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Birth Prevalence of Sickle Cell Disease and County-Level Social Vulnerability — Sickle Cell Data Collection Program, 11 States, 2016–2020

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Abstract

Sickle cell disease (SCD) remains a public health priority in the United States because of its association with complex health needs, reduced life expectancy, lifelong disabilities, and high cost of care. A cross-sectional analysis was conducted to calculate the crude and race-specific birth prevalence for SCD using state newborn screening program records during 2016–2020 from 11 Sickle Cell Data Collection program states. The percentage distribution of birth mother residence within Social Vulnerability Index quartiles was derived. Among 3,305 newborns with confirmed SCD (including 57% with homozygous hemoglobin S or sickle β-null thalassemia across 11 states, 90% of whom were Black or African American [Black], and 4% of whom were Hispanic or Latino), the crude SCD birth prevalence was 4.83 per 10,000 (one in every 2,070) live births and 28.54 per 10,000 (one in every 350) non-Hispanic Black newborns. Approximately two thirds (67%) of mothers of newborns with SCD lived in counties with high or very high levels of social vulnerability; most mothers lived in counties with high or very high levels of vulnerability for racial and ethnic minority status (89%) and housing type and transportation (64%) themes. These findings can guide public health, health care systems, and community program planning and implementation that address social determinants of health for infants with SCD. Implementation of tailored interventions, including increasing access to transportation, improving housing, and advancing equity in high vulnerability areas, could facilitate care and improve health outcomes for children with SCD.

Introduction

Sickle cell disease (SCD) is an inherited blood disorder caused by mutations in the hemoglobin subunit beta (*HBB*) gene and is associated with premature mortality (*1*) and significant morbidity, including vasoocclusive pain, stroke, and multiorgan damage. The protective association between variants in *HBB* and severe *Plasmodium falciparum* malaria results in a higher prevalence of *HBB* mutations in geographic areas with high malaria prevalences (*2*). The combination of this protective effect and the historical trans-Atlantic slave trade has resulted in SCD primarily affecting Black or African American (Black) persons in the United States, leading to exacerbation of high disease-associated morbidity in groups affected by

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structural racism and health inequities. Social determinants of health further contribute to poor outcomes among persons with SCD (*3*,*4*). Because of the associated health inequities, high risk of lifelong disabilities, and high cost of care, managing SCD remains a major national public health priority (*5*).

Although universal newborn screening for hemoglobinopathies, including SCD, has been implemented nationally since 2006 (*6*), SCD birth prevalence data remain scarce. The most recent race-specific birth prevalence (one in 365 Black newborns) is based on 2007 data (*7*). Data from 2015–2017 indicate an overall SCD birth prevalence of one in 2,024 U.S. newborns (*8*). The CDC-funded Sickle Cell Data Collection (SCDC) program is well suited to estimate SCD birth prevalence. At the time of this analysis, SCDC included 11 state-level surveillance programs from the southern, midwestern, and western United States. The programs collect and analyze data on newborns with SCD, including SCD type and geographic location, allowing for the assessment of county-level socioeconomic conditions that influence health outcomes among infants with SCD. Identifying these conditions can guide the planning and implementation of public health, health care systems, and community programs supporting persons with SCD. This report analyzed state newborn screening program records from 2016–2020 from 11 SCDC program states to provide updated crude and race-specific SCD prevalence among newborns and to describe the percentage of newborns with SCD by county-level socioeconomic characteristics among these states.

Methods

Data Sources

State newborn screening records from 2016–2020, combined with birth certificate data and confirmation testing results when available, were used to identify the most recent data across 11 SCDC program states (Alabama, California, Colorado, Georgia, Indiana, Michigan, Minnesota, North Carolina, Tennessee, Virginia, and Wisconsin). Newborns with a confirmed diagnosis of SCD were included if the infant's birth and their mother's residence county were within the SCDC program state. Confirmed SCD diagnosis was based on a positive Clinical Laboratory Improvement Amendments (CLIA)–certified laboratory SCD test result reported by a state newborn screening program with confirmatory testing or clinical diagnosis by a physician and documented confirmatory CLIA-certified laboratory testing after the newborn period. The mother's residence county and infant's race, ethnicity, sex, date of birth, and SCD type were extracted from newborn screening records or birth certificate data. Infants' race, ethnicity, and SCD type were based upon state-specific methodologies across newborn screening programs (*9*). The total number of live births and of live births among non-Hispanic Black persons by county were obtained from each state's health department.

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Data Analysis

Crude SCD birth prevalence (calculated by dividing the number of newborns with SCD by the total number of live births) and SCD birth prevalence among non-Hispanic Black newborns (calculated by dividing the number of Black* newborns with SCD by the total number of live births among non-Hispanic Black† persons) were reported per 10,000 newborns. Prevalence rates were calculated overall and by state.

County Social Vulnerability Index (SVI) characteristics were quantified using the 2020 state-specific SVI databases based on the birth mother's county of residence at birth. The state-specific SVI ranks each county relative to other counties within the state on 16 social factors. Percentile ranking values range from 0 to 1, with higher values indicating greater vulnerability. An overall SVI percentile ranking as well as percentile rankings measured on four themes (socioeconomic status, household characteristics, racial and ethnic minority status, and housing type and transportation)§ were categorized into quartiles from least to most vulnerable: low (0 to 0.25), medium (>0.25 to 0.5), high (>0.5 to 0.75), and very high (>0.75 to 1.0) vulnerability. The percentage distribution of birth mother residence within SVI quartiles was derived for the overall SVI measure and by SVI themes.

SAS (version 9.4; SAS Institute) was used for all analyses. Institutional review boards or ethics committees overseeing each state program either determined the analysis to be outside purview as public health surveillance or exempt and approved a waiver of consent. This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.¶

Results

Demographics and Birth Prevalence

During 2016–2020, a total of 3,305 SCD-affected newborns were recorded across the 11 SCDC program states (Table 1). The highest number of SCD-affected newborns (758) occurred in Georgia, followed by North Carolina (435), California (419), and Alabama (386). Approximately 50% of newborns with SCD were male, 90% were Black, and 4% were Hispanic or Latino. Overall, 1,882 (57%) infants had homozygous hemoglobin S (HbSS) or sickle β-null thalassemia ($HbS\beta^0$), 28% had hemoglobin SC disease, and 10% had sickle β-plus thalassemia ($HbS\beta^+$) or another SCD type.** Across the 11 states, crude SCD birth prevalence was 4.83 per 10,000 (one in every 2,070) live births (Table 2). SCD birth prevalence among non-Hispanic Black newborns was 28.54 per 10,000 (one in every 350) live births.

Social Vulnerability

Among all mothers of newborns with SCD, approximately two thirds (67%) lived in counties with high or very high social vulnerability (Figure). In five of the 11 SCDC program states, more than one half of birth mothers resided in very high SVI counties (Wisconsin [86%], Indiana [82%], Michigan [61%], Tennessee [58%], and California [56%]) (Supplementary Figure, https://stacks.cdc.gov/view/cdc/151052). Approximately one half (49%) of mothers of newborns with SCD resided in areas with high or very high socioeconomic vulnerability and household characteristic vulnerability (56%). In addition, approximately two thirds (64%) of mothers resided in counties with high or very high housing type and transportation vulnerability, and 89% resided in counties with high or very high racial and ethnic minority status vulnerability (Figure).

Discussion

In this analysis of birth prevalence and social vulnerability ranking of newborns with SCD across 11 SCDC program states, SCD affected one in every 2,070 newborns overall and one in every 350 non-Hispanic Black newborns. These findings align with previously reported estimates of SCD affecting one in every 2,024 newborns overall and one in every 365 non-Hispanic Black newborns (*7*,*8*); however, they expand on those reports by using more recent data from 2016–2020.

The finding that most mothers lived in counties with high or very high SVI highlights the insights that county-level data can provide to public health policymakers when considering the support that community-based programs can deliver to meet the complex health needs of newborns with SCD and their

* The number of newborns with SCD was reported to the SCDC programs with separate variables for race and ethnicity. As a result, the numerator in the calculation of SCD birth prevalence includes all Black newborns with SCD, regardless of ethnicity.

† The number of live births was reported to the SCDC programs with a single, combined variable for race and ethnicity. As a result, the denominator in the calculation of SCD birth prevalence includes only non-Hispanic Black newborns. Because the count of Black newborns with SCD included all ethnicities but the count of all Black live births included non-Hispanic newborns only, the non-Hispanic Black SCD birth prevalence could be overestimated.

§ https://www.atsdr.cdc.gov/placeandhealth/svi/data_documentation_download.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.

** Hemoglobin SC disease (HbSC) is usually the most severe type of SCD; children inherit a hemoblobin S gene from each parent. Persons with HbSC disease inherit a hemoglobin S gene from one parent, and a gene for abnormal hemoglobin C from the other parent; HbSC is usually milder than HbSS. Children with HbSβ inherit the hemoglobin S gene from one parent and a β thalassemia gene from the other parent. $HbS\beta^0$ is usually more severe than is $HbS\beta^+$. Rarer SCD types include HbSD, HbSE, and HbSO, in which an abnormal D, E, or O hemoglobin gene is inherited from one parent, and the hemoglobin S gene is inherited from the other parent. https://www.cdc.gov/ncbddd/sicklecell/facts.html

TABLE 1. Number of newborns with sickle cell disease, by sex, race, ethnicity, and confirmed sickle cell disease type (N = 3,305) — 11 Sickle Cell Data Collection program states, 2016–2020

State	Total no. of newborns with SCD	Sex			Race			Ethnicity*			Confirmed SCD type			
		Female	Male	Unk	Black or African American	Other	Unk	Hispanic or Latino	NH	Unk	HbSS or HbSβ^0	HbSC	HbSβ$^+$ or other	Unk
Alabama	**386**	179	159	—†	312	—	—	—	52	—	212	85	30	59
California	**419**	207	212	—	374	—	—	—	371	—	219	133	67	0
Colorado	**66**	27	39	—	54	—	—	—	56	—	40	18	—	—
Georgia	**758**	398	360	—	711	—	—	—	667	—	409	207	53	89
Indiana	**175**	74	101	—	144	—	—	—	142	—	108	51	16	0
Michigan	**315**	160	155	—	284	—	—	—	250	—	180	86	49	0
Minnesota	**90**	46	44	—	84	—	—	—	85	—	54	15	—	—
North Carolina	**435**	196	239	—	395	—	—	—	412	—	268	129	19	19
Tennessee	**224**	113	111	—	215	—	—	—	212	—	136	63	25	0
Virginia	**321**	161	159	—	289	—	—	—	218	—	188	106	27	0
Wisconsin	**116**	56	60	—	108	—	—	—	104	—	68	28	—	—
Total (row %)	**3,305 (100)**	**1,617 (48.9)**	**1,639 (49.6)**	**49 (1.5)**	**2,970 (89.9)**	**198 (6.0)**	**137 (4.1)**	**134 (4.1)**	**2,569 (77.7)**	**602 (18.2)**	**1,882 (56.9)**	**921 (27.9)**	**317 (9.6)**	**185 (5.6)**

Abbreviations: HbSC = hemoglobin SC disease; HBSS = sickle cell homozygous hemoglobin S; HbSβ^0 = sickle beta-null thalassemia; HbSβ$^+$ = sickle beta-plus thalassemia; NH = non-Hispanic; SCD = sickle cell disease; Unk = unknown.
* Ethnicity was unknown in 18% of cases; therefore, ethnicity results should be interpreted with caution.
† Dashes indicate data was censored because counts were <11 in one or more cells.

