10,935	2,271	241	22.1 (20.8–23.3)	23.1 (21.6–24.6)
Maryland	14,202	2,299	740	15.7 (14.9–16.6)	16.1 (15.1–17.0)
Massachusetts	7,127	1,233	990	17.9 (16.7–19.3)	18.2 (16.8–19.5)
Michigan	7,237	1,385	1,530	19.5 (18.3–20.8)	20.3 (19.0–21.7)
Minnesota	15,781	3,249	864	19.8 (19.0–20.6)	20.2 (19.4–21.0)
Mississippi	6,443	1,224	473	20.9 (19.5–22.3)	21.1 (19.6–22.6)
Missouri	9,162	1,975	1,086	22.8 (21.6–24.0)	23.4 (22.1–24.7)
Montana	6,283	1,310	191	22.6 (21.3–23.9)	23.4 (22.0–24.9)
Nebraska	14,748	2,304	245	16.8 (15.8–17.7)	17.0 (16.0–18.0)
Nevada	2,471	447	429	17.6 (15.6–19.7)	17.5 (15.5–19.6)
New Hampshire	6,411	1,285	238	21.5 (20.0–22.9)	22.5 (20.9–24.2)
New Jersey	11,312	1,832	1,055	15.2 (14.4–16.1)	15.6 (14.7–16.5)
New Mexico	6,984	1,207	284	17.6 (16.1–19.1)	17.8 (16.2–19.5)
New York	14,661	2,559	2,560	16.8 (15.9–17.7)	16.7 (15.9–17.7)
North Carolina	5,817	1,201	1,730	20.8 (19.6–22.2)	20.7 (19.4–22.1)
North Dakota	4,454	708	112	19.2 (17.6–21.0)	19.6 (17.9–21.5)
Ohio	14,592	3,242	2,005	22.0 (21.1–23.0)	22.8 (21.7–23.9)
Oklahoma	5,011	1,129	686	22.9 (21.4–24.4)	23.0 (21.5–24.6)
Oregon	5,380	1,152	712	21.2 (19.9–22.5)	21.4 (20.1–22.8)
Pennsylvania	5,520	1,108	2,056	20.2 (18.9–21.7)	20.9 (19.5–22.5)
Rhode Island	5,348	1,135	180	21.1 (19.5–22.9)	21.4 (19.6–23.3)
South Carolina	3,996	808	876	21.4 (19.8–23.1)	21.5 (19.7–23.3)
South Dakota	6,895	949	108	16.1 (14.1–18.3)	16.4 (14.3–18.8)
Tennessee	4,641	1,152	1,296	24.1 (22.4–25.8)	24.4 (22.6–26.2)
Texas	10,968	2,215	3,881	17.7 (16.4–19.1)	17.5 (16.2–18.9)
Utah	10,861	2,398	537	23.1 (22.1–24.2)	22.7 (21.8–23.7)
Vermont	6,511	1,443	118	23.3 (21.7–25.0)	24.2 (22.4–26.0)
Virginia	9,490	1,670	1,153	17.2 (16.2–18.3)	17.4 (16.3–18.5)
Washington	12,837	3,027	1,412	23.4 (22.5–24.4)	23.5 (22.5–24.5)
West Virginia	5,855	1,530	373	26.4 (25.0–27.8)	27.5 (25.9–29.1)
Wisconsin	5,078	913	904	19.8 (18.3–21.5)	20.5 (18.8–22.3)
Wyoming	4,791	709	81	18.3 (16.6–20.0)	18.9 (17.1–20.8)

* Respondents were classified as having depression if they responded "yes" to the question, "Has a doctor, nurse, or other health professional ever told you that you had a depressive disorder, including depression, major depression, dysthymia, or minor depression?"
† Weighted using the statistical weights provided in the Behavioral Risk Surveillance System data set.
§ Age-standardized to the 2000 projected U.S. Census Bureau population aged ≥18 years using four groups (18–24, 25–44, 45–64, and ≥65 years). https://www.cdc.gov/nchs/data/statnt/statnt20.pdf

The highest prevalence of having ever been diagnosed with depression by a health care professional was found among young adults (aged 18–24 years). Data from the National Survey on Drug Use and Health show that during 2015 to 2019, previous-year depression increased most rapidly among adolescents (aged 12–17 years) and young adults

FIGURE. Model-based age-standardized* county estimates of the percentage† of adults aged ≥18 years self-reporting a lifetime diagnosis of depression§ — Behavioral Risk Factor Surveillance System, United States, 2020



* Age-standardized to the 2000 projected U.S. Census Bureau population aged ≥18 years using 13 age groups (18–24, 25–29, 30–34, 35–39, 40–44, 45–49, 50–54, 50–59, 60–64, 65–69, 70–74, 75–79, and ≥80 years). https://www.cdc.gov/nchs/data/statnt/statnt20.pdf
† By quartile.
§ Respondents were classified as having depression if they responded "yes" to the question, "Has a doctor, nurse, or other health professional ever told you that you had a depressive disorder, including depression, major depression, dysthymia, or minor depression?"

(aged 18–25 years) (*4*). Depression can affect people differently by age,††† and the American Psychological Association provides clinical practice guidelines and decision aids for the treatment of depression by age group, including children and adolescents, adults, and older adults.§§§ Health promoting behaviors, including physical activity, quality sleep, and good nutrition, can help to manage symptoms of depression and support positive mental health across the lifespan (*7*).¶¶¶

There was considerable geographic variation in the prevalence of depression, with the highest state and county estimates of depression observed along the Appalachian and southern Mississippi Valley regions. Depression is a comorbidity for many chronic diseases, including diabetes, arthritis, and cardiovascular diseases (*8*). These diseases also occur in higher concentrations in states within the Appalachian region,**** suggesting that geographic variation in the prevalence of depression might partially reflect patterns of other chronic

††† https://www.nimh.nih.gov/health/publications/depression
§§§ https://www.apa.org/depression-guideline
¶¶¶ https://www.cdc.gov/mentalhealth/

**** https://www.arc.gov/wp-content/uploads/2020/06/Health_Disparities_in_Appalachia_August_2017.pdf

diseases. The variation in depression might also reflect the influence of social determinants of health[††††] in counties and states, including economic status and differences in access to health care. For example, adults in the Appalachian region tend to have lower incomes, higher poverty rates, and lower education levels, all of which can negatively affect health and well-being.[§§§§] The model-based county-level estimates provided in this report offer a starting point for identifying geographic disparities in depression. Incorporating additional neighborhood-level data and context can help guide local public health practitioners in the development and implementation of effective and targeted efforts to address mental health in their communities.

Population-level efforts to address prevention, treatment, and management of depression include tailored and targeted programs to address demographic and geographic disparities. CDC provides information about mental health resources and programs, including those focused on specific populations (e.g., children, older adults, and those with chronic conditions). Depression often co-occurs with other health conditions, and chronic disease self-management programs also help persons with chronic conditions manage their disease and improve their mental health.[¶¶¶¶] CDC's How Right Now[*****] is a communications campaign designed to promote and strengthen the emotional well-being and resilience of persons disproportionally affected by mental health challenges. The campaign offers evidence-based information and resources to address the emotional health needs of adults (*9*).

In addition, CPSTF provides communities with a list of recommended interventions to improve mental health or address mental illness.[†††††] Examples of recommended interventions include collaborative care for the management of depressive disorders, mental health benefits legislation, school-based cognitive behavioral therapy programs to reduce depression and anxiety symptoms (targeted and universal), and depression care management among older adults (clinic- and home-based). SAMHSA's Evidence-Based Practices Resource Center also provides communities, clinicians, policymakers and others with the information and tools to incorporate evidence-based practices into their communities or clinical settings.[§§§§§]

[††††] https://www.cdc.gov/chronicdisease/programs-impact/sdoh.htm
[§§§§] https://health.gov/healthypeople/priority-areas/social-determinants-health
[¶¶¶¶] https://www.cdc.gov/arthritis/interventions/self_manage.htm
[*****] https://www.cdc.gov/howrightnow/
[†††††] https://www.thecommunityguide.org/pages/task-force-findings-mental-health.html
[§§§§§] https://www.samhsa.gov/resource-search/ebp

Summary

What is already known about this topic?

Depression is a major cause of morbidity and mortality in the United States.

What is added by this report?

During 2020, 18.4% of U.S. adults reported having ever been diagnosed with depression; state-level age-standardized estimates ranged from 12.7% in Hawaii to 27.5% in West Virginia. Model-based age-standardized county-level prevalence estimates ranged from 10.7% to 31.9%, and there was considerable state-level and county-level variability.

What are implications for public health practice?

Decision-makers can use these estimates to guide resource allocation to areas where the need is greatest, possibly by implementing practices such as those recommended by The Guide to Community Preventive Services Task Force and the Substance Abuse and Mental Health Services Administration.

The findings in this report are subject to at least three limitations. First, BRFSS collects self-reported data about whether the respondent has ever received a diagnosis of depression from a health care professional and these data are susceptible to recall, nonresponse, cultural and social desirability, and other reporting biases (*10*). Differences in reporting could be attributed to sex, cultural, and generational differences, and a person's willingness to discuss symptoms with a health care provider, as well as their access to a provider. Second, data are collected via a landline and cell phone survey that excludes institutionalized populations or those who cannot be reached via this method, which might affect the representativeness of the samples. Finally, county estimates of prevalence might be imprecise because the multilevel regression modeling approach uses the U.S. Census Bureau Vintage 2020 county population estimates, which are estimates of the population rather than census counts.

This report provides current estimates of national, state-level, and county-level prevalence of adults reporting a lifetime diagnosis of depression. These estimates can help decision-makers guide resource allocation to areas where the need is greatest, which might include consideration of evidence-based interventions and practices such as those recommended by CPSTF and SAMHSA.

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Genomic Surveillance for SARS-CoV-2 Variants: Circulation of Omicron Lineages — United States, January 2022–May 2023

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CDC has used national genomic surveillance since December 2020 to monitor SARS-CoV-2 variants that have emerged throughout the COVID-19 pandemic, including the Omicron variant. This report summarizes U.S. trends in variant proportions from national genomic surveillance during January 2022–May 2023. During this period, the Omicron variant remained predominant, with various descendant lineages reaching national predominance (>50% prevalence). During the first half of 2022, BA.1.1 reached predominance by the week ending January 8, 2022, followed by BA.2 (March 26), BA.2.12.1 (May 14), and BA.5 (July 2); the predominance of each variant coincided with surges in COVID-19 cases. The latter half of 2022 was characterized by the circulation of sublineages of BA.2, BA.4, and BA.5 (e.g., BQ.1 and BQ.1.1), some of which independently acquired similar spike protein substitutions associated with immune evasion. By the end of January 2023, XBB.1.5 became predominant. As of May 13, 2023, the most common circulating lineages were XBB.1.5 (61.5%), XBB.1.9.1 (10.0%), and XBB.1.16 (9.4%); XBB.1.16 and XBB.1.16.1 (2.4%), containing the K478R substitution, and XBB.2.3 (3.2%), containing the P521S substitution, had the fastest doubling times at that point. Analytic methods for estimating variant proportions have been updated as the availability of sequencing specimens has declined. The continued evolution of Omicron lineages highlights the importance of genomic surveillance to monitor emerging variants and help guide vaccine development and use of therapeutics.

CDC's national genomic surveillance system integrates SARS-CoV-2 sequences from three sources: 1) the National SARS-CoV-2 Strain Surveillance (NS3) program,[†] 2) CDC-contracted commercial laboratories, and 3) public sequence data repositories, including the Global Initiative on Sharing All Influenza Data (GISAID) repository and National Center for Biotechnology Information (NCBI) GenBank.[§] Variant proportions generated by genomic surveillance are regularly updated on CDC's COVID Data Tracker and guide public health measures to address COVID-19[¶] (*1*,*2*).

Weekly SARS-CoV-2 consensus sequences[**] from the NS3 program, commercial laboratories, and data repositories were quality-filtered,[††] deduplicated, and assigned Pango lineages (*3*). During January 2022–May 2023, the median interval from specimen collection to data availability was 16 days. Weekly variant proportions were estimated at the national and U.S. Department of Health and Human Services (HHS) regional levels[§§] by specimen collection date for the 11 weeks before the most recent 3 weeks; lineages were included if they constituted ≥1% (unweighted) of sequences nationally and contained spike protein substitutions of potential therapeutic relevance. To estimate variant proportions for the most recent 3 weeks, nowcasts were generated using multinomial regression fit on the previous 21 weeks of data.[¶¶] All methods included weighting to account for the complex survey design and adjust

[*] These authors contributed equally to this report.

[†] https://www.cdc.gov/coronavirus/2019-ncov/variants/cdc-role-surveillance.html

[§] Sequences from public sequence data repositories are limited to those meeting baseline surveillance criteria, which ensures that they appropriately capture geographic, demographic, and clinical diversity. https://www.aphl.org/programs/preparedness/Crisis-Management/Documents/Technical-Assistance-for-Categorizing-Baseline-Surveillance-Update-Oct2021.pdf

[¶] https://covid.cdc.gov/covid-data-tracker/#variant-proportions; https://data.cdc.gov/Laboratory-Surveillance/SARS-CoV-2-Variant-Proportions/jr58-6ysp

[**] A consensus sequence is produced by aligning SARS-CoV-2 nucleotide sequences generated through sequencing a sample and then determining the most common nucleotide at each position. A consensus sequence is an interoperable genomic surveillance unit that can be combined from laboratory sources.

[††] Quality filters included limiting sequences to include only human-derived sources and U.S-specific sequences and excluding those with invalid state names and laboratory sources.

[§§] https://www.hhs.gov/about/agencies/iea/regional-offices/index.html

[¶¶] Before August 13, 2022, nowcasts were used to produce estimates for only the most recent 2 weeks.

for potential sampling biases.*** Nowcasts were conducted for any lineages with ≥0.5% prevalence beginning October 11, 2022,††† to improve accuracy by accounting for differential growth rates of grouped sublineages. Weekly numbers of COVID-19 cases attributable to variants were estimated by multiplying counts of positive nucleic acid amplification tests from COVID-19 electronic laboratory reporting (CELR) with variant proportions. Doubling times for proportions of specific lineages were estimated from the coefficients of the multinomial nowcasting model.§§§ Methodologic changes following the public health emergency expiration (*4*) were summarized. Biweekly estimates using the updated model were compared with weekly estimates from the previous model to assess consistency. Data were current as of June 1, 2023. This activity was reviewed by CDC and conducted consistent with applicable federal law and CDC policy.¶¶¶

During January 2, 2022–May 13, 2023, a total of 1,697,197 SARS-CoV-2 surveillance sequences from 56 U.S. jurisdictions**** were generated by or reported to CDC from NS3 (1%), commercial laboratories (60%), and repositories (38%); the percentage of sequences from repositories represented an increase from 10% during June 2021–January 2022 (*1*). The weekly number of sequenced specimens decreased from approximately 65,000 collected in January 2022 to approximately 4,400 in April 2023, as the number of COVID-19 cases declined (Supplementary Figure 1, https://stacks.cdc.gov/view/cdc/129515).

Omicron remained predominant during January 2, 2022–May 13, 2023, with various descendent lineages emerging and becoming predominant nationwide. The BA.1.1 lineage reached predominance by the week ending January 8, 2022, followed by BA.2 by March 26, BA.2.12.1 by May 14, and BA.5 by July 2 (Figure 1). The prevalence of these lineages peaked at 75.7% (95% CI = 73.8%–77.5%) for BA.1.1 by the week ending February 19, 2022; 73.4% (95% CI = 69.6%–77.0%) for BA.2 by April 16; 62.4% (95% CI = 60.7%–64.0%) for BA.2.12.1 by May 28; and 86.2% (95% CI = 85.2%–87.2%) for BA.5 by August 20. Circulation of these lineages coincided with surges in COVID-19 cases (Figure 1) (Supplementary Figure 2, https://stacks.cdc.gov/view/cdc/129516).

During the latter half of 2022, multiple Omicron descendants of BA.2, BA.4, and BA.5,†††† including BA.2.75, BA.4.6, BF.7, BQ.1, BQ.1.1, BA.5.2.6, BN.1, BF.11, and CH.1.1 accounted for >1% of circulating variants at different points (Figure 1). Several of these lineages independently acquired spike receptor binding domain (RBD) substitutions, including R346T, K444T, N460K, and F486S/P (Table). None attained predominance individually; however, BQ.1 (which includes K444T and N460K) and BQ.1.1 (which also includes R346T) reached a combined peak prevalence of 59.3% by December 24, 2022 (BQ.1, 22.1%; BQ.1.1, 37.2%), coinciding with a winter surge in cases (Figure 1) (Supplementary Figure 2, https://stacks.cdc.gov/view/cdc/129516).

In late fall 2022, the XBB lineage (recombinant of two BA.2 descendant lineages, BM.1.1.1 and BJ.1, with R346T, G446S, N460K, and F486S RBD substitutions) emerged in the United States, reaching <5% prevalence nationally. XBB.1.5, an XBB descendant (harboring an additional S486P substitution) was initially reported in New York City in October 2022 (*5*) and first reached predominance in HHS Region 2 (New York, New Jersey, Puerto Rico, and the U.S. Virgin Islands) on December 31, 2022, and Region 1 (Connecticut, Maine, Massachusetts, New Hampshire, Rhode Island, and Vermont) on January 7, 2023 (Figure 2). XBB.1.5 further spread south and west to attain national predominance by January 28, 2023, reaching a peak prevalence of 84.1% (95% CI = 81.4%–86.5%) by April 1 (Figure 1).

As of May 13, 2023, the commonly circulating Omicron lineages were XBB.1.5 (61.5%; 95% CI = 56.4%–66.4%), XBB.1.9.1 (10.0%; 95% CI = 6.8%–14.1%), and XBB.1.16 (9.4%; 95% CI = 6.9%–12.5%), with approximately a 19% combined prevalence of other circulating lineages, including XBB (5.3%), XBB.1.9.2 (4.5%), XBB.2.3 (3.2%), XBB.1.16.1 (2.4%), and XBB.1.5.1 (1.9%). Whereas many circulating XBB lineages share the XBB.1.5 spike sequence, XBB.1.16 and XBB.1.16.1 also contain the K478R RBD substitution and XBB.2.3 also contains the P521S substitution (Table). During the week ending May 13, 2023, the fastest doubling times

*** Variant proportion estimation methods account for the complex survey design, with weights based on the weekly estimated number of infections represented by each SARS-CoV-2 sequence; weights are trimmed to the 99th percentile. Each submitting laboratory source was considered a primary sampling unit, and the state and week of sequence sample collection were considered strata. The updated code, weight derivations, and nowcast model equations for the variant proportion estimation methods are available online. https://github.com/CDCgov/SARS-CoV-2_Genomic_Surveillance

††† Beginning October 11, 2022, growth rate and nowcast estimates were conducted for any lineages accounting for ≥0.5% of sequences nationwide (unweighted) in the last week before nowcast estimates. Lineages with a prevalence <1% or without spike protein substitutions of potential therapeutic or clinical relevance were aggregated with their parental lineage in the final estimates.

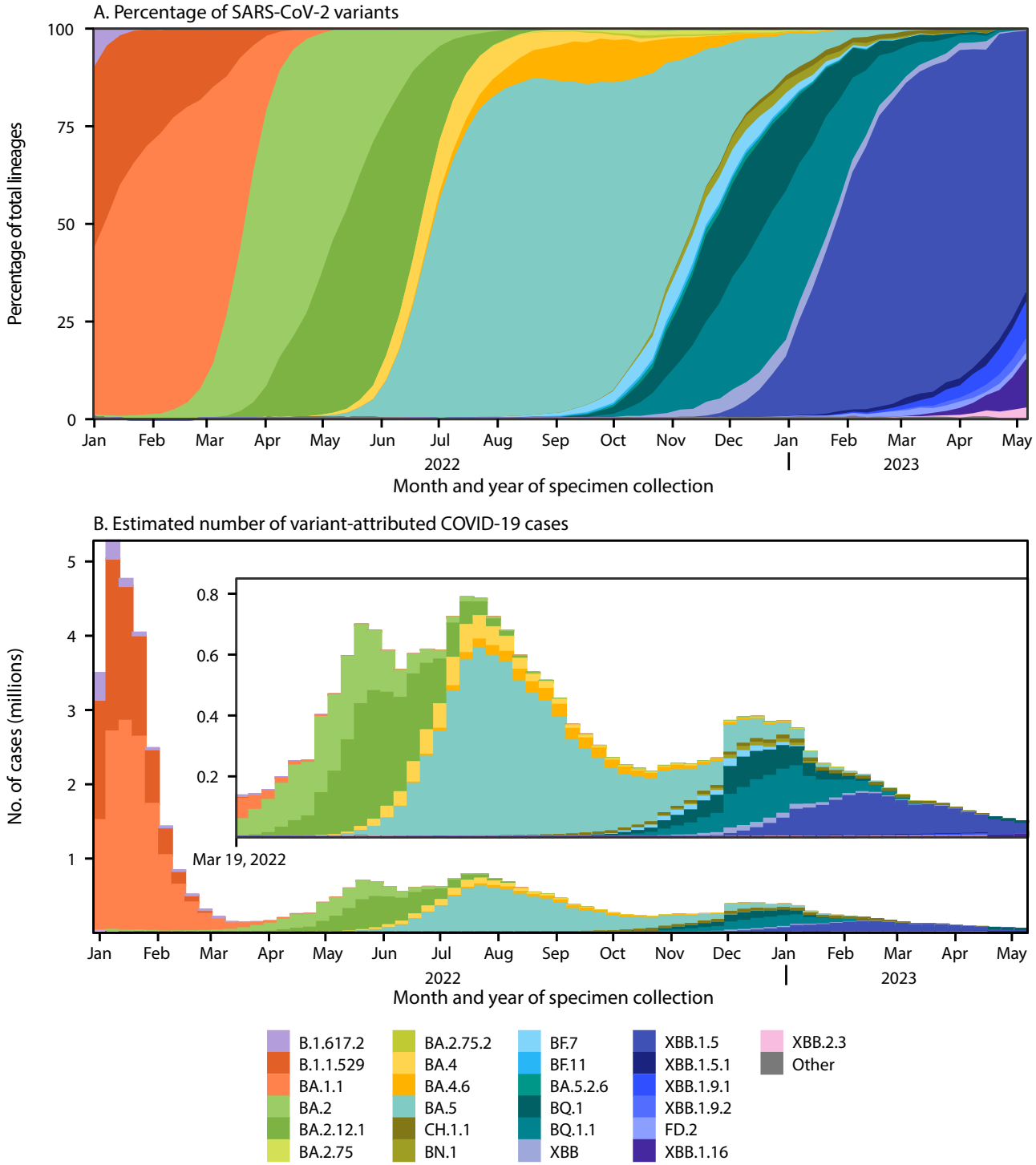
§§§ Doubling times for proportions of specific lineages are based on instantaneous growth rates from the multinomial nowcasting model. Doubling times were assessed either 1) when a lineage reached 1% prevalence, for comparisons of doubling times across all lineages, or 2) during the most recent week of data availability, to assess growth trajectories for currently circulating lineages.