TABLE 2. Sickle cell disease birth prevalence overall and among non-Hispanic Black or African American infants — 11 Sickle Cell Data Collection program states, 2016–2020

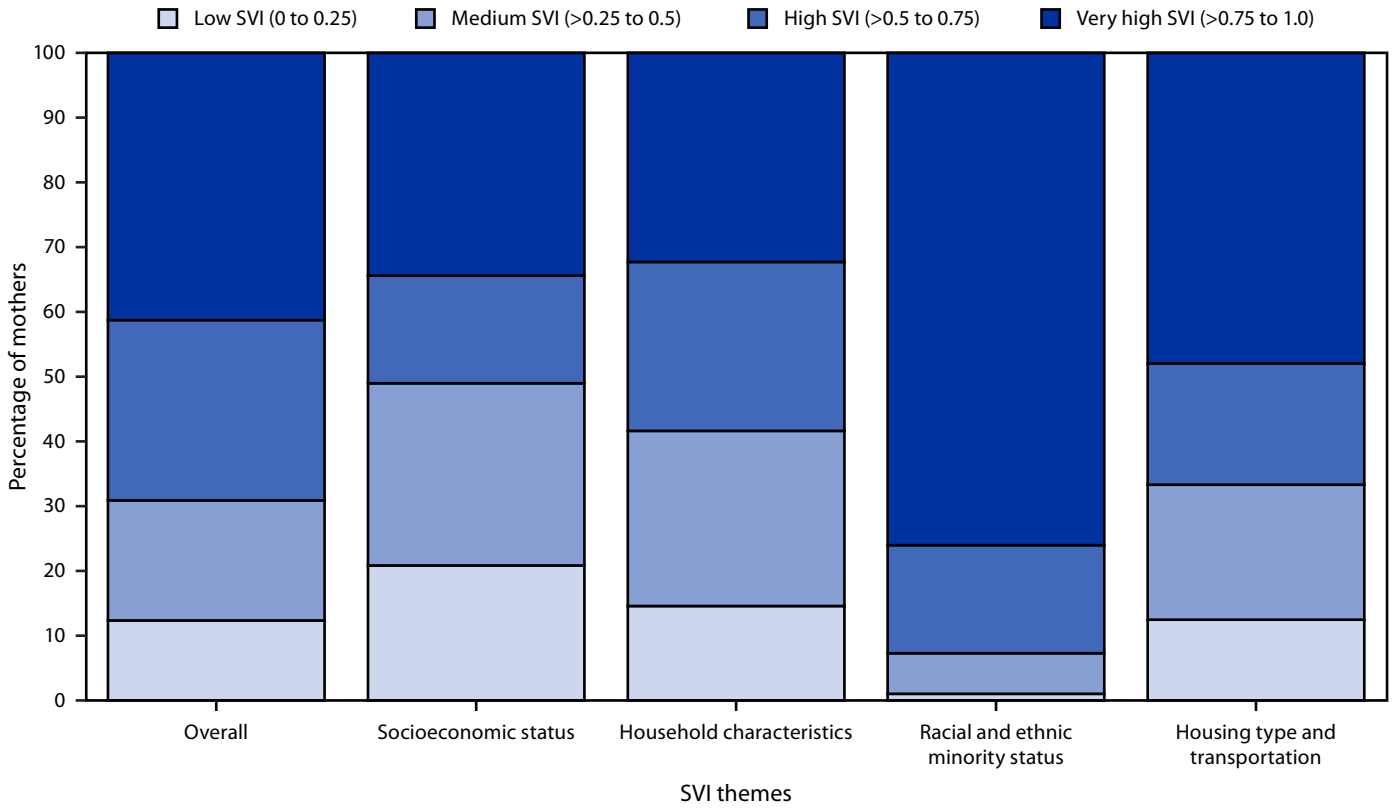
State	Total no. of newborns with SCD	Total no. of live births	Overall crude prevalence* of newborns with SCD	No. of Black newborns with SCD†	No. of NH Black live births§	Prevalence¶ of NH Black newborns with SCD
Alabama	**386**	**292,038**	13.22	312	91,467	34.11
California	**419**	**2,281,910**	1.84	374	136,485	27.40
Colorado	**66**	**540,370**	1.22	54	17,541	30.79
Georgia	**758**	**633,778**	11.96	711	228,199	31.16
Indiana	**175**	**406,382**	4.31	144	52,827	27.26
Michigan	**315**	**547,020**	5.76	284	107,109	26.52
Minnesota	**90**	**335,154**	2.69	84	43,514	19.30
North Carolina	**435**	**595,301**	7.31	395	143,595	27.51
Tennessee	**224**	**401,622**	5.58	215	81,995	26.22
Virginia	**321**	**493,627**	6.50	289	104,973	27.53
Wisconsin	**116**	**319,625**	3.63	108	33,073	32.66
Total	**3,305**	**6,846,827**	**4.83**	**2,970**	**1,040,778**	**28.54**

Abbreviations: Black = Black or African American; NH = non-Hispanic; SCD = sickle cell disease; SCDC = Sickle Cell Disease Collection.
* Crude prevalence of newborns with SCD were calculated by dividing the number of newborns with SCD by number of live newborns in each state and multiplying by 10,000.
† The number of newborns with SCD was reported to SCDC programs with separate variables for race and ethnicity. As a result, the numerator in the calculation of SCD birth prevalence includes all Black newborns with SCD, regardless of ethnicity.
§ The number of live births was reported to SCDC programs with a single, combined variable for race and ethnicity. As a result, the denominator in the calculation of SCD birth prevalence includes only NH Black newborns.
¶ Prevalence of NH Black newborns with SCD was calculated by dividing the number of Black newborns with SCD by number of live births among NH Black persons in each state during 2016–2020 and multiplying by 10,000. Birth rates among NH Black persons for Alabama, Colorado, and Indiana should be interpreted with caution because race was unknown for 9%–14% of newborns with SCD in these states; thus, the NH Black SCD birth prevalence for these states could be underestimated.

caregivers. The majority (64%) of mothers of newborns with SCD resided in counties with high or very high housing type and transportation social vulnerability, underscoring potential strategies to serve these communities, including medical transportation programs or development of innovative care models to facilitate access to comprehensive SCD care. For example, improving flexibility in scheduling of medical transportation, providing reimbursement for use of existing public transportation such as rideshares, and partnering with local faith- and community-based organizations for medical transport have the potential to improve access to care. Moreover, understanding the geographic location of SCD-affected newborns within a state can help guide specialty and primary care efforts to improve access to SCD care. Together, these findings provide data to Medicaid programs, the primary payer for SCD care,†† as they collaborate with state agencies to consider the effect

†† https://www.ncbi.nlm.nih.gov/books/NBK547764/

FIGURE. Percentage of mothers of newborns with sickle cell disease (N = 3,305), by overall and theme-specific Social Vulnerability Index quartiles* — 11 Sickle Cell Data Collection program states,† 2016–2020



Abbreviation: SVI = Social Vulnerability Index.

* The 2020 state-ranked SVI datasets based on mother's county of residence at birth were used (https://www.atsdr.cdc.gov/placeandhealth/svi/data_documentation_download.html). SVI values were state-specific and ranked each county relative to other counties within a state. The SVI ranks counties based on 16 social factors. Percentile ranking values range from 0 to 1, with higher values indicating greater vulnerability. Themes were socioeconomic status (<150% of the federal poverty level, unemployed, housing cost burden, no high school diploma, and no health insurance), household characteristics (age ≥65 years, age ≤17 years, civilian with a disability, single-parent households, and English language proficiency), racial and ethnic minority status (non-Hispanic American Indian or Alaska Native, non-Hispanic Asian, non-Hispanic Black or African American, non-Hispanic Native Hawaiian or other Pacific Islander, non-Hispanic two or more races, Hispanic or Latino of any race, and non-Hispanic other races), and housing type and transportation (multiunit structures, mobile homes, crowding, no vehicle, and group quarters). For 127 (4%) mothers of newborns with sickle cell disease, the county of residence at birth was unknown.

† Alabama, California, Colorado, Georgia, Indiana, Michigan, Minnesota, North Carolina, Tennessee, Virginia, and Wisconsin.

of housing and transportation vulnerabilities on infants with SCD. These Medicaid programs can also support partnerships created by public health programs, the communities they serve, and community-based organizations to ascertain specific resource needs of SCD-affected populations, as well as where and how resources can be deployed to drive more equitable outcomes.

Limitations

The findings in this report are subject to at least four limitations. First, because of the time needed to ascertain SCD type by public health surveillance systems, state newborn screening data are subject to a 3-year time lag. Despite this lag, SCD counts among newborns did not fluctuate significantly between years. Second, missing data hampered the ability to further disaggregate race and ethnicity categories, which might be important to understanding differential birth prevalences across states and tailoring programs to different racial and ethnic communities. Third, SVI was examined at the county level as opposed to U.S. Census Bureau tract level, which could mask variations of SVI within counties. Finally, SVI metrics are at the county level rather than the person level and might not reflect a comprehensive assessment of specific services needed by infants with SCD.

Implications for Public Health Practice

Understanding characteristics of the geographic residence of infants with SCD and their caregivers is critical to guiding local and state health departments and health agencies in prioritizing and developing programs that can mitigate specific social determinants of health and their attendant inequities.

Summary

What is already known about the topic?

Approximately one in every 365 Black or African American (Black) newborns in the United States has sickle cell disease (SCD), a condition associated with complex health needs.

What is added by this report?

During 2016–2020, 3,305 cases of SCD among newborns were recorded across 11 states participating in the Sickle Cell Data Collection program (SCD birth prevalence = 28.54 per 10,000 [one in every 350] non-Hispanic Black newborns). Approximately two thirds of mothers of newborns with SCD resided in counties with high or very high social vulnerability.

What are the implications for public health?

Implementation of tailored interventions, including increasing access to transportation, improving housing, and advancing equity in high vulnerability areas, could facilitate care and improve health outcomes for children with SCD.

Specifically, these data highlight the potential need to consider tailored interventions in high vulnerability areas to increase access to transportation, improve housing, and advance equity for infants with SCD. Developing programs in partnership with communities and community-based organizations is critical to allocating needed resources and determining how they might be effective in improving health outcomes for children with SCD.

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Ceftriaxone-Resistant Gonorrhea — China, 2022

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Abstract

Gonorrhea is a widespread sexually transmitted infection; in 2022, China reported 96,313 cases of gonorrhea, making it the fourth most common notifiable infectious disease in the country after viral hepatitis, pulmonary tuberculosis, and syphilis. The rise in prevalence in antimicrobial-resistant strains, particularly the international spread of ceftriaxone-resistant clones, poses a formidable challenge to gonorrhea control. The China Gonococcal Resistance Surveillance Program (China-GRSP), established in 1987 and covering 19 of 34 provincial-level administrative units, continuously monitors gonococcal antimicrobial resistance. In 2022, 13 China-GRSP sentinel sites collected 2,804 gonococcal isolates, representing 2.9% of all cases reported in China, and 4.1% of cases reported in the 13 participating provinces. The prevalence of *Neisseria gonorrhoeae* resistance to ceftriaxone was 8.1%, approximately three times the 2017 rate of 2.9%; five provinces reported >10% ceftriaxone resistance. Resistance prevalences to cefixime, azithromycin, tetracycline, penicillin, and ciprofloxacin were 16.0%, 16.9%, 77.1%, 77.8%, and 97.6%, respectively. Only one case of spectinomycin resistance was reported. These data highlight a substantial increase in ceftriaxone resistance from 2017 to 2022. Effective diagnosis and treatment and appropriate management of sex partners are essential to protect the health of infected persons and prevent ongoing transmission of gonorrhea, including transmission of resistant strains. Identifying reasons for the spread of ceftriaxone-resistant *N. gonorrhoeae* in China could guide strategies, such as antibiotic stewardship, to mitigate the rising resistance rate and curb the spread of resistant strains.

Introduction

Gonorrhea, a sexually transmitted bacterial infection caused by *Neisseria gonorrhoeae*, remains prevalent worldwide. The World Health Organization (WHO) estimated that approximately 82.4 million new gonorrhea cases were diagnosed among persons aged 15–49 years in 2020.[†] In China, a total of 96,313 gonorrhea cases were reported in 2022, representing a rate of 6.83 reported cases per 100,000 population, the fourth highest among class A and class B notifiable infectious diseases[§] in the country,[¶] after viral hepatitis, pulmonary tuberculosis, and syphilis. In the United States, in 2022, a total of 648,056 cases of gonorrhea were reported.[**]

In recent years, gonococcal resistance to multiple antibiotics has emerged (*1*). Ceftriaxone is recommended as the first-line treatment option for gonorrhea in China (single dose of 1 g, administered intramuscularly)[††] as well as in the United States (single dose of 500 mg for persons weighing <150 kg, administered intramuscularly).[§§] However, the emergence of ceftriaxone-resistant strains, particularly the ceftriaxone-resistant clone FC428 (*2*), has been identified worldwide. First identified in Beijing in 2016 (*3*), this resistant clone has become widely disseminated across various regions of China, with its proportion among all resistant clones steadily increasing since 2016, highlighting the challenge associated with addressing gonococcal resistance (*4*).

The China Gonococcal Resistance Surveillance Program (China-GRSP), established in 1987, monitors gonococcal resistance to azithromycin, cefixime, ceftriaxone, ciprofloxacin, penicillin, spectinomycin, and tetracycline in China (*5*). This report describes gonococcal resistance surveillance data from China for 2022, the most recent year for which data are available.

Methods

In 2022, China-GRSP conducted gonococcal resistance surveillance across 13 of the 19 provinces (among 34 national province-level administrative jurisdictions) that participate in the program, within six of seven regions of China (Supplementary Figure, https://stacks.cdc.gov/view/cdc/150923). *N. gonorrhoeae* isolates obtained from urethral (from males) or endocervical (from females) swab specimens were collected from the 2,804 identified cases included in the surveillance program from consecutively evaluated patients throughout the year. Consecutive evaluation involved specimen collection at each sentinel site from January through December, with some sites having larger sample sizes and sampling limitations that might result in data collection ending as early as September. Specimens were cultured on

[*] These authors contributed equally to this report.

[†] https://www.who.int/news-room/fact-sheets/detail/gonorrhoea-(neisseria-gonorrhoeae-infection)

[§] Two class A and 28 class B notifiable infectious diseases are recognized in China; class A diseases include cholera and plague, and class B diseases include those associated with a high risk for outbreaks or that are likely to result in rapid spread once an outbreak occurs, such as AIDS, gonorrhea, measles, syphilis, and tuberculosis.

[¶] http://www.nhc.gov.cn/guihuaxxs/s3585u/202309/6707c48f2a2b420fbfb739c393fcca92.shtml; data on rates of reported cases of COVID-19 were not available; therefore, SARS-CoV-2 infections were not included in these statistics.