¶¶¶ 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.0 Sect.552a; 44 U.S.C. Sect. 3501 et seq.

**** SARS-CoV-2 sequences originated from the 50 U.S. states, the District of Columbia, American Samoa, Guam, Northern Mariana Islands, Puerto Rico, and U.S. Virgin Islands.

†††† An unscaled dendrogram depicting the phylogenetic relationships between Omicron lineages is available on CDC's COVID Data Tracker. https://covid.cdc.gov/covid-data-tracker/#variant-summary

FIGURE 1. National estimates of weekly proportions* of SARS-CoV-2 variants† (A) and estimated number of variant-attributed cases§ (B) — United States, January 2, 2022–May 13, 2023



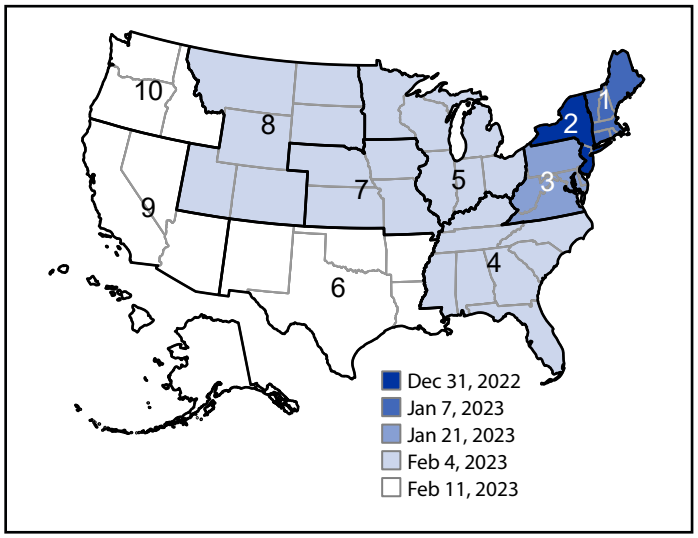
Abbreviations: CELR = COVID-19 electronic laboratory reporting; NS3 = National SARS-CoV-2 Strain Surveillance Program.

* Sequences are reported to CDC through NS3, contract laboratories, public health laboratories, and other U.S. institutions. Variant proportion estimation methods use a complex survey design and statistical weights to account for the probability that a specimen is sequenced. https://covid.cdc.gov/covid-data-tracker/#variant-proportions

† Lineages reaching a prevalence of ≥1% with spike protein substitutions of potential therapeutic relevance and separated out on the COVID Data Tracker website.

§ Estimated numbers of COVID-19 cases attributable to variants were calculated by multiplying weekly numbers of reported positive nucleic acid amplification tests from CELR with estimated variant proportions.

FIGURE 2. Omicron XBB.1.5 predominance,* by U.S. Department of Health and Human Services Region† and week that the variant became predominant — United States, December 25, 2022–February 11, 2023



Abbreviation: HHS = U.S. Department of Health and Human Services.

* The timing of XBB.1.5 predominance was defined as the week ending date during which the variant proportion estimate exceeded 50% in each HHS region. https://covid.cdc.gov/covid-data-tracker/#variant-proportions

† HHS Region 2 includes data from Puerto Rico and the U.S. Virgin Islands. HHS Region 3 includes data from the District of Columbia. HHS Region 9 includes data from American Samoa, Guam, and the Northern Mariana Islands. https://www.hhs.gov/about/agencies/iea/regional-offices/index.html

were observed for XBB.1.16 (15.7 days; 95% CI = 13.9–17.9), XBB.1.16.1 (16.7 days; 95% CI = 14.3–20.2), and XBB.2.3 (20.3 days; 95% CI = 16.6–26.0).

The fastest doubling times among lineages assessed at 1% prevalence during January 2, 2022–May 13, 2023, occurred for BA.2.12.1 (5.4 days; 95% CI = 4.8–6.1), BQ.1.1 (6.3 days; 95% CI = 5.5–7.2), BA.5 (6.8 days; 95% CI = 5.9–8.2), and XBB.1.5 (7.0 days; 95% CI = 5.8–8.6). In comparison, the doubling time for Omicron B.1.1.529 was 3.2 days (*1*). BA.5, XBB.1.5, and BA.1.1 remained predominant for the longest durations (19, 16, and 10 weeks, respectively). The number of cases attributed to each lineage was highest for BA.1.1 (14 million), B.1.1.529 (9.8 million) and BA.5 (8.0 million) (Figure 1) (Supplementary Figure 2, https://stacks.cdc.gov/view/cdc/129516). As of May 13, 2023, XBB.1.5 was associated with 1.8 million cases, with numbers expected to continue increasing.

Beginning May 13, 2023, after the expiration of the public health emergency declaration (*4*) and in response to declining numbers of cases and sequenced specimens, methodologic changes were made regarding the analysis of SARS-CoV-2 genomic surveillance data. The reporting cadence and unit of analysis changed from weekly to biweekly, with variant proportions estimated for 2-week periods and nowcast predictions conducted for the most recent 4 weeks,§§§§ and state-specific estimates were discontinued. For calculating survey weights, the level and source for information on positive test results changed to regional-level data from the National Respiratory and Enteric Virus Surveillance System (NREVSS)¶¶¶¶ (*6*). The previous and updated analytic methods using CELR- and NREVSS-derived survey weights, respectively, produced similar variant proportion estimates for all lineages. An example comparison of national and regional proportions of XBB.1.5 demonstrates the consistency between methodologies (Supplementary Figure 3, https://stacks.cdc.gov/view/cdc/129517).

Discussion

During January 2022–May 2023, CDC's genomic surveillance system detected the emergence and changing prevalence of multiple Omicron lineages nationwide. Predominant lineages included BA.1.1, BA.2, and BA.2.12.1 in the first half of 2022 and BA.5 and BQ.1/BQ.1.1 (combined) in the second half. Surges in COVID-19 cases were associated with the emergences of these variants. The rise of XBB.1.5 to predominance in 2023 was characterized by an expansion from the northeastern United States to southeastern and western regions. Multiple Omicron lineages independently acquired similar substitutions (e.g., R346T, K444T, N460K, and F486S/P) in the spike RBD, suggesting that these sites are under selective pressure in the population and drive enhanced viral circulation (*7*). Accordingly, these substitutions have been observed to be associated with escape from neutralizing antibodies, including previously authorized monoclonal antibody therapies (*7*,*8*), and the S486P substitution observed in some XBB-descendent lineages also has been observed to increase infectivity via enhanced angiotensin-converting enzyme 2 receptor binding affinity (*9*). XBB lineages with additional substitutions compared with XBB.1.5, namely XBB.1.16, XBB.1.16.1, and XBB.2.3, had the fastest doubling times as of May 13, 2023.

§§§§ Beginning May 11, 2023, weighted variant proportions were estimated for the six 2-week periods (12 weeks total) before the two most recent 2-week periods for select lineages accounting for ≥1% (unweighted) of sequences nationwide. Nowcast predictions were used to produce estimates for the two most recent 2-week periods. Nowcasts were also conducted for lineages accounting for ≥0.5% (unweighted) of sequences nationwide during the first 2-week nowcast period to improve accuracy by accounting for differential growth rates of grouped sublineages.

¶¶¶¶ Test positivity data (weekly numbers of positive specimens and total tests administered) from CELR were no longer available after the expiration of the public health emergency declaration (https://healthdata.gov/dataset/COVID-19-Diagnostic-Laboratory-Testing-PCR-Testing/j8mb-icvb). Beginning May 11, 2023, the percentage of positive nucleic acid amplification test results by HHS Region from NREVSS (https://www.cdc.gov/surveillance/nrevss/index.html), which correlate well with CELR data (https://doi.org/10.15585/mmwr.mm7219e2), were used with the number of positive specimens by state from CELR to estimate survey design weights.

TABLE. Predominant amino acid substitutions* in the receptor binding domain (residues 333–527) of the spike protein among Omicron lineages with ≥1% prevalence† relative to BA.4/BA.5 — United States, January 2, 2022–May 13, 2023

Lineage (partially expanded name)	Date added to CDT	Spike RBD (residues 333–527) amino acid substitutions																	
		339§	346§,¶	368	371	376	405	408	444§,¶	445¶	446§,¶	452§,¶	460§,¶	478	486§,¶	490§,¶	493§	496	521
BA.4/BA.5 reference sequence	**Jun 4, 2022**	**D**	**R**	**L**	**F**	**A**	**N**	**S**	**K**	**V**	**G**	**R**	**N**	**K**	**V**	**F**	**Q**	**G**	**P**
BA.4.6	Jul 30, 2022	—**	T	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
BA.5.2.6	Oct 29, 2022	—	T	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
BF.7 (BA.5.2.1.7)	Sep 17, 2022	—	T	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
BF.11 (BA.5.2.1.11)	Nov 19, 2022	—	T	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
BQ.1 (BA.5.3.1.1.1.1.1)	Oct 15, 2022	—	—	—	—	—	—	—	T	—	—	—	K	—	—	—	—	—	—
BQ.1.1 (BA.5.3.1.1.1.1.1.1)	Oct 15, 2022	—	T	—	—	—	—	—	T	—	—	—	K	—	—	—	—	—	—
BA.1.1	Feb 12, 2022	—	K	—	L	T	D	R	—	—	S	L	—	—	F	—	R	S	—
BA.2	Feb 5, 2022	—	—	—	—	—	—	—	—	—	—	L	—	—	F	—	R	—	—
BA.2.12.1	Apr 16, 2022	—	—	—	—	—	—	—	—	—	—	Q	—	—	F	—	R	—	—
BA.2.75	Sep 17, 2022	H	—	—	—	—	—	—	—	—	S	L	K	—	F	—	—	—	—
BN.1 (BA.2.75.5.1)	Nov 12, 2022	H	T	—	—	—	—	—	—	—	S	L	K	—	F	S	—	—	—
CH.1.1 (BA.2.75.3.4.1.1.1.1)	Jan 28, 2023	H	T	—	—	—	—	—	T	—	S	—	K	—	S	—	—	—	—
XBB/XBB.1	Nov 26, 2022	H	T	I	—	—	—	—	—	P	S	L	K	—	S	S	—	—	—
XBB.1.5	Dec 31, 2022	H	T	I	—	—	—	—	—	P	S	L	K	—	P	S	—	—	—
XBB.1.5.1	Mar 11, 2023	H	T	I	—	—	—	—	—	P	S	L	K	—	P	S	—	—	—
FD.2 (XBB.1.5.15.2)	Apr 15, 2023	H	T	I	—	—	—	—	—	P	S	L	K	—	P	S	—	—	—
XBB.1.9.1	Apr 1, 2023	H	T	I	—	—	—	—	—	P	S	L	K	—	P	S	—	—	—
XBB.1.9.2	Apr 15, 2023	H	T	I	—	—	—	—	—	P	S	L	K	—	P	S	—	—	—
XBB.1.16	Apr 15, 2023	H	T	I	—	—	—	—	—	P	S	L	K	R	P	S	—	—	—
XBB.1.16.1	May 27, 2023	H	T	I	—	—	—	—	—	P	S	L	K	R	P	S	—	—	—
XBB.2.3	May 6, 2023	H	T	I	—	—	—	—	—	P	S	L	K	—	P	S	—	—	S

Abbreviations: BA = B.1.1.529; CDT = COVID Data Tracker; RBD = receptor binding domain.

* Amino acid substitutions in the receptor binding domain (relative to a BA.4/BA.5 spike protein reference sequence) were included if they were present in ≥50% of sequences belonging to a given Pango lineage. The BA.4/BA.5 spike protein was used as a reference because of its inclusion in the bivalent mRNA COVID-19 booster vaccines. Residues conserved or with substitutions present in <50% of a lineage are not shown.

† Lineages reaching a prevalence of ≥1% with spike protein substitutions of potential therapeutic relevance and listed separately on the CDT website. https://covid.cdc.gov/covid-data-tracker/#variant-proportions

§ Indicates sites of independent substitutions in at least two different evolutionary lineages.

¶ Indicates sites identified in a previous study (https://doi.org/10.1038/s41586-021-04385-3) associated with in vitro reductions in binding by monoclonal antibodies that were previously authorized by the Food and Drug Administration.

** Dashes indicate no change from the BA.4/BA.5 reference sequence.

Data on SARS-CoV-2 Omicron variant proportions helped guide decisions to revoke the emergency use authorizations for different monoclonal antibody therapies with decreased clinical efficacy against various Omicron lineages starting winter 2021.***** Data on variant proportions were also used by the Food and Drug Administration (FDA) to recommend the inclusion of BA.4/BA.5 in updated (bivalent) vaccines in June 2022 and are expected to guide decisions about the composition of future COVID-19 vaccines.†††††

The findings in this report are subject to at least four limitations. First, early SARS-CoV-2 variant proportion estimates might have low precision because of relatively limited data availability and biases in the timing of specimen collection or sequence submission. These effects can be exacerbated by sequencing and reporting lag time (e.g., holidays) or laboratory issues, such as lineage-specific sequencing failures. Second, continued decreases in the number of sequencing specimens available over time affect precision; for this reason, state-specific estimates were discontinued in May 2023. Third, current analyses might differ from previous analyses because of fluctuations in sequencing data sources, changes in Pango lineage definitions, and methodologic updates. Finally, estimates of COVID-19 cases attributed to more recent lineages are affected by case underascertainment because of increasing at-home test use and other changes in test-seeking behaviors.

CDC has maintained national SARS-CoV-2 genomic surveillance since December 2020 to monitor variant proportions and aid in making timely decisions on prevention strategies, including vaccines and therapeutics. Analytic methods have been updated to maintain robust and representative estimates as the availability of sequencing specimens has declined; it is reassuring that the previous and updated weighting methodologies produced consistent estimates. Continued monitoring of SARS-CoV-2 variants in the U.S. population is key for

***** https://www.fda.gov/drugs/emergency-preparedness-drugs/emergency-use-authorizations-drugs-and-non-vaccine-biological-products; https://www.covid19treatmentguidelines.nih.gov/tables/variants-and-susceptibility-to-mabs/

††††† https://www.who.int/news/item/18-05-2023-statement-on-the-antigen-composition-of-covid-19-vaccines

Summary

What is already known about this topic?

CDC has used genomic surveillance to monitor trends in circulating U.S. SARS-CoV-2 variants since December 2020, including the emergence of the Omicron variant at the end of 2021.

What is added by this report?

Weekly estimates of variant proportions during January 2, 2022–May 13, 2023, identified the emergence and subsequent predominance of multiple Omicron lineages in the United States, including BA.2, BA.2.12.1, BA.5, and XBB.1.5. Repeated independent substitutions in the spike protein suggested convergent evolution related to immune evasion. Analytic methods for variant proportion estimation have been updated as numbers of cases and sequenced specimens have declined.

What are implications for public health practice?

Ongoing genomic surveillance can identify emerging SARS-CoV-2 variants and guide vaccine and therapeutic development and use.

guiding public health action, including FDA authorizations for COVID-19 therapeutics and strain selection for vaccines.

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Interim Recommendations for Use of Bivalent mRNA COVID-19 Vaccines for Persons Aged ≥6 Months — United States, April 2023

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Throughout the national public health emergency declared in response to the COVID-19 pandemic, CDC, guided by the Advisory Committee on Immunization Practices (ACIP), has offered evidence-based recommendations for the use of COVID-19 vaccines in U.S. populations after each regulatory action by the Food and Drug Administration (FDA). During August 2022–April 2023, FDA amended its Emergency Use Authorizations (EUAs) to authorize the use of a single, age-appropriate, bivalent COVID-19 vaccine dose (i.e., containing components from the ancestral and Omicron BA.4/BA.5 strains in equal amounts) for all persons aged ≥6 years, use of bivalent COVID-19 vaccine doses for children aged 6 months–5 years, and additional bivalent doses for immunocompromised persons and adults aged ≥65 years (*1*). ACIP voted in September 2022 on the use of the bivalent vaccine, and CDC made recommendations after the September vote and subsequently, through April 2023, with input from ACIP. This transition to a single bivalent COVID-19 vaccine dose for most persons, with additional doses for persons at increased risk for severe disease, facilitates implementation of simpler, more flexible recommendations. Three COVID-19 vaccines are currently available for use in the United States and recommended by ACIP: 1) the bivalent mRNA Pfizer-BioNTech COVID-19 vaccine, 2) the bivalent mRNA Moderna COVID-19 vaccine, and 3) the monovalent adjuvanted, protein subunit-based Novavax COVID-19 vaccine.* As of August 31, 2022, monovalent mRNA vaccines based on the ancestral SARS-CoV-2 strain are no longer authorized for use in the United States (*1*).

Since June 2020, ACIP has convened 35 public meetings to review data relevant to the potential use of COVID-19 vaccines.† The ACIP COVID-19 Vaccine Work Group, comprising experts in adult and pediatric medicine, infectious diseases, vaccinology, vaccine safety, public health, and ethics, has met weekly to review COVID-19 surveillance data, evidence for immunogenicity, efficacy, postauthorization effectiveness, safety of COVID-19 vaccines, and implementation considerations. To assess the evidence for benefits and harms associated with use of bivalent vaccines, and to guide deliberations, ACIP used the Evidence to Recommendations (EtR) Framework.§ Within this framework, ACIP considered the importance of COVID-19 as a public health problem, including during the Omicron-predominant era, as well as issues of resource use, benefits and harms, patients' values and preferences, acceptability, feasibility, and equity related to use of the vaccines. ACIP held three public meetings on September 1, 2022, February 24, 2023, and April 19, 2023, to discuss bivalent vaccine policy using the EtR Framework. ACIP voted on adult bivalent doses on September 1, 2022. Authorization for bivalent vaccines was subsequently extended to additional age groups, and CDC updated recommendations, guided by February 24, 2023, and April 19, 2023, input from ACIP (Box). To better protect against the Omicron variant, which emerged in November 2021, ACIP recommended a dose of bivalent mRNA vaccine (containing mRNA encoding the spike protein from both the ancestral SARS-CoV-2 and Omicron BA.4/BA.5 SARS-CoV-2 variants) in September 2022 (*2*). Among persons who had only received monovalent COVID-19 vaccines, bivalent COVID-19 vaccines have provided additional protection against infection and COVID-19–associated hospitalization; however, that protection might wane over time (*3*). From September 2022 to March 2023, vaccine effectiveness (VE) against emergency department and urgent care visits by adults aged 18–64 years waned from 53% (95% CI = 48%–58%) at 7–59 days after receipt of a bivalent dose to 42% (95% CI = 35%–47%) at 60–119 days. Protection against hospitalization among adults aged 18–64 years without an immunocompromising condition waned from 68% (95% CI = 53%–79%) at 7–59 days to 27% (95% CI = 2%–46%) at 60–119 days (*3*).

As of May 6, 2023, COVID-19–associated hospitalization rates were highest among adults aged ≥65 years (9.5 per 100,000 persons).¶ Bivalent booster doses are shown to provide the highest protection against hospitalization among

* Novavax is authorized as a 2-dose primary series and booster dose in limited situations (e.g., among persons for whom mRNA vaccines are contraindicated or who are unwilling to receive an mRNA vaccine). https://www.cdc.gov/vaccines/covid-19/clinical-considerations/interim-considerations-us.html

† https://www.cdc.gov/vaccines/hcp/acip-recs/vacc-specific/covid-19.html

§ https://www.cdc.gov/vaccines/acip/recs/grade/downloads/acip-evidence-recs-framework.pdf

¶ https://gis.cdc.gov/grasp/COVIDNet/COVID19_3.html (Accessed May 29, 2023).