[**] https://www.cdc.gov/std/statistics/2022/overview.htm#Gonorrhea

[††] https://doi.org/10.1097/JD9.0000000000000072

[§§] https://www.cdc.gov/std/treatment-guidelines/gonorrhea-adults.htm

selective gonococcal culture media, and *N. gonorrhoeae* (an oxidase-positive, gram-negative diplococcus) was identified by microscopic examination of Gram-stained material, detection of a rapid oxidase reaction, and carbohydrate utilization test results.¶¶ The susceptibility of isolates to azithromycin, cefixime, ceftriaxone, ciprofloxacin, penicillin, spectinomycin, and tetracycline was determined using the agar dilution method. Antibiotic resistance breakpoints were applied based on the European Committee on Antimicrobial Susceptibility Testing criteria,*** except for azithromycin, for which WHO criteria were used. WHO *N. gonorrhoeae* reference strains were used for quality assurance. The determination of antibiotic resistance was based on the minimum inhibitory concentration (MIC) values obtained through agar dilution. The antibiotic resistance breakpoints were as follows: azithromycin MIC >0.5 mg/L, cefixime MIC >0.125 mg/L, ceftriaxone MIC >0.125 mg/L, ciprofloxacin MIC >0.06 mg/L, penicillin MIC >1 mg/L, spectinomycin MIC >64 mg/L, and tetracycline MIC >1 mg/L. Resistance rate was expressed as the percentage of resistant isolates among the total number of isolates. This activity was reviewed and approved by the Medical Ethics Committee at the Institute of Dermatology, Chinese Academy of Medical Sciences & Peking Union Medical College, and the National Center for AIDS/STD Control and Prevention in China.

Results

In 2022, a total of 2,804 isolates (4.1% of 68,217 gonococcal infection cases) from 13 provinces in China were tested for antimicrobial susceptibility. The largest numbers of cases were reported in Guangdong (22,171) and Zhejiang (13,460) provinces. Rates of reported cases ranged from 2.13 to 20.58 per 100,000 population, with highest rates reported in Zhejiang, Guangdong, Yunnan, Hainan, and Guangxi provinces (Table 1).

Percentages of isolates tested by province ranged from 2.1% (Yunnan) to 18.1% (Tianjin). Among isolates submitted, resistance was identified to ciprofloxacin (97.6%), penicillin (77.8%), tetracycline (77.1%), azithromycin (16.9%), cefixime (16.0%), and ceftriaxone (8.1%) (Table 2). Only one isolate was resistant to spectinomycin. Among 2,804 isolates, those from 18 cases were identified as resistant to all antibiotics except spectinomycin.

Antibiotic resistance rates differed among provinces. Whereas ceftriaxone resistance detected in most sentinel sites was ≤5% during the past decade, in 2022, five provinces (Chongqing, Jiangsu, Sichuan, Tianjin, and Xinjiang) reported >10% ceftriaxone resistance, with rates in Sichuan, Tianjin, and Xinjiang surpassing 20%; only Hainan, Hunan, Shanghai, and Zhejiang reported ≤5% ceftriaxone resistance (Figure). Among other antibiotics, overall resistance to cefixime was 16.0%, with rates in Jiangsu, Sichuan, Tianjin, and Xinjiang exceeding 25%. Azithromycin resistance was >35% in Hunan and Shanghai and >20% in Chongqing, Guangdong, Tianjin, and Xinjiang. Resistance to ciprofloxacin remained consistently high nationwide (97.6%), with Hunan, Shaanxi, Shanghai, Sichuan, Tianjin, and Yunnan reaching 100%. Overall resistance to tetracycline was 77.1%, ranging from 28.3% in Tianjin to 100% in Xinjiang. Penicillin resistance was 77.8% nationwide and was >70% in most provinces; the highest penicillin resistance rate (98.2%) was reported by Shanghai province.

Discussion

The prevalence of ceftriaxone resistance among gonococcal isolates in China nearly tripled since 2017, increasing from

¶¶ https://www.who.int/publications/i/item/9789241505840
*** www.eucast.org/clinical_breakpoints/

TABLE 1. Reported cases and rates of gonorrhea and proportion of isolates available for antimicrobial susceptibility tests, by province — 13 Gonococcal Resistance Surveillance Program sentinel sites,* China, 2022

Province	Population	No. of reported gonorrhea cases	Rate†	No. of isolates tested for antimicrobial susceptibility (%)
Chongqing	32,119,942	2,498	7.78	66 (2.6)
Guangdong	126,840,013	22,171	17.48	751 (3.4)
Guangxi	50,369,886	6,162	12.23	719 (11.7)
Hainan	10,199,964	1,466	14.37	57 (3.9)
Hunan	66,220,222	3,016	4.55	66 (2.2)
Jiangsu	85,050,277	5,354	6.30	248 (4.6)
Shanghai	24,889,864	1,339	5.38	111 (8.3)
Shanxi	39,539,596	1,405	3.55	65 (4.6)
Sichuan	83,721,532	3,235	3.86	120 (3.7)
Tianjin	13,730,084	293	2.13	53 (18.1)
Xinjiang	25,889,690	905	3.50	27 (3.0)
Yunnan	46,899,911	6,913	14.74	146 (2.1)
Zhejiang	65,400,126	13,460	20.58	375 (2.8)

* Data from 13 of 19 provincial sentinel surveillance sites were included in the analysis; only 2,804 isolates were tested for antimicrobial susceptibility, accounting for 4.1% of all reported cases in the 13 participating provinces.
† Per 100,000 population.

TABLE 2. Resistance of gonococcal isolates to ciprofloxacin, penicillin, tetracycline, azithromycin, cefixime, ceftriaxone, and spectinomycin — 13 Gonococcal Resistance Surveillance Program sentinel sites,* China, 2022

Province	Antibiotic/MIC, no. of resistant isolates (%)						
	Ciprofloxacin/ >0.06 mg/L†	Penicillin/ >1 mg/L†	Tetracycline/ >1 mg/L†	Azithromycin/ >0.5 mg/L†	Cefixime/ >0.125 mg/L†	Ceftriaxone/ >0.125 mg/L†	Spectinomycin/ >64 mg/L†
Chongqing	64 (97.0)	43 (65.2)	28 (42.4)	14 (21.2)	16 (24.2)	9 (13.6)	0 (—)
Guangdong	741 (98.7)	604 (80.4)	509 (67.8)	161 (21.4)	172 (22.9)	66 (8.8)	0 (—)
Guangxi	714 (99.3)	538 (74.8)	631 (87.8)	115 (16.0)	65 (9.0)	45 (7.6)	1 (0.1)
Hainan	53 (93.0)	19 (33.3)	25 (43.9)	2 (3.5)	1 (1.8)	1 (1.8)	0 (—)
Hunan	66 (100.0)	59 (89.4)	26 (39.4)	25 (38.0)	10 (15.2)	2 (3.0)	0 (—)
Jiangsu	209 (84.3)	184 (74.2)	197 (79.4)	32 (12.9)	55 (28.2)	24 (12.3)	0 (—)
Shanghai	111 (100.0)	109 (98.2)	60 (54.1)	42 (37.8)	14 (12.6)	0 (—)	0 (—)
Shanxi	65 (100.0)	54 (83.0)	49 (75.4)	0 (—)	6 (9.2)	4 (6.2)	0 (—)
Sichuan	120 (100.0)	86 (71.7)	101 (84.2)	11 (9.2)	44 (36.7)	30 (25.0)	0 (—)
Tianjin	53 (100.0)	47 (88.7)	15 (28.3)	12 (22.6)	19 (35.9)	14 (26.4)	0 (—)
Xinjiang	21 (77.8)	19 (70.4)	27 (100.0)	6 (22.2)	7 (25.9)	7 (25.9)	0 (—)
Yunnan	146 (100.0)	130 (89.0)	139 (95.2)	25 (17.1)	12 (8.2)	10 (6.9)	0 (—)
Zhejiang	374 (99.7)	289 (77.1)	356 (94.9)	28 (7.5)	20 (5.3)	10 (2.8)	0 (—)
Total	**2,737 (97.6)**	**2,181 (77.8)**	**2,163 (77.1)**	**473 (16.9)**	**441 (16.0)**	**222 (8.1)**	**1 (<1)**

Abbreviation: MIC = minimum inhibitory concentration.
* Data from 13 of 19 provincial sentinel surveillance sites were included in the analysis.
† Concentrations listed are the MIC thresholds used to categorize resistant isolates.

2.9% to 8.1% in 2022; this rate is relatively high compared with that in other countries (*1*). For example, in 2022, the percentage of strains with reduced susceptibility to ceftriaxone (MIC >0.03 mg/L) in the United Kingdom was 0.21%.††† According to the U.S. CDC's Gonococcal Isolate Surveillance Project report, the prevalence of isolates exhibiting elevated ceftriaxone MICs (≥0.125 μg/mL) fluctuated at approximately 0.2% during 2016–2020.§§§ In Canada, prevalence of decreased susceptibility to ceftriaxone has remained relatively stable, at approximately 0.6% during 2017–2021 (*6*).

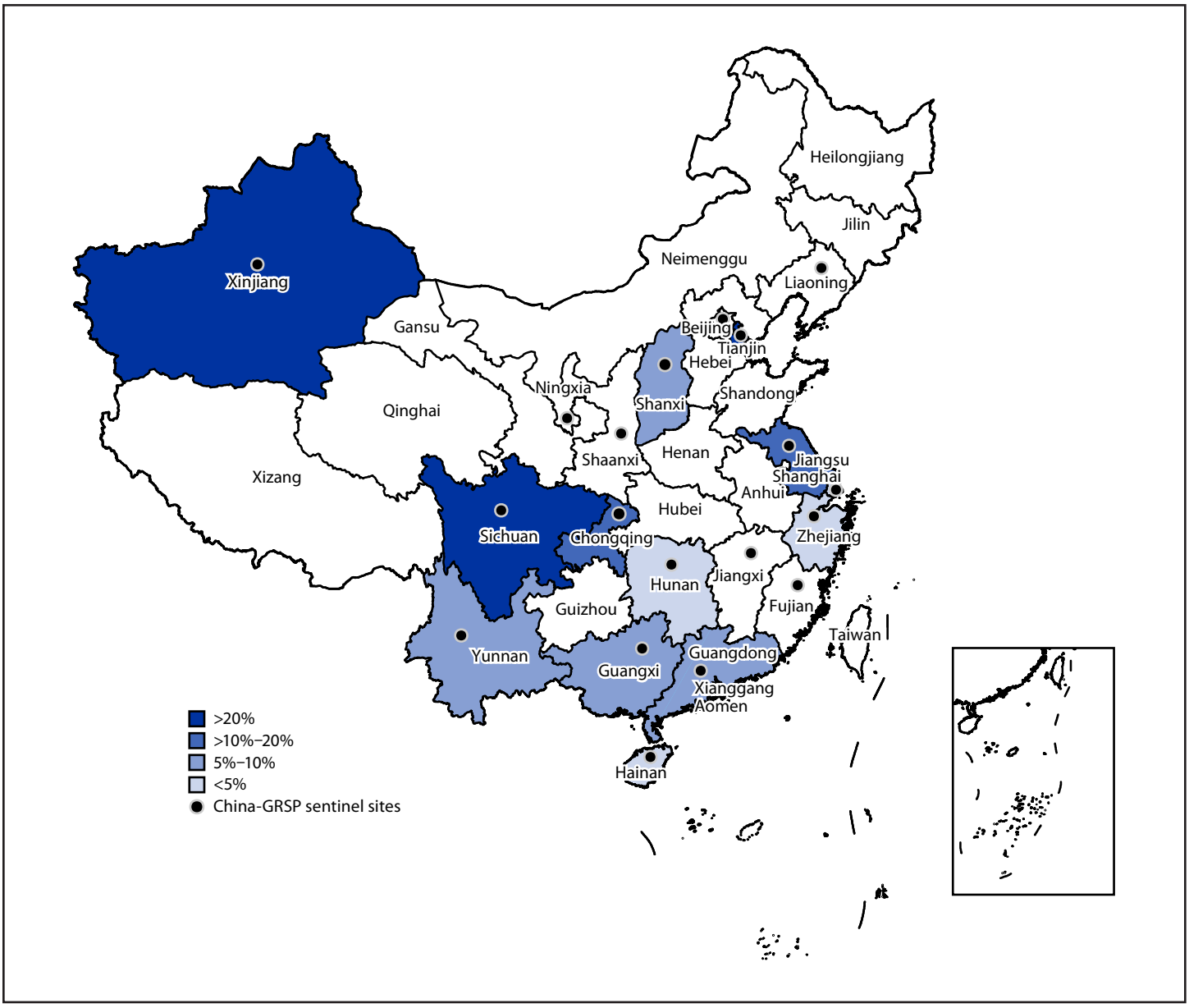
These findings underscore the urgent need for a comprehensive approach to address antibiotic-resistant *N. gonorrhoeae* in China, including identifying factors contributing to this high resistance rate, especially in provinces where the percentage of gonococcal isolates resistant to ceftriaxone is >10%. Factors that could contribute to ceftriaxone resistance include spread of the ceftriaxone-resistant FC428 strain, gaps in gonorrhea screening, treatment, and partner management, and nonrecommended prescribing or use of antibiotics (although antibiotics are only available by prescription in China). Understanding these factors is crucial to guiding the development and implementation of targeted interventions and preventive measures. The preliminary investigation revealed that the widespread dissemination of ceftriaxone-resistant FC428 clones might be the underlying reason for the high resistance rate in China (*3*,*4*,*7*), although whole-genome sequencing of isolates collected in 2022 is ongoing. These resistant clones have spread internationally (*8*–*10*), and collaborative cross-border efforts will be essential to monitoring and mitigating its further spread. These findings also reinforce the pivotal role of programs such as the China-GRSP in the ongoing monitoring and adapting of strategies to address evolving resistance patterns. The observed resistance rates for other antibiotics emphasize the complex landscape of gonococcal antimicrobial resistance, further highlighting the urgent need to develop alternative treatment strategies, including vaccines to counter this growing threat.¶¶¶

Limitations

The findings in this report are subject to at least four limitations. First, relying on reported cases of gonorrhea might underestimate the actual incidence, because asymptomatic cases or those among patients not seeking medical attention might go unrecorded. Second, in 2022, China-GRSP only covered one third of the country, and fewer than 3% of isolates were available for testing, leading to potential bias, and results might not be representative of the entire country. Third, this analysis focused on antimicrobial resistance rates and did not address broader sociodemographic factors influencing gonorrhea transmission. Finally, the lack of detailed patient information hampers the identification of specific risk factors contributing to the observed resistance patterns. Future research should address these limitations for a more nuanced understanding of *N. gonorrhoeae* epidemiology in China.

††† https://www.gov.uk/government/publications/gonococcal-resistance-to-antimicrobials-surveillance-programme-grasp-report/grasp-report-data-to-june-2023
§§§ https://www.cdc.gov/std/statistics/gisp-profiles/default.htm
¶¶¶ https://www.who.int/publications-detail-redirect/9789240039827

FIGURE. Reported rates of ceftriaxone resistance — 13 Gonococcal Resistance Surveillance Program sentinel sites,* China, 2022



Abbreviation: GRSP = Gonococcal Resistance Surveillance Program.
* Data from 13 of 19 provincial sentinel surveillance sites were included in the analysis.

Implications for Public Health Practice

The increasing prevalence of ceftriaxone resistance in *N. gonorrhoeae* in China highlights a pressing public health concern. Effective diagnosis and treatment and appropriate management of sex partners are essential to protect the health of infected persons and prevent ongoing transmission of gonorrhea, including transmission of resistant strains. Public health practitioners should prioritize assessment of screening practices, particularly in regions with higher reported rates of gonorrhea cases and resistance rates. Understanding the factors that could contribute to the spread of resistance, such the nonrecommended use of antimicrobials, is also crucial to guide prevention efforts. Collaborative efforts and ongoing surveillance to monitor the international spread of resistant strains, as exemplified by programs like China-GRSP, are vital for a global response. International collaboration and information sharing are critical to prevent the further cross-border spread of resistant strains and to identify alternative treatment options for gonorrhea. Given the identified limitations, future research

Summary

What is already known about this topic?

Gonorrhea is the fourth most reported notifiable infectious disease in China. Emergence and spread of ceftriaxone-resistant clones of *Neisseria gonorrhoeae* in China have posed a challenge to gonorrhea treatment.

What is added by this report?

During 2017–2022, the prevalence of antibiotic-resistant strains of *N. gonorrhoeae* increased in China, with resistance to ceftriaxone, the first-line treatment for gonorrhea, approximately tripling. Resistance varied by geographic region. Gonorrhea strains were resistant to other antibiotics at prevalences up to 97.6%, varying by antibiotic type.

What are the implications for public health practice?

Effective diagnosis and treatment are essential to protect the health of infected persons and prevent ongoing transmission of antibiotic-resistant gonorrhea. Identifying reasons for the spread of ceftriaxone-resistant *N. gonorrhoeae* in China could guide strategies, such as antibiotic stewardship, to curb the spread of resistant strains.

should aim to broaden surveillance coverage, incorporate detailed patient information, and conduct a comprehensive analysis of sociodemographic factors. These efforts could improve understanding of gonococcal infections and antibiotic resistance in China. The findings underscore the dynamic nature of this public health issue, emphasizing the ongoing need for adaptive and collaborative approaches to address the growing threat of antibiotic-resistant *N. gonorrhoeae* effectively.

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Implications of Measles Inclusion by Commercial Syndromic Polymerase Chain Reaction Panels — United States, May 2022–April 2023

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Abstract

Syndromic polymerase chain reaction (PCR) panels are used to test for pathogens that can cause rash illnesses, including measles. Rash illnesses have infectious and noninfectious causes, and approximately 5% of persons experience a rash 7–10 days after receipt of a measles, mumps, and rubella (MMR) vaccine. MMR vaccine includes live attenuated measles virus, which is detectable by PCR tests. No evidence exists of person-to-person transmission of measles vaccine virus, and illness does not typically result among immunocompetent persons. During September 2022–January 2023, the Tennessee Department of Health received two reports of measles detected by syndromic PCR panels. Both reports involved children (aged 1 and 6 years) without known risk factors for measles, who were evaluated for rash that occurred 11–13 days after routine MMR vaccination. After public health responses in Tennessee determined that both PCR panels had detected measles vaccine virus, six state health departments collaborated to assess the frequency and characteristics of persons receiving a positive measles PCR panel test result in the United States. Information was retrospectively collected from a commercial laboratory testing for measles in syndromic multiplex PCR panels. During May 2022–April 2023, among 1,548 syndromic PCR panels, 17 (1.1%) returned positive test results for measles virus. Among 14 persons who received a positive test result and for whom vaccination and case investigation information were available, all had received MMR vaccine a median of 12 days before specimen collection, and none had known risk factors for acquiring measles. All positive PCR results were attributed to detection of measles vaccine virus. Increased awareness among health care providers about potential measles detection by PCR after vaccination is needed. Any detection of measles virus by syndromic PCR testing should be immediately reported to public health agencies, which can use measles vaccination history and assessment of risk factors to determine the appropriate public health response. If a person recently received MMR vaccine and has no risk factors for acquiring measles, additional public health response is likely unnecessary.

Introduction

Syndromic polymerase chain reaction (PCR) panels are used to test for pathogens that can cause rash illnesses, including measles. Rash illnesses have infectious and noninfectious causes, and approximately 5% of persons experience a rash 7–10 days after receipt of a measles, mumps, and rubella (MMR) vaccine (*1*). A component of MMR vaccines is live attenuated measles virus (genotype A). Although measles vaccine virus is detectable by PCR tests that target the nucleocapsid gene, no evidence of person-to-person transmission exists (*2,3*). Measles vaccine virus does not cause measles infection and does not typically cause illness among immunocompetent persons (*1,4*).

During September 2022–January 2023, the Tennessee Department of Health received two reports of measles in children aged 1 and 6 years, who were evaluated for rash illnesses without documented exposures or plausible epidemiologic risk factors for measles. Rashes occurred 11–13 days after administration of their routine first dose of MMR vaccine.[†] Both children received a positive measles test result on syndromic PCR panels for rash illnesses, a platform that simultaneously tests for multiple pathogens. Public health investigations of both reports concluded that positive test results represented detection of the live attenuated measles virus used in MMR vaccine.

Syndromic PCR platforms that report positive measles test results in persons without measles infection could result in extensive, unnecessary public health responses to measles vaccine virus detected after MMR vaccination. To guide future public health response to syndromic PCR panel detection of measles virus, six state health departments[§] assessed the frequency and characteristics of persons receiving positive measles PCR panel test results in the United States since a commercial platform became available in May 2022.[¶]

[*] These authors contributed equally to this report.

[†] In this report, MMR vaccines refer to both MMR vaccines and measles, mumps, rubella, and varicella vaccines.

[§] The state health departments of Florida, Illinois, North Carolina, Tennessee, Texas, and Virginia partnered for this investigation.

[¶] Two syndromic panels that use target-enriched multiplex PCR technology available from one commercial laboratory were used for this analysis. Both are marketed for evaluating skin rash illnesses by testing oropharyngeal specimens for *Streptococcus pyogenes* and either seven or nine viruses, including measles.

Methods

A commercial laboratory that included measles testing as part of a syndromic multiplex PCR panel provided the numbers of such panels ordered in the United States during May 2022–April 2023 and the number that detected measles virus by state. Six state health departments in states where syndromic PCR panels had detected measles virus partnered to collect patient information from laboratory reports, including age, sex, location and date of specimen collection, and whether other pathogens were detected. State immunization information systems were queried to identify patient MMR vaccination status and date of vaccination. Clinicians who ordered tests were asked about the patients' clinical signs and symptoms** and epidemiologic risk factors for measles (i.e., recent international travel or known exposure to a person with measles virus infection). For the initial two test results reported in Tennessee, findings were collected from subsequent measles testing, including a measles vaccine assay (MeVA) or viral genotype†† (*2,5,6*). This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.§§

Results

Detection of Measles Virus by Syndromic PCR Panels

During May 2022–April 2023, clinicians nationwide ordered 1,548 syndromic PCR panels from the participating commercial laboratory. In the 25 states where these clinicians practiced, a median of 13 tests were ordered per state (range = 1–368 tests). Among all tests conducted, 17 (1.1%) detected measles virus (Figure). Tennessee clinicians ordered the most tests (368) and detected measles most frequently (seven; 1.9%). Laboratory reports were available for 14 (82.4%) of 17 syndromic PCR panels that detected measles; these tests were ordered at pediatric (10), urgent care (three), and family practice (one) clinics.¶¶

Characteristics of Persons with Measles Virus Detected by Syndromic PCR Panels

Among 14 children with detectable measles virus for whom laboratory reports were available, the median age was 1 year (range = 1–6 years), and 11 (78.6%) were female. All 14 had received an MMR vaccine dose before specimen collection, including 13 who were vaccinated within 21 days of specimen collection (median = 12 days; range = 8–115 days). One outlier (measles virus detected 115 days after vaccination) occurred in a test on a specimen collected from a child whose measles serology was consistent with immunity (measles immunoglobulin G–positive and immunoglobulin M–negative). Seven of the 14 syndromic PCR panels detected one or more additional viruses, including human herpesvirus type 6 (six), enterovirus (four), human herpesvirus type 7 (three), and Epstein-Barr virus (two). Public health agencies were immediately notified by clinicians about the initial two persons in Tennessee and retrospectively followed up with clinicians about the 12 remaining persons whose positive test results had not been previously reported. All 14 children had been evaluated for rash illness. Fever was reported for at least eight children, including four for whom cough or coryza were also reported, thereby meeting the Council of State and Territorial Epidemiologists' measles clinical case definition. None of the 14 children had any known epidemiologic risk factors for measles, and no subsequent measles cases were linked to them. For two specimens with test results initially reported to the Tennessee Department of Health, subsequent genetic typing was conducted by CDC. For one, MeVA was inconclusive,***

** According to the Council of State and Territorial Epidemiologists' measles case definition, measles is an acute illness characterized by a generalized maculopapular rash lasting ≥3 days; temperature of ≥101°F (≥38.3°C); and cough, coryza, or conjunctivitis. https://ndc.services.cdc.gov/case-definitions/measles-2013

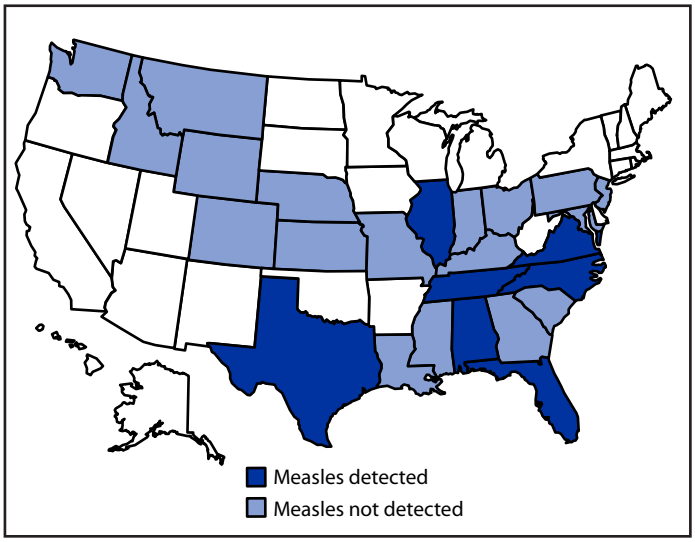
†† MeVa is a real-time reverse transcriptase-PCR assay that detects measles vaccine strains.

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

¶¶ The pediatric and family practice clinics also provide walk-in clinic services.

*** The MeVA result was inconclusive, likely because media used by the commercial laboratory is incompatible with MeVA testing and requires genotyping to detect measles vaccine strains.

FIGURE. Measles detections using syndromic polymerase chain reaction panel testing (N = 17), by state* — United States, May 2022–April 2023



* Measles virus was detected in panels in the following states: Alabama (three detections), Florida (two), Illinois (one), North Carolina (two), Tennessee (seven), Texas (one), and Virginia (one).

and for the other, genotyping results were consistent with measles vaccine virus (genotype A).

Discussion

These measles virus detections by syndromic PCR panels were attributed to previous MMR vaccination because nearly all occurred in persons without risk factors for measles and shortly after receipt of MMR vaccine. Detection of the strain of measles virus used in MMR vaccine typically occurs within 21 days of vaccination, but detection >100 days later has been reported (*7*), a period that aligns with findings described here. Children frequently experience symptoms of rash and fever from many causes, including other viral illnesses and typical vaccine side effects. This investigation identified an alternative viral etiology for rash for one half of the patients with measles virus detections.

Measles is a highly contagious airborne infection that can infect 90% of susceptible contacts (*1*). Preventing measles is essential for population and personal health. Prodromal signs and symptoms include high fever (up to 105°F [40.6°C]) and either cough, coryza, or conjunctivitis. The prodrome is followed by a maculopapular rash that spreads from head to trunk to lower extremities (*8*). Severe complications include pneumonia, encephalitis, and death. Viral transmission can occur from 4 days before to 4 days after rash onset. A single MMR vaccine dose is 93% effective in preventing measles, and receipt of 2 doses is 97% effective (*4*). In the United States, 90% of children receive MMR vaccines by age 24 months (*1*). Although measles is not endemic in the United States, cases and outbreaks occur sporadically when cases are imported from parts of the world where measles remains endemic (*8*). Preventing further measles transmission after detection of a case requires a rapid and robust public health response that can include isolating ill persons, verifying immunity of exposed persons, offering postexposure prophylaxis with measles vaccine or immunoglobulin, and implementation of quarantine measures if necessary (*8*). Notifying public health agencies immediately is imperative to determine which response measures are needed when measles is detected or clinically suspected.