BOX. Timeline of COVID-19 bivalent vaccine authorizations, by Food and Drug Administration and CDC vaccine recommendations — United States, August 2022–April 2023

August and September 2022

FDA authorizes and CDC recommends, with a single ACIP vote, 1) a single dose of Pfizer-BioNTech bivalent vaccine for persons aged ≥12 years 2 or more months after receipt of a primary series or previous monovalent booster dose and 2) a single dose of Moderna bivalent vaccine for adults aged ≥18 years 2 or more months after receipt of a primary series or previous monovalent booster dose.

October 2022

FDA authorizes and CDC recommends, with ACIP input, a single dose of Pfizer-BioNTech bivalent vaccine for children aged 5–11 years 2 or more months after receipt of a primary series or previous monovalent booster dose.

December 2022

FDA authorizes and CDC recommends, with ACIP input, a single dose of Moderna bivalent vaccine for children aged 6 months–5 years 2 or more months after receipt of a primary series.

FDA authorizes and CDC recommends, with ACIP input, a single dose of Pfizer-BioNTech bivalent vaccine for children aged 6 months–4 years as the third dose in a primary series 8 or more weeks after receipt of 2 monovalent doses of Pfizer-BioNTech vaccine.

March 2023

FDA authorizes and CDC recommends, with ACIP input, a single dose of Pfizer-BioNTech bivalent vaccine for children aged 6 months–4 years who received 3 monovalent doses of Pfizer-BioNTech as a primary series.

April 2023

FDA authorizes and CDC recommends, with ACIP input, a single dose of bivalent vaccine for all persons aged ≥6 years who are unvaccinated or 2 or more months after receipt of a previous monovalent dose.

FDA authorizes and CDC recommends, with ACIP input, at the time of initial vaccination (depending on vaccine product) 2 or 3 doses of bivalent vaccine for children aged 6 months–4 years and 1 or 2 doses of bivalent vaccine for children aged 5 years.

FDA authorizes and CDC recommends, with ACIP input, that persons aged ≥65 years may receive a single additional bivalent vaccine dose 4 or more months after receipt of their first bivalent dose.

FDA authorizes and CDC recommends, with ACIP input, that persons aged ≥6 months who are moderately or severely immunocompromised may receive an optional additional bivalent dose 2 or more months after the most recent bivalent dose and additional bivalent doses as needed.

Abbreviations: ACIP = Advisory Committee on Immunization Practices; FDA = Food and Drug Administration.

adults, with protection sustained through at least 179 days against critical outcomes, including intensive care unit admission or in-hospital death (*4*). However, only 17% of the U.S. population overall and 43.3% of adults aged ≥65 years have received a bivalent dose.** Primary series coverage (i.e., receipt of a complete COVID-19 vaccination series) follows a similar pattern: it is highest among older adults and lowest among young children.

Recommendations for Use of Bivalent COVID-19 Vaccines in Persons Aged ≥6 Years Without Immunocompromising Conditions

On April 18, 2023, FDA authorized and, on April 20, 2023, CDC recommended a single, age-appropriate bivalent mRNA dose for unvaccinated persons aged ≥6 years without moderate or severe immunocompromise. Previously vaccinated persons without moderate or severe immunocompromise were recommended to receive the vaccine ≥2 months after receipt of any monovalent vaccine dose (Table).

CDC's recommendation was based on input from ACIP during public meetings held on February 24, 2023, and April 19, 2023. At these meetings, discussions were guided by clinical trial data demonstrating that bivalent vaccines induce an immune response when administered as a primary series. Immunogenicity data demonstrated that a primary series of an Omicron BA.1-containing bivalent vaccine induced neutralization titers against BA.1 that were approximately 25 times those induced by the original monovalent vaccine†† (*5*). The percentage of patients reporting solicited systemic and local

** https://covid.cdc.gov/covid-data-tracker/#vaccination-demographics-trends (Accessed June 6, 2023).

†† Among 58 participants aged 6 months–5 years who received 25 μg of the Moderna Omicron BA.1–containing bivalent primary series and had available immunogenicity data, geometric mean ratios of neutralization titers 57 days after the BA.1-containing dose had 25.4 times the Omicron SARS-CoV-2 antibodies compared with titers in those receiving a monovalent dose, meeting superiority criteria. Superiority is considered met when the lower bound of the 97.5% CI of the geometric mean ratio, the ratio of neutralization titers in the intervention versus the control group, is >1.

TABLE. COVID-19 vaccines recommended for persons aged ≥6 months, by immunocompromise status and age group — CDC, United States, April 2023*

Immunocompromise status	Age group	Recommendation
Not moderately or severely immunocompromised	6 mos–5 yrs	At the time of initial vaccination, depending on vaccine product: 2 or 3 doses of bivalent vaccine for children aged 6 mos–4 yrs (Pfizer-BioNTech); and 1 or 2 doses of bivalent vaccine for children aged 5 yrs (Moderna)†
	≥6 yrs	A single bivalent dose
	≥65 yrs	A single bivalent dose and 1 additional, optional, bivalent dose
Moderately or severely immunocompromised	≥6 mos	A single bivalent dose and additional, optional, bivalent doses as needed

* https://www.cdc.gov/vaccines/covid-19/clinical-considerations/interim-considerations-us.html
† https://www.cdc.gov/vaccines/covid-19/clinical-considerations/interim-considerations-us.html#not-immunocompromised

reactogenicity after receiving the BA.1-containing vaccine was similar to or less than the percentage reporting these reactions after a receipt of a monovalent vaccine.§§ Unsolicited adverse events generally represented illnesses and commonly reported events during infancy and childhood (*5*).

CDC recommendations were also guided by ACIP discussions of seroprevalence data indicating that, for most older children, adolescents, and adults, future doses will provide an additional boost after previous infection, previous vaccination, or both. In a March–December 2022 nationwide seroprevalence study conducted among children aged 6 months–17 years, most children and adolescents had evidence of infection-induced immunity; prevalence of infection-induced immunity was highest among persons aged 5–11 and 12–17 years (93%) and lowest among children aged 6–11 months (63%) (*6*). Most adults also had preexisting antibodies against SARS-CoV-2. In a January–March 2022 seroprevalence study of adult blood donors aged ≥16 years, 96% had evidence of immunity from either previous infection, previous vaccination, or both (*7*).

A rare risk for myocarditis and pericarditis has been identified after receipt of monovalent mRNA COVID-19 vaccines, primarily in adolescent and young adult males. Because data are limited, the risk for myocarditis or pericarditis after receipt of a bivalent dose is not known; however, preliminary estimates suggest that the risk is lower than that observed after a second primary series monovalent dose (*8*). Higher rates of myocarditis have also been associated with a shorter interval between doses (*9*). Because of the small number of doses administered among adolescent and young adult males, estimating the incidence of myocarditis after a bivalent dose was not possible; however, only a single case of myopericarditis has been observed in the Vaccine Safety Datalink (a postauthorization vaccine safety monitoring system) during the 7 days after receipt of a bivalent dose in a male aged 18–29 years (*8*).

Recommendations from CDC were also guided by ACIP discussions of the benefits (i.e., reduction in the number of hospitalizations, intensive care unit admissions, and the number of deaths prevented) per 1 million primary series and bivalent vaccine doses administered, stratified by both age group and interval between primary series completion and receipt of a first bivalent dose. Benefits of a primary series and bivalent dose were seen among all age groups and at all intervals; however, the largest observed benefits were among the oldest age groups and those with the longest interval (i.e., ≥11 months) between completion of the primary series and receipt of the bivalent dose (*10*). Regular review of safety data, including myocarditis and pericarditis risk after bivalent doses, will continue in national safety surveillance systems.

Recommendations for Use of Bivalent COVID-19 Vaccine for Children Aged 6 Months–5 Years

During December 2022–April 2023, FDA amended multiple authorizations for bivalent mRNA vaccines for children aged 6 months–5 years. During this period, CDC updated recommendations, with input from ACIP, for children in this age group for use of bivalent doses based on a child's vaccination history (Table).

Among children aged 6 months–4 years, either mRNA vaccine may be used; however, all doses administered to a given child must be from the same manufacturer. Among those receiving Moderna vaccine, ≥2 doses are authorized, including ≥1 bivalent vaccine dose. Among those receiving Pfizer-BioNTech vaccine, ≥3 doses are authorized, including ≥1 bivalent vaccine dose.

Based on FDA authorizations, unvaccinated children aged 5 years are authorized to receive 2 doses of Moderna bivalent vaccine (with 4–8 weeks between doses) or 1 dose of Pfizer-BioNTech vaccine. Children aged 5 years who received 1 or 2 doses of monovalent Moderna vaccine are authorized to receive 1 dose of either the bivalent Moderna or Pfizer-BioNTech vaccine.¶¶ Those who received ≥1 doses of monovalent Pfizer-BioNTech vaccine are authorized to receive ≥1 bivalent Pfizer-BioNTech vaccine doses.

§§ Safety analysis was conducted among 142 children aged 6 months–5 years with available safety data.

¶¶ https://www.cdc.gov/vaccines/covid-19/clinical-considerations/interim-considerations-us.html#not-immunocompromised

CDC recommendations for pediatric immunization were guided by ACIP discussion of studies of bivalent vaccine given as a primary series in children, as well as booster doses among adults, demonstrating that a bivalent dose of either Moderna or Pfizer-BioNTech vaccine broadens the immune response in persons who have received a primary series and a previous monovalent booster dose (*5*). Compared with a monovalent booster dose (based on the ancestral SARS-CoV-2 strain), the immune response to Omicron was superior and that to the ancestral strain was noninferior among bivalent vaccine booster dose recipients. Monovalent booster doses of Moderna COVID-19 vaccines were studied in a clinical trial of 145 children aged 17 months–5 years who had received a Moderna primary series 8–13 months previously. Antibody levels after receipt of the monovalent booster dose in a subset of 56 children without previous SARS-CoV-2 infection were four times higher than were levels after the primary series in 294 young adults (*11*). Reactogenicity was similar to that observed after receipt of booster doses in other age groups. In a subset of 60 Pfizer-BioNTech pediatric trial participants aged 6 months–4 years who received a single bivalent Pfizer-BioNTech vaccine dose after completion of a 3-dose monovalent primary series, Omicron BA.4/BA.5–specific antibodies were higher compared with those among children who completed the 3-dose primary series of monovalent Pfizer-BioNTech vaccine and did not receive the bivalent booster dose. The bivalent dose was generally well-tolerated, with a lower frequency of postvaccination local and systemic reactions than previously observed in this age group with monovalent doses; no new or concerning safety findings were identified (*12*).