As demonstrated by this analysis, inclusion of measles virus in syndromic PCR panels can result in incidental detection of measles vaccine virus. Some clinicians who received reports of measles detection by syndromic PCR panels anecdotally shared with health departments that they had neither suspected measles infection in the patient nor realized that the test panel included measles. These clinicians had diagnosed common childhood illnesses, such as roseola or impetigo before receiving test results. When choosing diagnostic tests to evaluate skin rash illnesses, clinicians should consider likely etiologies and determine whether laboratory findings will guide treatment recommendations. Syndromic PCR panels provide the opportunity to rapidly test for multiple pathogens, including those unlikely to cause the illness in question. Inability of these testing panels to differentiate between measles virus causing illness and incidental detection of measles vaccine virus RNA can have significant public health reporting and response ramifications, potentially leading to misdiagnosis of measles virus infection. Any detection of measles virus by syndromic PCR testing, even if suspected to be incidental detection of vaccine strain, should be reported to public health agencies immediately so that appropriate investigation and additional testing can proceed if indicated.

In collaboration with CDC, the state health departments that conducted this analysis developed a process to assist public health agencies in determining response measures that consider risk factors and pretest probability of measles infection when measles virus is detected by syndromic PCR panels (Box). Investigators should determine MMR vaccination status and date of receipt and assess whether the person has epidemiologic risk factors for measles. Because signs and symptoms of vaccine reactions can be similar to those associated with measles infection (*9*), clinical presentations consistent with the measles case definition should be interpreted within the context of identified risk factors for measles. If a person was not recently vaccinated, public health response measures to prevent measles virus transmission are necessary and should include specimen referral for genotyping. However, if the person who received the positive test result was vaccinated during the preceding 21 days and has no epidemiologic risk factors (e.g., travel to a region with endemic measles or a known exposure to a person with measles), further public health response is likely unnecessary, because the positive test result likely represents detection of the attenuated vaccine strain measles virus. For persons who were vaccinated within the preceding 21 days and have a risk factor for measles, public health measures to prevent measles transmission should continue while testing for measles vaccine virus by MeVA or genotype. Genetic confirmation of vaccine reaction might also be considered if a person was vaccinated >21 days earlier and has no epidemiologic risk factors.

Limitations

The findings in this report are subject to at least three limitations. First, 12 persons with measles detected by syndromic PCR panels were not reported to public health agencies, and descriptions of their clinical signs, symptoms, and risk factors are limited to clinician recall and documentation, increasing susceptibility for recall bias. Second, the small number of syndromic PCR panels and measles detections in only a subset of states limits generalizability. Finally, because of delayed reporting to public health officials, only two specimens underwent confirmatory molecular testing.

BOX. Proposed public health approach* to incidental detection of measles virus, by syndromic polymerase chain reaction panels

Public health evaluation

- Documentation of receipt of measles vaccine
- Evaluation of clinical signs and symptoms†
- Assessment of risk factors
  - Epidemiologic link to a measles case§
  - Elicitation of travel history¶

Public health response

- No recent vaccination**
  - Full public health response††
- Recent vaccination** with risk factor
  - Full public health response while awaiting confirmatory testing§§
- Recent vaccination** without risk factor
  - No further public health response

* Proposed approach developed by CDC and state health departments of Florida, Illinois, North Carolina, Tennessee, Texas, and Virginia.

† Measles infection typically appears as a prodrome of fever with cough, coryza, and conjunctivitis followed by a descending maculopapular rash. Because vaccine reactions can occur with similar symptoms, signs and symptoms consistent with the measles case definition should be interpreted in the context of identified risk factors for measles.

§ Including exposure to persons with confirmed measles infection and persons with compatible signs and symptoms.

¶ Including travel to areas with measles virus transmission or travel through an international airport.

** Recent vaccination is defined here as receipt of a measles-containing vaccine within the preceding 21 days. If measles virus is detected after 21 days in a vaccinated person without risk factors or signs and symptoms consistent with measles infection, health departments could consider confirmatory testing for vaccine strain to differentiate between wild-type and vaccine strains of measles virus.

†† A full public health response includes identifying persons exposed to measles, checking presumptive evidence of immunity, offering postexposure prophylaxis, and recommending isolation or quarantine measures as appropriate to contain the spread of measles.

§§ Confirmatory testing by measles vaccine assay real-time reverse transcription–polymerase chain reaction or genotyping is available through the Association of Public Health Laboratories (https://www.aphl.org/aboutAPHL/publications/Documents/VPD-Reference-Guide.pdf) and CDC Vaccine Preventable Diseases Reference Centers (https://www.cdc.gov/measles/lab-tools/genetic-analysis.html).

Summary

What is already known about this topic?

Syndromic polymerase chain reaction panels test for pathogens that can cause rash illnesses, including measles. Rash illnesses have many causes. Approximately 5% of patients experience a rash after receipt of a measles, mumps, and rubella vaccine.

What is added by this report?

Among syndromic panels conducted by a commercial laboratory, approximately 1% were positive for measles. Patients who received these results were children without known measles risk factors who had been vaccinated against measles, the majority <3 weeks previously. Their results were attributed to detection of measles vaccine virus.

What are the implications for public health practice?

After vaccination, syndromic panels can detect measles vaccine virus, which is not transmitted to others and does not cause disease in immunocompetent persons. Any detection of measles virus should be immediately reported to public health agencies to determine appropriate public health response.

Implications for Public Health Practice

During the first year of measles inclusion in commercial syndromic multiplex PCR panels, approximately 1% of tests reported a positive measles test result after recent routine childhood MMR vaccination. These positive test results most likely represented detection of measles vaccine virus in patients with rashes from a vaccine reaction or other cause, rather than measles infection. To facilitate appropriate public health response, clinicians should notify their local public health agency immediately if they are concerned about possible measles infection or patients receive positive measles test results. Commercial laboratories should critically evaluate use of measles in syndromic PCR panels and rapidly notify public health officials of any measles-positive specimens. When measles infection is not clinically suspected but detected by syndromic PCR testing, public health agencies should consider the likelihood of incidental measles vaccine virus detection by assessing measles vaccination history and risk factors. Because 1 dose of MMR vaccine is 93% effective in preventing measles (*4*), if a person recently received MMR vaccine and has no risk factors for acquiring measles, additional public health response is likely unnecessary. However, if a person has not recently received MMR vaccine, subsequent public health response should include necessary measures to prevent measles transmission. For a person who recently received MMR vaccine and has a risk factor for acquiring measles, additional testing for measles vaccine virus is needed to determine subsequent response measures.

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Tuberculosis — United States, 2023

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Abstract

After 27 years of declining U.S. tuberculosis (TB) case counts, the number of TB cases declined considerably in 2020, coinciding with the COVID-19 pandemic. For this analysis, TB case counts were obtained from the National TB Surveillance System. U.S. Census Bureau population estimates were used to calculate rates overall, by jurisdiction, birth origin, race and ethnicity, and age group. Since 2020, TB case counts and rates have increased each year. During 2023, a total of 9,615 TB cases were provisionally reported by the 50 U.S. states and the District of Columbia (DC), representing an increase of 1,295 cases (16%) as compared with 2022. The rate in 2023 (2.9 per 100,000 persons) also increased compared with that in 2022 (2.5). Forty states and DC reported increases in 2023 in both case counts and rates. National case counts increased among all age groups and among both U.S.-born and non-U.S.–born persons. Although TB incidence in the United States is among the lowest in the world and most U.S. residents are at minimal risk, TB continues to cause substantial global morbidity and mortality. This postpandemic increase in U.S. cases highlights the importance of continuing to engage communities with higher TB rates and their medical providers in TB elimination efforts and strengthening the capacity in public health programs to carry out critical disease control and prevention strategies.

Introduction

Despite being both preventable and curable, tuberculosis (TB) remains one of the world's leading infectious disease killers (*1*). The United States has one of the lowest TB rates globally (*1*) and has a goal of eliminating TB (elimination defined as less than one case per 1 million population) by 2035 (*2*). During 1995–2014, health departments and CDC TB control efforts prevented as many as 300,000 persons from developing TB disease and averted up to $14.5 billion in costs (*3*). After 27 years of declining U.S. TB cases, the number of TB cases declined considerably in 2020 to 7,171, coinciding with the COVID-19 pandemic (*4*); however, TB case counts and rates increased in 2021 and 2022. This report provides provisional TB surveillance data for 2023 in the United States.

Methods

Tuberculosis Case Counts and Incidence

The 50 U.S. states and DC report each TB case that meets the Council of State and Territorial Epidemiologists' surveillance case definition* to CDC's National Tuberculosis Surveillance System (NTSS).† National case counts, along with counts by jurisdiction, birth origin,§ race and ethnicity, and age group, were obtained from NTSS. National and jurisdictional TB rates per 100,000 persons were calculated using the midyear U.S. Census Bureau population estimates,¶ and rates by birth origin (i.e., U.S.-born versus non-U.S.–born), race and ethnicity, and age group were calculated using the Current Population Survey** midyear estimates. Percentage changes in TB case counts and rates for 2023 compared with 2022 were calculated overall and by jurisdiction and demographic characteristics. Annual number and rate of TB cases are reported by birth origin for 2013 through 2023. SAS software (version 9.4; SAS Institute) was used for all analyses. This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.††

Population Characteristics

Self-reported race and ethnicity were categorized according to federal guidelines.§§ Persons of Hispanic or Latino (Hispanic) origin might be of any race but are categorized as Hispanic; all racial groups are non-Hispanic. Non-Hispanic persons who reported more than one race were categorized as "multiple race."

* https://ndc.services.cdc.gov/case-definitions/tuberculosis-2009
† This report is limited to National Tuberculosis Surveillance System data verified as of February 17, 2024. Updated data will be available in CDC's annual TB surveillance report later in 2024.
§ Persons born in the United States or certain U.S. territories or elsewhere to at least one U.S. citizen parent are categorized as U.S.-born. All other persons are categorized as non-U.S.–born.
¶ Short-term projections from the monthly population estimates by age, sex, and race and ethnicity were used for the 2023 population. Vintage 2022 Estimates were used for 2023 and 2022, and Vintage 2010 Estimates were used for 2013–2019. https://www.census.gov/programs-surveys/popest/data/tables.html
** https://www.census.gov/programs-surveys/cps.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.
§§ https://www.census.gov/topics/population/race/about.html

Results

Tuberculosis Incidence by Jurisdiction

In 2023, the 50 U.S. states and DC provisionally reported 9,615 TB cases, an increase of 1,295 cases (16%) compared with the 8,320 cases reported in 2022, an 8% increase compared with the 2019 prepandemic case count (8,895), and the highest number of cases reported since 2013 (9,556) (Figure). Overall, the U.S. TB rate increased by 15%, from 2.5 per 100,000 persons in 2022 to 2.9 in 2023 (Table 1). Forty states and DC reported an increase in both case counts and rates compared with those in 2022. As in 2022, California reported the highest number of cases in 2023 (2,113), and Alaska reported the highest rate (10.6). Eight states and DC reported TB rates higher than the national rate of 2.9 per 100,000 in 2023.

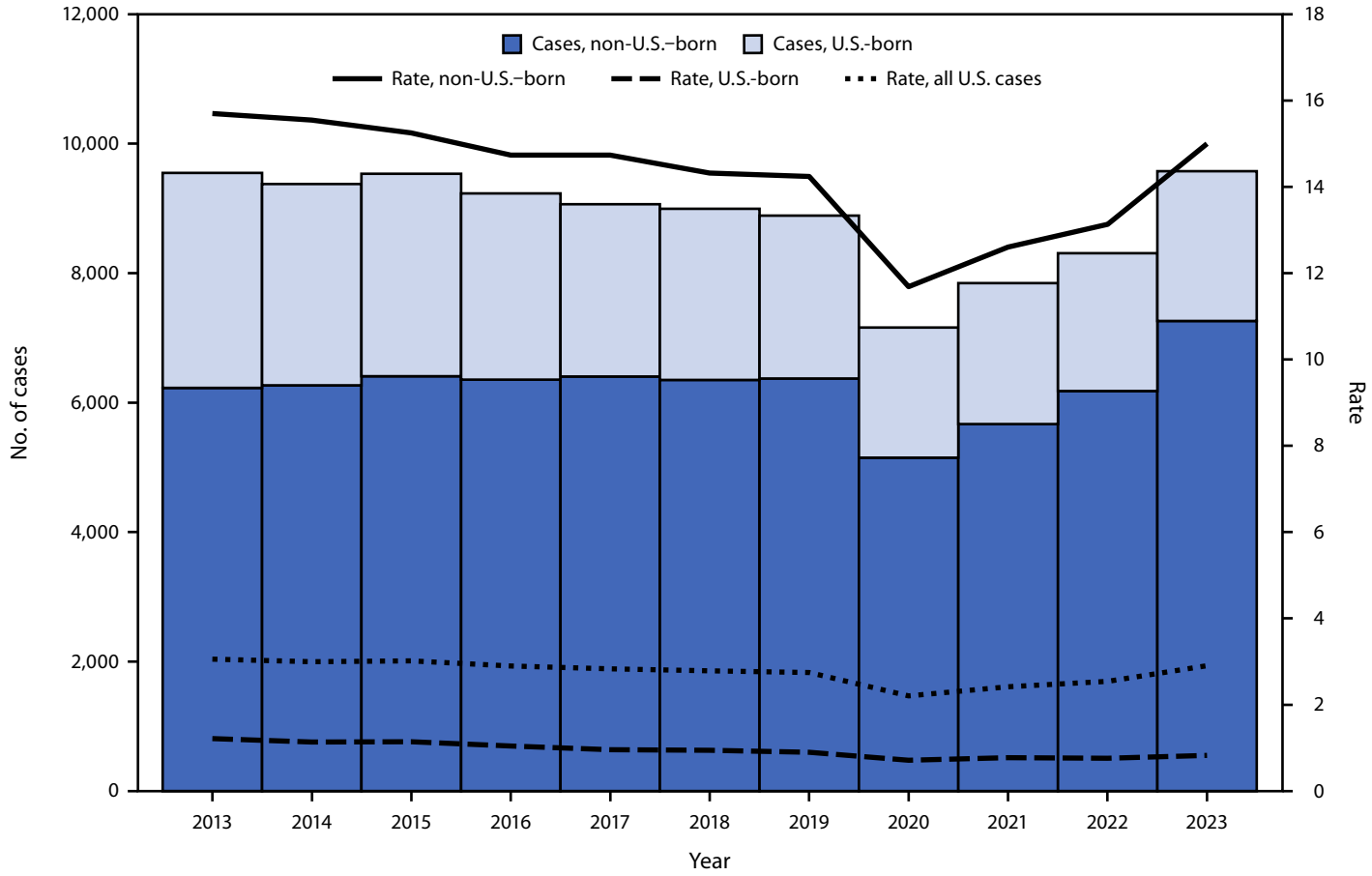
Tuberculosis Incidence by Demographic Characteristics