Additional Bivalent COVID-19 Doses for Adults Aged ≥65 Years and for Persons Aged ≥6 Months Who Are Moderately or Severely Immunocompromised

In April 2023, FDA granted an EUA for additional bivalent doses for adults aged ≥65 years and for persons aged ≥6 months with immunocompromise. Adults aged ≥65 years have the option to receive 1 additional bivalent vaccine dose ≥4 months after receipt of the most recent bivalent dose (Table). Persons aged ≥6 months who are moderately or severely immunocompromised have the option to receive ≥1 additional bivalent doses ≥2 months after receipt of the most recent bivalent dose and additional bivalent mRNA doses, as indicated, based on individual circumstances and clinical judgment.*** The option to receive ≥1 additional bivalent mRNA vaccine doses may be based on the clinical judgment of a health care provider, a person's risk for severe COVID-19 because of the presence of underlying medial conditions and age, and personal preference and circumstances.

CDC made recommendations based on ACIP discussions of VE and clinical epidemiology of COVID-19 among moderately or severely immunocompromised persons and adults aged ≥65 years. Effectiveness of a bivalent vaccine booster dose against hospitalization in adults aged ≥18 years with immunocompromising conditions was 30% (95% CI = 12%–44%) at 7–59 days postvaccination and 31% (95% CI = 4%–50%) at 120–179 days (*3*). Among adults aged ≥65 years, waning of absolute VE has been noted after receipt of a bivalent dose. Effectiveness of bivalent vaccines against COVID-19–associated emergency department or urgent care encounters among immunocompetent adults aged ≥65 years declined from 61% (95% CI = 57%–64%) 7–59 days after vaccination to 25% (95% CI = 16%–34%) at 120–179 days (*3*). VE against COVID-19–associated hospitalization declined from 64% (95% CI = 59%–69%) 7–59 days after vaccination to 39% (95% CI = 26%–50%) at 120–179 days (*3*).

Implementation Considerations

Before the authorization of a bivalent dose for most persons, 11 mRNA COVID-19 vaccine products were licensed or authorized for use. Authorization of a bivalent dose for most persons reduced the total number of vaccine products to five and eliminated vials that appear similar (i.e., look-alike vials) (*13*); these recommendations will thereby simplify implementation for COVID-19 vaccine providers. Reducing the number of products will expand providers' storage space and, in conjunction with the elimination of look-alike vials, might reduce vaccine administration errors.

The transition from a monovalent primary series to a single bivalent dose for most persons, and additional bivalent doses for populations at higher risk for severe disease, allows the COVID-19 vaccination program to progress toward simpler, more flexible, evidence-based recommendations. COVID-19 vaccination remains critical to protecting against serious consequences of COVID-19, and all persons aged ≥6 months should stay up to date with recommended COVID-19 vaccination, including receiving ≥1 bivalent vaccine dose.

Before vaccination, providers should provide the EUA Fact Sheet for the vaccine being administered and counsel vaccine recipients about expected systemic and local adverse reactions (reactogenicity). Additional clinical education materials are available,††† including further clinical considerations.§§§ These interim recommendations and clinical considerations

*** https://www.cdc.gov/vaccines/covid-19/clinical-considerations/interim-considerations-us.html#covid-vaccines

††† https://www.cdc.gov/vaccines/covid-19/index.html

§§§ https://www.cdc.gov/vaccines/covid-19/clinical-considerations/covid-19-vaccines-us.html

are based on currently available information regarding bivalent COVID-19 vaccine doses and might change as more evidence becomes available.

Reporting of Vaccine Adverse Events

Adverse events that occur after receipt of any COVID-19 vaccine should be reported to the Vaccine Adverse Event Reporting System (VAERS, https://vaers.hhs.gov or 1-800-822-7967). Vaccination providers are required by FDA to report vaccine administration errors, serious adverse events, cases of myocarditis, cases of pericarditis, cases of multisystem inflammatory syndrome, hospitalization or death, and cases of COVID-19 that result in hospitalization or death after administration of COVID-19 vaccine under EUA. Reporting is encouraged for any clinically significant adverse event even if it is uncertain whether the vaccine caused the event.

Summary

What is already known about this topic?

During August–October 2022, CDC recommended a bivalent COVID-19 mRNA vaccine dose for all persons aged ≥5 years who had received a monovalent primary vaccination series.

What is added by this report?

During December 2022–April 2023, CDC made recommendations for a single bivalent vaccine dose for most persons aged ≥6 years, bivalent vaccines for children aged 6 months–5 years, and optional additional bivalent booster doses for moderately or severely immunocompromised persons aged ≥6 months and adults aged ≥65 years.

What are the implications for public health practice?

Transition to a single bivalent COVID-19 vaccine dose for most persons, with additional doses for persons at increased risk for severe disease, facilitates implementation of simpler, more flexible recommendations. All persons aged ≥6 months should receive ≥1 bivalent vaccine dose.

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Notes from the Field

Increase in Meningococcal Disease Among Persons with HIV — United States, 2022

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Meningococcal disease, caused by the bacterium *Neisseria meningitidis*, is a sudden-onset, life-threatening illness that typically occurs as meningitis or meningococcemia. The most common signs and symptoms of meningitis include fever, headache, and stiff neck; the most common signs and symptoms of meningococcemia are fever, chills, fatigue, vomiting, diarrhea, cold hands and feet, and severe aches or pain.* Quadrivalent meningococcal conjugate vaccination (MenACWY) is routinely recommended for adolescents and persons at increased risk for meningococcal disease (*1*), including those with HIV. In 2016, a 2-dose series of MenACWY was recommended by the Advisory Committee on Immunization Practices (ACIP) for persons with HIV and incorporated into the U.S. immunization schedule. Coverage among persons with HIV, however, remains low: in a study of administrative claims data during January 2016–March 2018, only 16.3% of persons with HIV received ≥1 doses of MenACWY vaccine within 2 years after their diagnosis (*2*). This report describes an increase in meningococcal disease among persons with HIV in the United States in 2022. Data are typically finalized in the fall of the next year; therefore, this report is based on preliminary data for 2022.

Meningococcal disease cases are reported through the National Notifiable Diseases Surveillance System, with additional epidemiologic information and isolates obtained through Enhanced Meningococcal Disease Surveillance. Isolates are characterized using whole genome sequencing to determine serogroup and molecular typing information. This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.†

During 2017–2021, five to 15 meningococcal disease cases were reported each year among persons with HIV, representing 1.5%–4.3% of all meningococcal disease cases annually (Figure). Based on preliminary data, 29 meningococcal disease cases have been reported among persons with HIV in 2022, accounting for 9.8% of all cases. This case count might increase when reporting is complete.

Among the 29 meningococcal disease cases among persons with HIV in 2022, 22 had not received MenACWY vaccine, six had unknown MenACWY vaccination history, and one had received MenACWY vaccine, but the number of doses received was unknown. Fifteen of the 29 cases were part of a large serogroup C outbreak that occurred primarily among men who have sex with men (MSM); however, after excluding MSM outbreak-associated cases for all years, a substantial increase in meningococcal disease cases among persons with HIV in 2022 remained (i.e., 14 cases compared with four to eight cases per year during 2017–2021) (Figure). Of the 14 cases among persons with HIV in 2022 that were not related to the outbreak primarily among MSM, nine were caused by a single strain of *N. meningitidis* serogroup Y clonal complex CC174 sequence type ST-1466. Eight of these nine cases occurred in Black or African American persons, and seven occurred among MSM. The nine cases caused by a single strain were reported from three states with no identified connections among cases. The remaining five cases were not clustered geographically and had no identified epidemiologic connections.

MenACWY vaccine coverage among persons with HIV is low; given the recent increase in meningococcal disease cases in this population, health care providers should ensure that all persons with HIV are up to date with MenACWY vaccination per ACIP recommendations, as well as other vaccines recommended for this population. Health care providers should also maintain a high index of suspicion for meningococcal disease among persons with HIV who have symptoms of meningococcal disease. CDC recommends that all persons be screened for HIV at least once in their lifetime (*3*). Providers should ensure that patients with meningococcal disease and unknown HIV status are screened for HIV.

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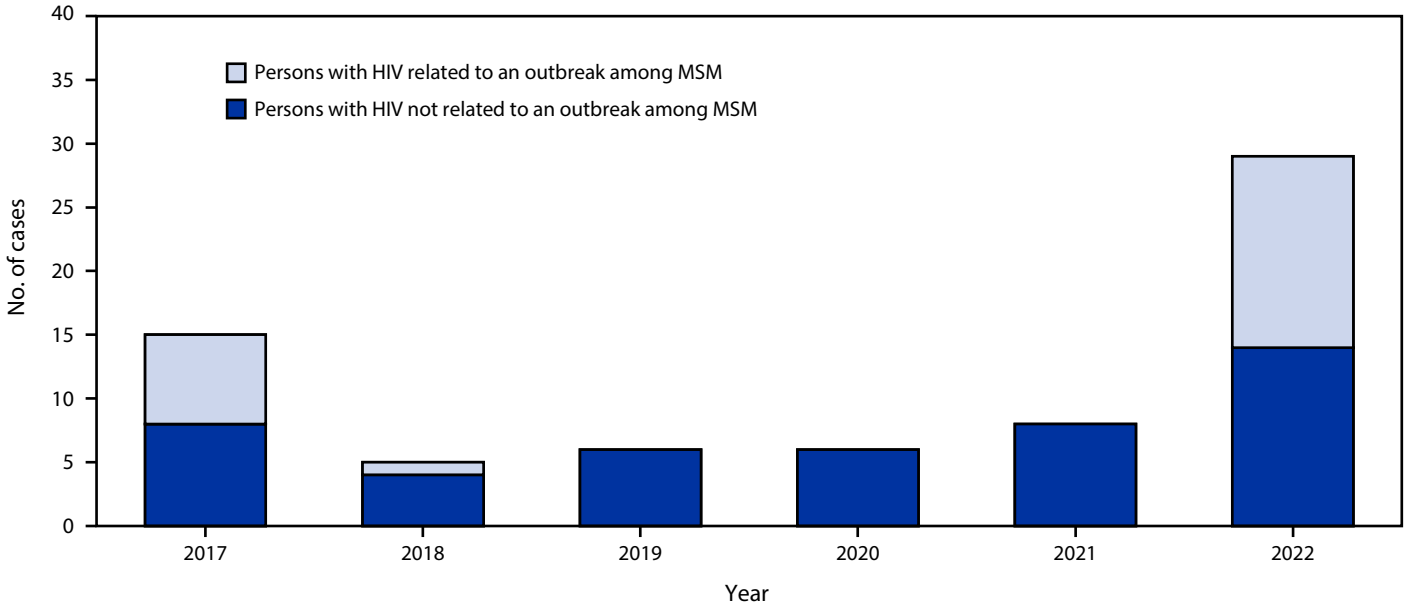
*https://www.cdc.gov/meningococcal/about/symptoms.html

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

FIGURE. Meningococcal disease cases among persons with HIV, by year — United States, 2017–2022*



Abbreviation: MSM = men who have sex with men.
* Data for 2022 are not yet final, and these numbers might increase when reporting is complete for the year.

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Notes from the Field

Tetanus in an Unvaccinated Man from Mexico — Oregon, 2022

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During June 2022, a non–English-speaking, Mexican-born male construction worker aged 42 years was evaluated at an Oregon emergency department (ED) complaining of 2 days of difficulty opening his mouth and pain in his back, arms, and neck. After receiving intravenous (IV) fluids and diazepam, he improved and was discharged. The following day, he visited a different ED with worsening symptoms, but again was discharged following administration of IV fluids and diazepam. He returned hours later with trismus and diffuse body spasms at which time a clinical diagnosis of tetanus was made. Immunization history was not documented during the first two ED visits. During the third ED visit, his family reported he had recently stepped on a nail at work and that he had no known history of tetanus immunization.

He was admitted to the hospital where he received IV metronidazole, tetanus immune globulin, tetanus toxoid, reduced diphtheria toxoid, and acellular pertussis vaccine (Tdap). Shortly thereafter, he experienced respiratory distress and was intubated. He was transferred to the intensive care unit (ICU) at a larger hospital, where a punctate callus was noted on the sole of the right foot. A tracheostomy was placed on day 13. He remained in the ICU through day 45. The tracheostomy was removed on day 48. At the time of discharge (day 50), he could speak, eat, drink, and walk short distances.

Tetanus is caused by a neurotoxin expressed by *Clostridium tetani*, an anaerobic, spore-forming gram-positive bacterium commonly found in soil and introduced through open wounds. Often life-threatening, tetanus can require months of medical care before recovery. During 2017, the cost for an unvaccinated pediatric patient in Oregon hospitalized with tetanus for 57 days exceeded $800,000 (*1*). Tetanus is preventable through a primary 3-dose diphtheria and tetanus toxoids and acellular pertussis (DTaP) vaccination series at 2, 4, and 6 months, with booster doses at ages 15–18 months and 4–6 years. Persons aged 11–18 years should receive a single booster dose of Tdap, preferably during a preventive care visit at age 11–12 years. To ensure continued protection against tetanus and diphtheria, booster doses of Td or Tdap should be administered every 10 years throughout life. CDC recommends that adults with no history of vaccination against tetanus receive tetanus toxoid–containing vaccines recommended by the Advisory Committee on Immunization Practices.* Migrant workers might be at increased risk for tetanus: their occupational injury risk has been shown to be twice that of U.S.-born workers (*2*).

Health care providers should be on alert for reemerging vaccine-preventable diseases as a result of declines in vaccination coverage attributable to the COVID-19 pandemic.† Providers should also be aware that migrant populations often have lower vaccination coverage rates and suffer higher rates of vaccine-preventable diseases than do nonmigrants (*3*). In the United States, vaccination coverage is significantly lower among non- U.S-born than among U.S.-born adults (*4*). Across the Americas, national vaccination schedules have largely reached parity during recent decades, ensuring high coverage among children and young adults; however, coverage among adults is lower. Mexico, the country representing the largest U.S. migrant population, lags behind the United States in immunization metrics: during 2022, 3-dose DTaP coverage among Mexican children aged 1 year was 74%, compared with 93% in the United States, and receipt of 2 measles-containing vaccine doses by the nationally recommended age was 78% in Mexico and 85% in the United States.§ Providers in the United States should remain particularly vigilant for vaccine-preventable diseases among non–U.S.-born patients and take every opportunity to administer recommended vaccines.

Ineffective communication between providers and patients can delay treatment. The patient described in this report did not have his immunization history documented until his third ED visit, and only after the diagnosis of tetanus was apparent. To mitigate language barriers, clinical care settings should provide interpreter services for non–English-speaking communities. Providers should be mindful that some Hispanic or Latino immigrants in the United States have limited health literacy, hindering quality of care (*5*). To address issues of health literacy, providers should consider use of both written and oral formats, photonovelas (picture stories), and "teach-back" methods¶.

This preventable tetanus case highlights the importance of equitable communication practices in health care settings, vigilance for serious but rare vaccine-preventable diseases, early ascertainment of immunization history, and awareness of possible lower vaccination coverage among migrant populations. Persons lacking verified immunization should be offered vaccination expeditiously.

* https://www.cdc.gov/mmwr/volumes/69/wr/mm6903a5.htm
† https://www.who.int/news/item/15-07-2022-covid-19-pandemic-fuels-largest-continued-backslide-in-vaccinations-in-three-decades
§ https://www.who.int/publications/i/item/9789240051157
¶ https://doi.org/10.3912/OJIN.Vol14No03Man02

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Notes from the Field

Comparison of COVID-19 Mortality Rates Among Adults Aged ≥65 Years Who Were Unvaccinated and Those Who Received a Bivalent Booster Dose Within the Preceding 6 Months — 20 U.S. Jurisdictions, September 18, 2022–April 1, 2023

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Updated (bivalent) COVID-19 vaccines were first recommended by CDC on September 1, 2022.* An analysis of case and death rates by vaccination status shortly after authorization of bivalent COVID-19 vaccines showed that receipt of a bivalent booster dose provided additional protection against SARS-CoV-2 infection and associated death (*1*). In this follow-up report on the durability of bivalent booster protection against death among adults aged ≥65 years, mortality rate ratios (RRs) were estimated among unvaccinated persons and those who received a bivalent booster dose by time since vaccination during three periods of Omicron lineage predominance (BA.5 [September 18–November 5, 2022], BQ.1/BQ.1.1 [November 6, 2022–January 21, 2023], and XBB.1.5 [January 22–April 1, 2023]).†

During September 18, 2022–April 1, 2023, weekly counts of COVID-19–associated deaths§ among unvaccinated persons and those who received a bivalent booster dose¶ were reported from 20 U.S. jurisdictions** that routinely link case surveillance data to immunization registries and vital registration databases (*1*). Vaccinated persons who did not receive a bivalent COVID-19 booster dose were excluded. Rate denominators were calculated from vaccine administration data and 2019 U.S. intercensal population estimates,†† with numbers of unvaccinated persons estimated by subtracting numbers of vaccinated persons from the 2019 intercensal population estimates, as previously described§§ (*1*). Average weekly mortality rates were estimated based on date of specimen collection¶¶ during each variant period by vaccination status and time since bivalent booster dose receipt. RRs were calculated by dividing rates among unvaccinated persons by rates among bivalent booster dose recipients; after detrending the underlying linear changes in weekly rates, 95% CIs were estimated from the

* https://www.cdc.gov/coronavirus/2019-ncov/vaccines/stay-up-to-date.html

† National weighted estimates of weekly proportions of circulating SARS-CoV-2 variants are reported by CDC (https://covid.cdc.gov/covid-data-tracker/#variant-proportions). Analysis periods were categorized based on Omicron lineage predominance (>50% of sequenced lineages) for BA.5 (September 18–November 5, 2022) and XBB.1.5 (January 22–April 1, 2023). The BQ.1/BQ.1.1 period (November 6, 2022–January 21, 2023) also included other lineages with similar mutations and was defined based on when BA.5 reached <50% related to the rise of these other lineages.

§ A COVID-19–associated death occurred in a person with a documented COVID-19 diagnosis who died and whose report local health authorities reviewed to make that determination (e.g., using vital records, public health investigation, or other data sources). Per national guidance, this group should include persons whose death certificate lists COVID-19 or SARS-CoV-2 as an underlying cause or a significant condition contributing to death (https://preparedness.cste.org/wp-content/uploads/2022/12/CSTE-Revised-Classification-of-COVID-19-associated-Deaths.Final_.11.22.22.pdf). In some jurisdictions, deaths that were not laboratory-confirmed were included.

¶ Unvaccinated persons did not receive any COVID-19 vaccine doses. Persons vaccinated with a bivalent booster dose received a primary series and an authorized bivalent COVID-19 vaccine dose on or after September 1, 2022, and ≥14 days before the positive specimen collection date; bivalent vaccines reported as first or second doses are classified as bivalent booster doses. Reinfections occurring ≥90 days after a previous infection were included.

** The 20 jurisdictions included in this analysis represent 41% of the U.S. population: Alabama, Arizona, Colorado, District of Columbia, Georgia, Idaho, Indiana, Kentucky, Louisiana, Michigan, Minnesota, Nebraska, New Jersey, New Mexico, New York City, North Carolina, Tennessee, Texas, Utah, and West Virginia.

†† https://www.census.gov/programs-surveys/popest/data/tables.2019.html

§§ A continuity correction was applied to denominators by capping vaccination coverage at 95%; it was assumed that ≥5% of each age group would be unvaccinated in each jurisdiction. Adding this correction ensures that there is always a reasonable denominator for the unvaccinated population and prevents incidence and death rates from growing unrealistically large because of potential overestimates of vaccination coverage.

¶¶ For deaths that were not laboratory-confirmed, alternative reference dates were used in lieu of positive specimen collection date (i.e., symptom onset date or date of death or report date when symptom onset date was unavailable).

remaining variation in rates observed*** (*1*). SAS (version 9.4; SAS Institute) and R (version 4.1.2; R Foundation) software were used to conduct all analyses. This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.†††

Among adults aged ≥65 years who were unvaccinated or had received a bivalent COVID-19 vaccine booster dose, 8,161 COVID-19–associated deaths in the 20 U.S. jurisdictions were reported during September 18, 2022–April 1, 2023. Overall, 58% of deaths occurred among adults aged ≥80 years; this distribution was consistent among vaccinated and unvaccinated persons and across the three variant periods. Mortality rates among adults aged ≥65 years peaked in December 2022 during the BQ.1/BQ.1.1 predominance period. Higher mortality rates were observed among unvaccinated persons during all three periods of Omicron lineage predominance (Table).

In time-stratified analyses comparing mortality rates among unvaccinated persons with those among vaccinated persons 2 weeks–2 months after receipt of a bivalent booster dose, mortality RRs significantly declined from 16.3 during the BA.5-predominant period to 8.4 during the XBB.1.5-predominant period, representing a modest reduction in crude vaccine effectiveness from 94% to 88%.§§§ Mortality RRs were similar among persons who had received a bivalent booster dose either 2 weeks–2 months earlier or 3–6 months earlier in the BQ.1/BQ.1.1-predominant period (11.4 and 11.0, respectively) and in the XBB.1.5-predominant period (8.4 and 7.3, respectively).¶¶¶

*** 95% CIs were calculated after detrending underlying linear changes in weekly rates using piecewise linear regression. Each 95% CI represents the remaining variation in observed weekly rates and resulting RRs. The number of observations leading to each 95% CI reflects the number of weeks per period: BA.5 (7 weeks), BQ.1/BQ.1.1 (11 weeks), and XBB.1.5 (10 weeks).