In 2023, among 9,573 TB cases in persons for whom birth origin was known, 7,259 (76%) occurred among non-U.S.–born persons, an 18% increase compared with the 6,177 such cases reported in 2022 (Table 2). The number of cases in U.S.-born persons in 2023 increased 9%, from 2,131 in 2022 to 2,314.[¶¶] The rate increased among non-U.S.–born persons from 13.1 in 2022 to 15.0 in 2023, and the rate among U.S.-born persons remained at 0.8 cases per 100,000 persons.

Among U.S.-born persons with TB, 33% (753) identified as Black or African American (Black), 27% (614) as Hispanic, 26% (591) as White, 6% (130) as Asian, 5% (106) as American

[¶¶] Proportions using birth origin are calculated excluding 12 cases in 2022 and 42 cases in 2023 for which birth origin was missing or unknown.

FIGURE. Annual number* and rate† of cases of tuberculosis disease, by birth origin§ — United States, 2013–2023



* Case counts are based on data from the National Tuberculosis Surveillance System as of February 17, 2024.
† Annual tuberculosis rate is calculated as cases per 100,000 persons. The Current Population Survey provides the population denominators used to calculate tuberculosis rate according to birth origin. https://www.census.gov/programs-surveys/cps.html (Accessed February 2, 2024).
§ Persons born in the United States or certain U.S. territories or elsewhere to at least one U.S. citizen parent are categorized as U.S.-born. All other persons are categorized as non-U.S.–born. Persons for whom birth origin was unknown (range = 7 [2013] to 42 [2023]) are not included in this figure.

TABLE 1. Tuberculosis case counts and rate, by jurisdiction — United States, 2022 and 2023

Jurisdiction	No. of cases*		% Change 2022 to 2023§	TB rate†		% Change 2022 to 2023§
	2022	2023		2022	2023	
All	**8,320**	**9,615**	16	**2.5**	**2.9**	15
Alabama	65	92	42	1.3	1.8	41
Alaska	95	78	−18	13	10.6	−18
Arizona	154	202	31	2.1	2.7	30
Arkansas	68	83	22	2.2	2.7	21
California	1,842	2,113	15	4.7	5.4	15
Colorado	57	89	56	1.0	1.5	55
Connecticut	67	66	−1	1.9	1.8	−2
Delaware	13	21	62	1.3	2.0	60
District of Columbia	15	26	73	2.2	3.8	71
Florida	535	624	17	2.4	2.8	15
Georgia	261	248	−5	2.4	2.2	−6
Hawaii	100	116	16	6.9	8.1	16
Idaho	11	15	36	0.6	0.8	35
Illinois	298	353	18	2.4	2.8	19
Indiana	99	130	31	1.4	1.9	31
Iowa	60	67	12	1.9	2.1	11
Kansas	52	46	−12	1.8	1.6	−12
Kentucky	70	75	7	1.6	1.7	7
Louisiana	95	97	2	2.1	2.1	2
Maine	17	26	53	1.2	1.9	52
Maryland	157	198	26	2.5	3.2	26
Massachusetts	154	224	45	2.2	3.2	45
Michigan	120	149	24	1.2	1.5	24
Minnesota	132	160	21	2.3	2.8	21
Mississippi	53	41	−23	1.8	1.4	−23
Missouri	71	72	1	1.1	1.2	1
Montana	6	8	33	0.5	0.7	32
Nebraska	29	33	14	1.5	1.7	13
Nevada	62	86	39	2.0	2.7	38
New Hampshire	11	14	27	0.8	1.0	27
New Jersey	289	330	14	3.1	3.6	14
New Mexico	30	41	37	1.4	1.9	37
New York	709	894	26	3.6	4.6	27
North Carolina	164	215	31	1.5	2.0	29
North Dakota	10	9	−10	1.3	1.1	−11
Ohio	146	193	32	1.2	1.6	32
Oklahoma	77	66	−14	1.9	1.6	−15
Oregon	73	78	7	1.7	1.8	7
Pennsylvania	173	216	25	1.3	1.7	25
Rhode Island	17	27	59	1.6	2.5	59
South Carolina	101	90	−11	1.9	1.7	−12
South Dakota	10	14	40	1.1	1.5	39
Tennessee	106	118	11	1.5	1.7	10
Texas	1,100	1,235	12	3.7	4.0	11
Utah	33	34	3	1.0	1.0	2
Vermont	3	3	0	0.5	0.5	0
Virginia	195	207	6	2.2	2.4	6
Washington	251	222	−12	3.2	2.8	−12
West Virginia	11	15	36	0.6	0.8	37
Wisconsin	52	54	4	0.9	0.9	3
Wyoming	1	2	100	0.2	0.3	99

* Case counts are based on data reported to the National Tuberculosis Surveillance System as of February 17, 2024.
† Annual tuberculosis rate is calculated as cases per 100,000 persons using midyear population estimates from the U.S. Census Bureau. Short-term projections from the monthly population estimates by age, sex, and race and ethnicity were used for the 2023 population. Vintage 2022 estimates were used for 2022 and 2023. https://www.census.gov/programs-surveys/popest/data/tables.html
§ Percentage change in rate was calculated with unrounded numbers.

TABLE 2. Characteristics of persons with tuberculosis — United States, 2022 and 2023

Characteristic	No. of cases* (%)		% Change 2022 to 2023§	TB rate†		% Change 2022 to 2023§
	2022	2023		2022	2023	
Overall	**8,320**	**9,615**	**16**	**2.5**	**2.9**	**15**
Age group,¶ yrs						
0–4	199 (2)	233 (2)	17	1.1	1.3	17
5–14	163 (2)	231 (2)	42	0.4	0.6	45
15–24	844 (10)	1,017 (11)	21	2.0	2.3	16
25–44	2,450 (29)	3,001 (31)	22	2.8	3.4	21
45–64	2,416 (29)	2,597 (27)	7	2.9	3.2	9
≥65	2,248 (27)	2,530 (26)	13	4.0	4.3	9
Race and ethnicity						
U.S.-born,††,§§**	2,131 (26)	2,314 (24)	9	0.8	0.8	8
American Indian or Alaska Native	113 (5)	106 (5)	−6	4.5	4.1	−9
Asian	142 (7)	130 (6)	−8	1.7	1.5	−12
Black or African American	672 (32)	753 (33)	12	1.9	2.1	12
Native Hawaiian or other Pacific Islander	51 (2)	62 (3)	22	6.4	7.7	20
White	569 (27)	591 (26)	4	0.3	0.3	4
Hispanic or Latino	542 (25)	614 (27)	13	1.3	1.5	11
Multiple races	20 (1)	18 (1)	−10	0.3	0.2	−14
Non-U.S.–born,§§,¶¶**	6,177 (74)	7,259 (76)	18	13.1	15.0	14
American Indian or Alaska Native***	0 (—)	6 (1)	—	0.0	12.3	—
Asian	2,739 (44)	2,804 (39)	2	22.9	22.5	−2
Black or African American	650 (11)	922 (13)	42	14.2	18.2	28
Native Hawaiian or other Pacific Islander	105 (2)	115 (2)	10	28.4	36.6	29
White	274 (4)	300 (4)	9	3.4	3.7	10
Hispanic or Latino	2,278 (37)	2,876 (40)	26	10.5	12.9	23
Multiple races	68 (1)	64 (1)	−6	28.3	25.8	−9

Abbreviation: TB = tuberculosis.

* Case counts are based on data reported to the National Tuberculosis Surveillance System as of February 17, 2024.

† Annual tuberculosis rate is calculated as cases per 100,000 persons using midyear population estimates from the U.S. Census Bureau. Short-term projections from the monthly population estimates by age, sex, and race and ethnicity were used for the 2023 population. Vintage 2022 estimates were used for 2022 and 2023. https://www.census.gov/programs-surveys/popest/data/tables.html

§ Percentage change in rate was calculated with unrounded numbers.

¶ Age was missing or unknown for zero cases in 2022 and six cases in 2023.

** Persons born in the United States or certain U.S. territories or elsewhere to at least one U.S. citizen parent are categorized as U.S.-born. All other persons are categorized as non-U.S.–born.

†† Birth origin was missing or unknown for 12 cases in 2022 and 42 cases in 2023.

§§ Race and ethnicity was missing or unknown for 22 cases in 2022 and 40 cases in 2023 among U.S.-born persons.

¶¶ Race and ethnicity was missing or unknown for 63 cases in 2022 and 172 cases in 2023 among non-U.S.–born persons.

*** No TB cases reported among American Indian or Alaska Native persons in 2022.

Indian or Alaska Native, 3% (62) as Native Hawaiian or other Pacific Islander, and 1% (18) as multiple race. Among U.S.-born persons, the rate of TB in 2023 compared with 2022 increased 20% (11 cases) among Native Hawaiian or other Pacific Islander, 12% (81 cases) among Black, 11% (72 cases) among Hispanic, and 4% (22 cases) among White persons, and the rate declined 9% (–7 cases) among American Indian or Alaska Native, and 12% (–12 cases) among Asian persons. Among non-U.S.–born persons with TB, 40% (2,876) identified as Hispanic, 39% (2,804) as Asian, 13% (922) as Black, 4% (300) as White, 2% (115) as Native Hawaiian or other Pacific Islander, 1% (64) as multiple race, and 0.1% (six) as American Indian or Alaska Native persons. Among non-U.S.–born persons, the TB rate in 2023 compared with 2022 increased 29% (10 cases) among Native Hawaiian or other Pacific Islander, 28% (272 cases) among Black, 23% (598 cases) among Hispanic, and 10% (26) among White persons, among non-U.S.–born Asian persons, the rate declined 2% (65 cases).***

TB incidence increased in every age group in 2023 compared with 2022, with the largest relative increase among children aged 5–14 years (68 cases, corresponding to a 42% increase in case count and a 45% increase in rate). Among the 83% (8,013) of persons with TB in 2023 for whom HIV status was known, 5% were coinfected with TB and HIV.

Discussion

Provisional national surveillance data show that TB case counts and rates have increased since the COVID-19 pandemic, returning to the number of cases last observed in 2013 (*4*). Increases occurred in every age group and all except

*** Percentage change is calculated from unrounded numbers. For demographic groups with small populations (e.g., non-U.S.–born American Indian or Alaska Native), changes in rates should be interpreted cautiously because of the increased volatility of these rates.

10 U.S. states. Case counts increased among both U.S.-born and non-U.S.–born persons, with the most substantial increase, 18%, among non-U.S.–born persons (1,082 cases).

The United States has one of the lowest TB rates in the world (*1*) and most U.S. residents are at minimal risk for TB (*2*,*4*). The overall epidemiology of TB continues to reflect persistent disparities by birth origin, and race and ethnicity in the United States. TB rates in 2023 were highest among non-U.S.–born persons which is consistent with prepandemic trends. Among U.S.-born persons, rates remained <1.0 overall but were highest among those who identified as Native Hawaiian or other Pacific Islander, American Indian or Alaska Native, or Black.

Approximately 85% of TB cases in the United States are attributed to reactivation of latent TB infection (LTBI) rather than recent transmission (*2*,*4*). Therefore, sustained transmission of TB in the United States leading to outbreaks is uncommon. Essential TB elimination activities include TB testing among populations at risk and treating persons with LTBI or TB disease. To prevent transmission and reduce morbidity, TB disease must be detected quickly; effective treatment must be initiated promptly; and all exposed persons identified, evaluated, and treated if infected (*5*). This approach led to a 66% reduction in TB cases and 73% reduction in the TB rate in the United States in the first 25 years of implementation (*4*).

TB prevention and control interventions are primarily conducted by staff members in state and local public health programs. The decades-long downward trend in TB in the United States and the high TB disease treatment completion rates (*4*) underscore the success of these TB programs. However, during the COVID-19 pandemic, TB programs were severely taxed with many staff members and activities diverted to the COVID-19 response (*6*). Timely diagnosis and treatment of TB disease also suffered because of pandemic-related disruptions in health care access and health care workers focusing on identifying persons with COVID-19, who often have symptoms similar to those of pulmonary TB (*7*). These factors, along with changes in migration volume (*8*), probably contributed to the decrease in the number of cases observed in 2020, and to the subsequent rise in case counts and rates since 2020. Identification of TB cases possibly increased after the pandemic because of renewed attention to infectious diseases other than COVID-19.

The number of persons who received a new TB diagnosis has also risen globally. In 2022, the World Health Organization reported a second consecutive year of increasing TB case counts, with the global estimate of TB cases equaling that of 2016 (*1*). TB is not the only preventable communicable disease resurging after the COVID-19 pandemic. For example, influenza (*9*) and measles (*10*) have also experienced postpandemic surges. Setbacks to TB elimination in the United States illustrate the power of pandemics and other large-scale crises to have long-lasting effects on public health, a phenomenon also observed at the onset of the HIV epidemic when the number of TB cases increased after 3 decades of decline (*4*). Renewed progress toward TB elimination will require strengthened capacity of public health programs to carry out critical TB control and prevention strategies and engagement of providers and affected communities in TB elimination efforts. In addition, because most TB cases in the United States occur among non-U.S.–born persons, collaboration of public health entities in the United States with international partners is important to reduce TB morbidity globally.

Summary

What is already known about this topic?

For years, the United States has had one of the lowest tuberculosis (TB) rates in the world. In the first year of the COVID-19 pandemic, reported TB case counts dropped substantially, followed by increasing case counts every year since 2020.

What is added by this report?

During 2023, tuberculosis case counts increased among all age groups, among U.S-born and non-U.S.–born persons, and in most reporting jurisdictions. Overall, cases increased from 8,320 in 2022 to 9,615 in 2023, an increase of 1,295 cases. The rate also increased from 2.5 per 100,000 persons in 2022 to 2.9 in 2023.

What are the implications for public health practice?

Continued progress toward TB elimination will require strong public health systems that are capable of maintaining essential disease prevention and control activities and prepared to withstand the next pandemic or other large-scale crisis.

Limitations

The findings in this report are subject to at least two limitations. First, this analysis is limited to provisional surveillance data for 2023, and case counts might change before CDC's annual TB surveillance report is published. Second, rates are based on midyear population estimates from the U.S. Census Bureau that are subject to ongoing refinement.

Implications for Public Health Practice

The U.S. TB case count increases in 2023 underscores the ongoing global TB-associated morbidity and mortality. Renewed progress toward TB elimination will require strong public health systems both domestically and globally that are responsive to health disparities, capable of maintaining essential disease prevention and control activities, and prepared to withstand the next pandemic or other large-scale crisis.

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Interim Effectiveness of Updated 2023–2024 (Monovalent XBB.1.5) COVID-19 Vaccines Against COVID-19–Associated Hospitalization Among Adults Aged ≥18 Years with Immunocompromising Conditions — VISION Network, September 2023–February 2024

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Abstract

In September 2023, CDC's Advisory Committee on Immunization Practices recommended updated 2023–2024 (monovalent XBB.1.5) COVID-19 vaccination for all persons aged ≥6 months to prevent COVID-19, including severe disease. As with past COVID-19 vaccines, additional doses may be considered for persons with immunocompromising conditions, who are at higher risk for severe COVID-19 and might have decreased response to vaccination. In this analysis, vaccine effectiveness (VE) of an updated COVID-19 vaccine dose against COVID-19–associated hospitalization was evaluated during September 2023–February 2024 using data from the VISION VE network. Among adults aged ≥18 years with immunocompromising conditions, VE against COVID-19–associated hospitalization was 38% in the 7–59 days after receipt of an updated vaccine dose and 34% in the 60–119 days after receipt of an updated dose. Few persons (18%) in this high-risk study population had received updated COVID-19 vaccine. All persons aged ≥6 months should receive updated 2023–2024 COVID-19 vaccination; persons with immunocompromising conditions may get additional updated COVID-19 vaccine doses ≥2 months after the last recommended COVID-19 vaccine.

Introduction

On September 12, 2023, CDC's Advisory Committee on Immunization Practices recommended updated 2023–2024 COVID-19 vaccination with a monovalent XBB.1.5–derived vaccine for all persons aged ≥6 months to prevent COVID-19, including severe disease (*1*). Most persons aged ≥5 years are recommended to receive 1 updated dose. Persons with moderate or severe immunocompromising conditions, who are at higher risk for severe COVID-19 and might have a decreased response to vaccination, have the option to receive additional doses, guided by the clinical judgment of a health care provider and personal preference and circumstances* (*2*). Understanding vaccine effectiveness (VE) among persons with immunocompromising conditions is important to guiding vaccine policy and patient and provider decisions. This analysis estimated effectiveness of updated 2023–2024 COVID-19 vaccines against COVID-19–associated hospitalizations among adults aged ≥18 years with immunocompromising conditions during September 2023–February 2024.

Methods

Methods for Virtual SARS-CoV-2, Influenza, and Other respiratory viruses Network (VISION) VE analyses have been reported (*3*). VISION is a multisite† electronic health care records (EHR)–based network that utilizes a test-negative design to estimate COVID-19 VE. This analysis included hospitalizations among adults aged ≥18 years with immunocompromising conditions§ and who had COVID-19–like

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

† Sites from the CDC-funded VISION network that contributed data for this analysis were HealthPartners (Minnesota and Wisconsin), Intermountain Health (Utah), Kaiser Permanente Northern California (California), Kaiser Permanente Northwest (Oregon and Washington), Regenstrief Institute (Indiana), and University of Colorado (Colorado).

§ Immunocompromising conditions were obtained from *International Classification of Diseases, Tenth Revision* (ICD-10) discharge codes. The specific codes used were hematological malignancy: C81.*, C82.*, C83.*, C84.*, C85.*, C86.*, C88.*, C90.*, C91.*, C92.*, C93.*, C94.*, C95.*, C96.*, D46.*, D61.0*, D61.2, D61.9, D70.0, and D71.*; solid malignancy: C00.*, C01.*, C02.*, C03.*, C04.*, C05.*, C06.*, C07.*, C08.*, C09.*, C10.*, C11.*, C12.*, C13.*, C14.*, C15.*, C16.*, C17.*, C18.*, C19.*, C20.*, C21.*, C22.*, C23.*, C24.*, C25.*, C26.*, C27.*, C28.*, C29.*, C30.*, C31.*, C32.*, C33.*, C34.*, C35.*, C36.*, C37.*, C38.*, C39.*, C40.*, C41.*, C42.*, C43.*, C44.*, C45.*, C46.*, C47.*, C48.*, C49.*, C50.*, C51.*, C52.*, C53.*, C54.*, C55.*, C56.*, C57.*, C58.*, C59.*, C60.*, C61.*, C62.*, C63.*, C64.*, C65.*, C66.*, C67.*, C68.*, C69.*, C70.*, C71.*, C72.*, C73.*, C74.*, C75.*, C76.*, C77.*, C78.*, C79.*, C7A.*, C7B.*, C80.*, Z51.0, Z51.1*, and C4A.*; transplant: T86.0*, T86.1*, T86.2*, T86.3*, T86.4*, T86.5*, T86.81*, T86.85*, D47.Z1, Z48.2.*, Z94.*, and Z98.85; rheumatologic/inflammatory disorders: D86.*, E85.1, E85.2, E85.3, E85.4, E85.8*, E85.9, G35.*, J67.9.*, L40.54, L40.59, L93.0.*, L93.2.*, L94.*, M05.*, M06.*, M07.*, M08.*, M30.*, M31.3*, M31.5*, M32.*, M33.*, M34.*, M35.3*, M35.8*, M35.9*, M46.*, and T78.40*; other intrinsic immune condition or immunodeficiency: D27.9, D72.89, D80.*, D81.0, D81.1, D81.2, D81.4, D81.5, D81.6, D81.7, D81.8*, D81.9, D82.*, D83.*, D84.*, D87.89, D89.0, D89.1, D89.3, D89.4*, D89.8*, D89.9, K70.3*, K70.4*, K72.*, K74.3, K74.4, K74.5, K74.6, N04.*, R18.0; HIV: B20.*, B21.*, B22.*, B23.*, B24.*, B97.35, O98.7*, and Z21*. All ICD-10 codes with * include all child codes under the specific parent code.

illness[¶] with SARS-CoV-2 molecular testing during the 10 days preceding admission or up to 72 hours after admission. Case-patients were persons who received a positive SARS-CoV-2 test result using a molecular test and received a negative or indeterminate or had an unknown test result for both respiratory syncytial virus and influenza, and control patients were those who received a negative SARS-CoV-2 test result using a molecular test and received a negative influenza test result or had an unknown influenza test result. Nine persons who received >1 updated COVID-19 vaccine dose were included.[**] Odds ratios (ORs) and 95% CIs were estimated using multivariable logistic regression comparing persons who received an updated COVID-19 vaccine dose with those who did not, irrespective of the number of previous original or bivalent COVID-19 vaccine doses received (if any), among case- and control patients. Regression models were adjusted for age, sex, race and ethnicity, calendar time, and geographic region. VE was calculated as (1 – adjusted OR) × 100%. Analyses were conducted using R software (version 4.3.2; R Foundation). This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.[††] VISION activities were reviewed and approved by the Westat and site institutional review boards.

[¶] COVID-19–like illness diagnoses were obtained from ICD-10 discharge codes. The specific codes used were COVID-19 pneumonia: J12.81 and J12.82; influenza pneumonia: J09.X1, J10.0, J10.00, J10.01, J10.08, J11.0, J11.00, and J11.08; other viral pneumonia: J12*; bacterial and other pneumonia: J13, J14, J15*, J16*, J17, and J18*; influenza disease: J09*, J10.1, J10.2, J10.8*, J11.1, J11.2, and J11.8*; acute respiratory distress syndrome: J80; chronic obstructive pulmonary disease with acute exacerbation: J44.1; asthma acute exacerbation: J45.21, J45.22, J45.31, J45.32, J45.41, J45.42, J45.51, J45.52, J45.901, and J45.902; respiratory failure: J96.0*, J96.2*, and R09.2; other acute lower respiratory tract infections: B97.4, J20*, J21*, J22, J40, J44.0, J41*, J42, J43*, J47*, J85, J85.0, J85.1, J85.2, J85.3, and J86*; acute and chronic sinusitis: J01* and J32*; acute upper respiratory tract infections: J00*, J02*, J03*, J04*, J05*, and J06*; acute respiratory illness signs and symptoms: R04.2, R05, R05.1, R05.2, R05.4, R05.8, R05.9, R06.00, R06.02, R06.03, R06.1, R06.2, R06.8, R06.81, R06.82, R06.89, R07.1, R09.0*, R09.1, R09.2, R09.3, and R09.8*; acute febrile illness signs and symptoms: R50*, R50.81, and R68.83; acute nonrespiratory illness signs and symptoms: M79.10, M79.18, R19.7, R43*, R51.9, R65*, R53.81, R53.83, R57.9, R41.82, R40.0, R40.1, R53.1, R11.0, R11.10, R11.11, R11.15, R11.2, R21*, R10.0, R10.1*, R10.2, R10.3*, R10.81*, R10.84, and R10.9; respiratory failure, unspecified: J96.9*; febrile convulsions: R56.0; viral and respiratory diseases complicating pregnancy, childbirth, and puerperium: O98.5*, O98.8*, O98.9*, and O99.5*. All ICD-10 codes with * include all child codes under the specific parent code. One VISION site, representing 33% of case-patients, did not include the following codes in its definition: B97.4, J96.9*, O98.5*, O98.8*, O98.9*, O99.5*, and R56.0.

[**] The Advisory Committee on Immunization Practices recommendations allow optional additional doses for persons with moderate or severe immunocompromise. Because only nine persons in participating sites received >1 updated COVID-19 vaccine dose, statistical power to estimate VE separately in this group was insufficient.

[††] 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.

Results

Among 14,586 patients with immunocompromising conditions who were hospitalized with COVID-19–like illness, 1,392 case-patients and 13,194 control patients were included (Table 1). The most common immunocompromising conditions among both case-patients and control patients were solid organ malignancy (36% and 43%, respectively) and other intrinsic immune conditions or immunodeficiency (38% and 35%, respectively). A total of 195 (14%) case-patients had received an updated COVID-19 vaccine dose compared with 2,401 (18%) control patients. VE against COVID-19–associated hospitalization was 38% in the first 7–59 days after receipt of an updated COVID-19 vaccine dose and 34% in the 60–119 days after receipt of an updated dose (Table 2).

Discussion

In this multisite analysis among adults with immunocompromising conditions during September 2023–February 2024, receiving an updated 2023–2024 COVID-19 vaccine dose provided additional protection against COVID-19–associated hospitalizations, compared with not receiving an updated vaccine dose. Effectiveness estimates in this report were slightly lower than those in a recently published analysis from VISION and another CDC VE network showing COVID-19 VE against COVID-19-associated hospitalizations in adults without immunocompromising conditions was approximately 50%, but this report includes the analysis of an additional month of data compared with the previous report (*3*). However, lower COVID-19 VE among adults with immunocompromising conditions compared with adults without immunocompromising conditions has been previously reported (*4*,*5*); persons with moderate or severe immunocompromising conditions are at higher risk for severe COVID-19 and might have decreased response to vaccination (*2*).