††† 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.0 Sect.552a; 44 U.S.C. Sect. 3501 et seq.

§§§ To interpret RR changes, age group-specific crude vaccine effectiveness was estimated as (1 – [incidence in vaccinated / incidence in unvaccinated]) x 100%.

¶¶¶ The median time since vaccination during the 2 weeks–2 months postvaccination category (14–89 days) was 22 days for the BA.5 period, 58 days for the BQ.1/BQ.1.1 period, and 72 days for the XBB.1.5 period. For the period 3–6 months since vaccination (90–212 days), the median time was 101 days during the BQ.1/BQ.1.1 period and 132 days for the XBB.1.5 period.

TABLE. Average weekly mortality rates* and rate ratios for unvaccinated adults aged ≥65 years compared with those vaccinated with a bivalent COVID-19 vaccine booster dose,† by time since vaccination and variant period§ — 20 U.S. jurisdictions,¶ September 18, 2022–April 1, 2023

		Vaccination status				
			Vaccinated with bivalent booster dose, by time since vaccination**			
		Unvaccinated	2 wks–2 mos		3–6 mos	
Period (predominant Omicron lineage)	Total	No. of deaths (mortality rate)	No. of deaths (mortality rate)	RR (95% CI)††	No. of deaths (mortality rate)	RR (95% CI)
Sep 18–Nov 5, 2022 (BA.5)	**1,717**	1,623 (13.5)	94 (0.8)	16.3 (13.8–19.1)	NA§§	NA§§
Nov 6, 2022–Jan 21, 2023 (BQ.1/BQ.1.1)	**4,537**	3,532 (18.8)	794 (1.6)	11.4 (9.4–13.9)	211 (1.8)	11.0 (8.4–14.4)
Jan 22–Apr 1, 2023 (XBB.1.5)	**1,907**	1,247 (7.3)	114 (0.9)	8.4 (6.1–11.7)	546 (1.0)	7.3 (6.1–8.7)

Abbreviations: NA = not applicable; RR = rate ratio.

* Deaths per 100,000 persons aged ≥65 years. A COVID-19–associated death occurred in a person with a documented COVID-19 diagnosis who died and whose report local health authorities reviewed to make that determination (e.g., using vital records, public health investigation, or other data sources). Per national guidance, this group should include persons whose death certificate lists COVID-19 or SARS-CoV-2 as an underlying cause or a significant condition contributing to death (https://preparedness.cste.org/wp-content/uploads/2022/12/CSTE-Revised-Classification-of-COVID-19-associated-Deaths.Final_.11.22.22.pdf). In some jurisdictions, deaths that were not laboratory-confirmed were included.

† Unvaccinated persons did not receive any COVID-19 vaccine doses. Persons vaccinated with a bivalent booster dose received a primary series and an authorized bivalent COVID-19 vaccine dose on or after September 1, 2022, and ≥14 days before the positive specimen collection date; bivalent vaccines reported as first or second doses are classified as bivalent booster doses. Reinfections occurring ≥90 days after a previous infection were included.

§ National weighted estimates of weekly proportions of circulating SARS-CoV-2 variants are reported by CDC (https://covid.cdc.gov/covid-data-tracker/#variant-proportions). Analysis periods were categorized based on Omicron lineage predominance (>50% of sequenced lineages) for BA.5 (September 18–November 5, 2022) and XBB.1.5 (January 22–April 1, 2023). The BQ.1/BQ.1.1 period (November 6, 2022–January 21, 2023) also included other lineages with similar mutations and was defined based on when BA.5 reached <50% related to the rise of these other lineages.

¶ The 20 jurisdictions included in this analysis represent 41% of the overall U.S. population: Alabama, Arizona, Colorado, District of Columbia, Georgia, Idaho, Indiana, Kentucky, Louisiana, Michigan, Minnesota, Nebraska, New Jersey, New Mexico, New York City, North Carolina, Tennessee, Texas, Utah, and West Virginia.

** Time since receipt of last bivalent booster dose categories was restricted to outcomes occurring during eligible weeks based on the timing of the first bivalent booster dose recommendation on September 1, 2022: 2 weeks–2 months (starting September 18, 2022) and 3–6 months (starting December 4, 2022). Unvaccinated persons were compared with persons who received a bivalent booster dose for the same time frame in each category. The median time since vaccination in the 2 weeks–2 months category (14–89 days) was 22 days for the BA.5 period, 58 days for the BQ.1/BQ.1.1 period, and 72 days for the XBB.1.5 period. For the period 3–6 months since vaccination (90–212 days), the median time was 101 days during the BQ.1/BQ.1.1 period and 132 days for the XBB.1.5 period.

†† RRs were calculated as the ratio between rates among unvaccinated persons compared with rates among bivalent booster dose recipients by time since vaccination (2 weeks–2 months and 3–6 months). 95% CIs were calculated after detrending underlying linear changes in weekly rates using piecewise linear regression. Each 95% CI represents the remaining variation in observed weekly rates and resulting RRs. The number of observations leading to each 95% CI reflects the number of weeks per period: BA.5 (7 weeks), BQ.1/BQ.1.1 (11 weeks), and XBB.1.5 (10 weeks).

§§ Based on the timing of the authorization of the bivalent vaccine on September 1, 2022.

The findings in this report are subject to at least six limitations. First, this ecologic study using surveillance data could not adjust for important confounders, such as variations in infection-derived immunity, comorbidities, and testing or prevention behaviors, which might contribute to mortality rate differences by vaccination status. Second, a decrease in mortality during the XBB.1.5 period limited sample sizes and statistical power. Third, only seven of 20 jurisdictions were able to include COVID-19–associated deaths without laboratory-confirmation, which have increased over time.**** Fourth, potential misclassification of bivalent and monovalent booster doses could influence RRs (*2*). Fifth, a small proportion (0.3%) of persons received a second bivalent booster before April 1, 2023, although this was not authorized for some persons until April 19, 2023.†††† Finally, these data represent approximately 41% of the U.S. population, and therefore, might not be generalizable.

In this assessment of the durability of protection afforded by a bivalent booster dose against COVID-19–associated death among adults aged ≥65 years, receipt of a bivalent booster dose provided substantial protection, with no significant evidence of waning up to 6 months postvaccination; this finding is similar to other studies assessing vaccine effectiveness against critical illness and death (*1*,*3*,*4*). However, some immune evasion was observed during the Omicron XBB.1.5 period (evidenced by a 6% decrease in vaccine effectiveness compared with that during the BA.5 period), likely related to changes in the spike protein relative to the BA.4/BA.5 spike contained in the bivalent vaccine. These findings are relevant to future decisions on COVID-19 vaccine composition.§§§§ With the expiration of the COVID-19 public health emergency declaration on May 11, 2023, routine monitoring of incidence, hospitalization rates, and death rates by vaccination status has been discontinued; however, CDC will continue to monitor vaccine effectiveness through well-controlled studies (e.g., the VISION and IVY networks) (*5*). All persons should stay up to date with recommended COVID-19 vaccines, including ≥1 bivalent dose for persons aged ≥6 months. Additional bivalent vaccine doses are optional for adults aged ≥65 years and immunocompromised persons.

**** https://www.cdc.gov/coronavirus/2019-ncov/science/data-review/index.html
†††† https://www.cdc.gov/media/releases/2023/s0419-covid-vaccines.html
§§§§ https://www.who.int/news/item/18-05-2023-statement-on-the-antigen-composition-of-covid-19-vaccines

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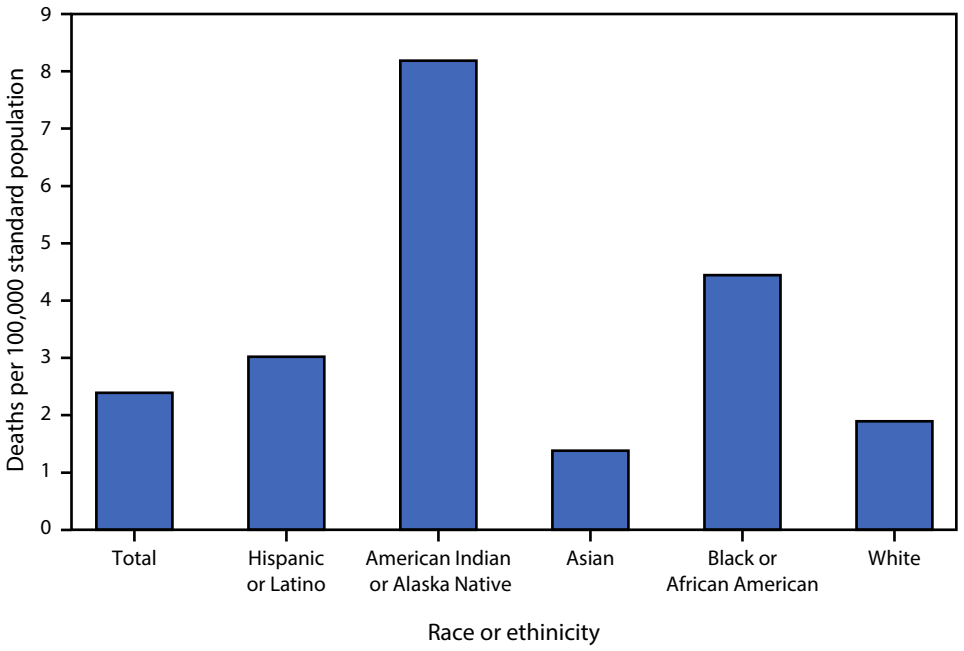
QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Age-Adjusted Death Rates*,† for Pedestrians Involved in a Collision with a Motor Vehicle,§ by Race and Hispanic Origin¶ — National Vital Statistics System, United States, 2021



* Deaths per 100,000 U.S. standard population.
† Death rates for Asian, American Indian or Alaska Native, and Hispanic or Latino (Hispanic) persons might be affected by misclassification of race and Hispanic origin on death certificates. https://www.cdc.gov/nchs/data/series/sr_02/sr02_172.pdf
§ Deaths from pedestrians involved in a collision with a motor vehicle, including traffic and non-traffic accidents, as the underlying cause of death were identified using the *International Classification of Diseases, Tenth Revision* codes V02–V04, V09[.0,.2].
¶ Hispanic persons could be of any race. All reported race groups are non-Hispanic.

In 2021, a total of 8,392 deaths from pedestrian-involved collisions with motor vehicles occurred. The age-adjusted death rate from such collisions was highest for American Indian or Alaska Native persons (8.2 deaths per 100,000 standard population), followed by Black or African American (4.4), Hispanic or Latino (3.0), White (1.9), and Asian (1.4) persons.

Source: National Vital Statistics System, Underlying Cause of Death, 2018–2021. https://wonder.cdc.gov/ucd-icd10-expanded.html

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