Relatively few persons in this analysis had received an updated COVID-19 vaccine dose, despite those with immunocompromising conditions being at higher risk for severe COVID-19. For example, among those with an organ or stem cell transplant, a group known to be at particularly high risk for severe COVID-19 (*6*), only 18% had received an updated dose, representing a missed opportunity to prevent severe COVID-19.

Limitations

The findings in this report are subject to at least two limitations. First, the use of selected discharge diagnoses as surrogates for presumed immunocompromise status and the absence of medication and other relevant data might have led to misclassification of immunocompromise status, which might have biased estimated VE in either direction. Second,

TABLE 1. Characteristics of hospitalizations among immunocompromised adults aged ≥18 years with COVID-19–like illness, by COVID-19 vaccination status and SARS-CoV-2 test result status — VISION, September 2023–February 2024

Characteristic	Overall, no. (col. %) N = 14,586	SARS-CoV-2 status, no. (column %)			Vaccination status, no. (row %)			
		Case-patients* (n = 1,392)	Control patients† (n = 13,194)	SMD§	No updated dose¶ (n = 11,990)	Updated dose, 7–59 days earlier (n = 1,381)	Updated dose, 60–119 days earlier (n = 1,215)	SMD§
Site**								
HealthPartners	**966 (7)**	91 (7)	875 (7)	0.18	709 (73)	141 (15)	116 (12)	0.49
Intermountain Health	**1,608 (11)**	201 (14)	1,407 (11)		1,358 (84)	125 (8)	125 (8)	
KPNC	**5,790 (40)**	466 (33)	5,324 (40)		4,430 (77)	709 (12)	651 (11)	
KPNW	**863 (6)**	72 (5)	791 (6)		659 (76)	124 (14)	80 (9)	
Regenstrief Institute	**3,541 (24)**	353 (25)	3,188 (24)		3,154 (89)	206 (6)	181 (5)	
University of Colorado	**1,818 (12)**	209 (15)	1,609 (12)		1,680 (92)	76 (4)	62 (3)	
COVID-19 vaccination status								
No updated dose¶	**11,990 (82)**	1,197 (86)	10,793 (82)	0.12	11,990 (100)	0 (—)	0 (—)	NA
Updated dose, ≥7 days earlier	**2,596 (18)**	195 (14)	2,401 (18)		0 (—)	1,381 (53)	1,215 (47)	
Updated dose, 7–59 days earlier	**1,381 (9)**	100 (7)	1,281 (10)		0 (—)	1,381 (100)	0 (—)	
Updated dose, 60–119 days earlier	**1,215 (8)**	95 (7)	1,120 (8)		0 (—)	0 (—)	1,215 (100)	
Median age, yrs (IQR)	**70 (60–79)**	72 (63–80)	70 (60–78)	0.16	69 (59–78)	74 (66–81)	75 (68–82)	0.36
Age group, yrs								
18–64	**5,017 (34)**	393 (28)	4,624 (35)	0.15	4,524 (90)	288 (6)	205 (4)	0.43
≥65	**9,569 (66)**	999 (72)	8,570 (65)		7,466 (78)	1,093 (11)	1,010 (11)	
Female sex	**7,420 (51)**	669 (48)	6,751 (51)	0.06	6,159 (83)	675 (9)	586 (8)	0.06
Race and ethnicity								
Black or African American, non-Hispanic	**1,390 (10)**	110 (8)	1,280 (10)	0.12	1,196 (86)	113 (8)	81 (6)	0.14
White, non-Hispanic	**10,008 (69)**	1,022 (73)	8,986 (68)		8,126 (81)	996 (10)	886 (9)	
Hispanic or Latino	**1,620 (11)**	127 (9)	1,493 (11)		1,378 (85)	135 (8)	107 (7)	
Other, non-Hispanic††	**1,419 (10)**	121 (9)	1,298 (10)		1,157 (82)	130 (9)	132 (9)	
Unknown§§	**149 (1)**	12 (1)	137 (1)		133 (89)	7 (5)	9 (6)	
No. of chronic medical condition categories¶¶ in addition to immunocompromising conditions								
0	**555 (4)**	31 (2)	524 (4)	0.13	495 (89)	33 (6)	27 (5)	0.17
1	**1,310 (9)**	144 (10)	1,166 (9)		1,138 (87)	91 (7)	81 (6)	
2	**2,681 (18)**	267 (19)	2,414 (18)		2,204 (82)	255 (10)	222 (8)	
3	**4,115 (28)**	400 (29)	3,715 (28)		3,307 (80)	404 (10)	404 (10)	
4	**3,378 (23)**	333 (24)	3,045 (23)		2,741 (81)	354 (10)	283 (8)	
≥5	**2,547 (17)**	217 (16)	2,330 (18)		2,105 (83)	244 (10)	198 (8)	
Chronic respiratory condition***	**6,192 (42)**	550 (40)	5,642 (43)	0.07	5,012 (81)	628 (10)	552 (9)	0.07
Type of immunocompromising condition†††								
Solid organ malignancy	**6,185 (42)**	500 (36)	5,685 (43)	0.15	5,052 (82)	600 (10)	533 (9)	0.03
Hematologic malignancy	**2,124 (15)**	241 (17)	1,883 (14)	0.08	1,699 (80)	234 (11)	191 (9)	0.06
Rheumatologic or inflammatory disorder	**3,684 (25)**	411 (30)	3,273 (25)	0.11	3,025 (82)	345 (9)	314 (9)	0.01
Other intrinsic immune condition or immunodeficiency	**5,140 (35)**	525 (38)	4,615 (35)	0.06	4,304 (84)	445 (9)	391 (8)	0.08
Organ or stem cell transplant	**1,191 (8)**	162 (12)	1,029 (8)	0.13	974 (82)	122 (10)	95 (8)	0.02
HIV/AIDS	**315 (2)**	17 (1)	298 (2)	0.08	258 (82)	34 (11)	23 (7)	0.02
ICU admission	**3,386 (23)**	283 (20)	3,103 (24)	0.08	2,871 (85)	298 (9)	217 (6)	0.10
Receipt of invasive mechanical ventilation								
Yes	**1,467 (10)**	117 (8)	1,350 (10)	0.07	1,271 (87)	107 (7)	89 (6)	0.27
No	**10,967 (75)**	1,059 (76)	9,908 (75)		8,788 (80)	1,155 (11)	1,024 (9)	
Unknown	**2,152 (15)**	216 (16)	1,936 (15)		1,931 (90)	119 (6)	102 (5)	
In-hospital death§§§	**1,479 (10)**	112 (8)	1,367 (10)	0.08	1,249 (84)	125 (8)	105 (7)	0.05
Month and year of COVID-19–like illness hospitalization								
Sep 2023	**931 (6)**	68 (5)	863 (7)	0.20	931 (100)	0 (—)	0 (—)	1.10
Oct 2023	**3,045 (21)**	247 (18)	2,798 (21)		2,901 (95)	144 (5)	0 (—)	
Nov 2023	**3,015 (21)**	285 (20)	2,730 (21)		2,503 (83)	496 (16)	16 (1)	
Dec 2023	**3,394 (23)**	394 (28)	3,000 (23)		2,596 (76)	482 (14)	316 (9)	
Jan 2024	**3,214 (22)**	337 (24)	2,877 (22)		2,334 (73)	223 (7)	657 (20)	
Feb 2024	**987 (7)**	61 (4)	926 (7)		725 (73)	36 (4)	226 (23)	
SARS-CoV-2 JN.1 lineage predominant period¶¶¶	**5,089 (35)**	512 (37)	4,577 (35)	0.04	3,732 (73)	346 (7)	1,011 (20)	0.69

See table footnotes on the next page.

TABLE 1. (*Continued*) Characteristics of hospitalizations among immunocompromised adults aged ≥18 years with COVID-19–like illness, by COVID-19 vaccination status and SARS-CoV-2 test result status — VISION, September 2023–February 2024

Abbreviations: ICU = intensive care unit; KPNC = Kaiser Permanente Northern California; KPNW = Kaiser Permanente Northwest; NA = not applicable; SMD = standardized mean or proportion difference; VISION = Virtual SARS-CoV-2, Influenza, and Other respiratory viruses Network.

* Patient received a positive SARS-CoV-2 test result using a molecular test and received a negative or indeterminate test result or had an unknown test result for both respiratory syncytial virus and influenza.

† Patient received a negative SARS-CoV-2 test result using a molecular test and received a negative influenza test result or had an unknown influenza test result.

§ A larger SMD indicates a larger difference in variable distributions between hospitalizations for vaccinated versus unvaccinated patients, or for patients who received a positive SARS-CoV-2 test result versus patients who received a negative SARS-CoV-2 test result. For mRNA COVID-19 vaccination status, a single SMD was calculated by averaging the absolute SMDs obtained from pairwise comparisons of each vaccinated category versus unvaccinated. Specifically, SMD was calculated as the average of the absolute value of the SMDs for 1) updated dose, 7–59 days earlier versus no updated dose; and 2) updated dose, 60–119 days earlier versus no updated dose.

¶ The "no updated dose" group included all eligible persons who did not receive an updated COVID-19 vaccine dose, regardless of number of previous (i.e., original monovalent and bivalent) doses (if any) received.

** Date ranges of hospitalizations by site: HealthPartners (September 21, 2023–February 17, 2024), Intermountain Health (September 21, 2023–February 17, 2024), KPNC (September 21, 2023–February 17, 2024), KPNW (September 21, 2023–February 17, 2024), Regenstrief Institute (September 21, 2023–February 13, 2024), and University of Colorado (September 21, 2023–February 4, 2024).

†† "Other, non-Hispanic" race persons reporting non-Hispanic ethnicity and any of the following options for race: American Indian or Alaska Native, Asian, Native Hawaiian or other Pacific Islander, other races not listed, and multiple races; because of small numbers, these categories were combined.

§§ "Unknown" includes persons with missing race and ethnicity in their electronic health records.

¶¶ Underlying condition categories included pulmonary, cardiovascular, cerebrovascular, musculoskeletal, neurologic, hematologic, endocrine, renal, and gastrointestinal. All persons in the analysis had one or more immunocompromising condition.

*** Chronic respiratory condition was defined using *International Classification of Diseases, Tenth Revision* discharge codes for asthma, chronic obstructive pulmonary disease, cystic fibrosis, or other lung disease.

††† Persons included in the analysis might have one or more immunocompromising conditions; therefore, column totals might add to more than 100%.

§§§ In-hospital death was defined as death while hospitalized within 28 days after admission.

¶¶¶ The JN.1 predominant period was considered to have started December 24, 2023.

TABLE 2. Effectiveness of updated 2023–2024 (monovalent XBB.1.5) COVID-19 vaccination against laboratory-confirmed COVID-19–associated hospitalization among immunocompromised adults aged ≥18 years — VISION, September 2023–February 2024

COVID-19 vaccination dosage pattern	Total	Positive SARS-CoV-2 test result, no. (%)	Median interval since last dose, days (IQR)	Unadjusted VE, %* (95% CI)	Adjusted VE, %† (95% CI)
No updated dose§ (Ref)	**11,990**	1,197 (10)	587 (381–766)	Ref	Ref
Received updated dose	**2,596**	195 (8)	56 (32–81)	27 (14–37)	36 (25–46)
7–59 days earlier	**1,381**	100 (7)	34 (21–46)	30 (13–43)	38 (23–50)
60–119 days earlier	**1,215**	95 (8)	83 (71–98)	24 (5–38)	34 (16–47)

Abbreviations: Ref = referent group; VE = vaccine effectiveness; VISION = Virtual SARS-CoV-2, Influenza, and Other respiratory viruses Network.

* VE was calculated as (1 – odds ratio) × 100%, with odds ratios calculated using logistic regression.

† The odds ratio was adjusted for age, sex, race and ethnicity, geographic region, and calendar time (days since January 1, 2021).

§ The "no updated dose" group included all eligible persons who did not receive an updated COVID-19 vaccine dose, regardless of number of previous (i.e., original monovalent and bivalent) doses (if any) received.

immunocompromising conditions are heterogeneous and likely to create differential risk for severe COVID-19, as well as differential response to vaccination (*2*). This analysis did not have statistical power to estimate VE by individual risk group or for those receiving more than one dose of the updated COVID-19 vaccine; however, CDC will continue to monitor VE in these groups. In addition, this analysis is subject to limitations similar to those in previous VISION VE analyses, including the potential that case-patients might have been hospitalized for reasons other than COVID-19, potential misclassification of vaccination status, no accounting for previous infection status, and potential residual confounding (*3*).

Implications for Public Health Practice

Receipt of an updated COVID-19 vaccine dose provided increased protection against COVID-19–associated hospitalization among adults with immunocompromising conditions compared with no receipt of an updated dose. CDC will continue to monitor VE of updated COVID-19 vaccines in populations at high risk, including those with immunocompromising conditions. All persons aged ≥6 months should receive updated 2023–2024 COVID-19 vaccination; persons with immunocompromising conditions may get additional updated COVID-19 vaccine doses ≥2 months after the last recommended COVID-19 vaccine.

Summary

What is already known about this topic?

In September 2023, CDC's Advisory Committee on Immunization Practices recommended updated 2023–2024 (monovalent XBB.1.5) COVID-19 vaccination for all persons aged ≥6 months to prevent COVID-19, including severe disease, with optional additional doses for persons with immunocompromising conditions; such persons are at higher risk for severe COVID-19 and might also have reduced immune responses to vaccination.

What is added by this report?

Among adults aged ≥18 years with immunocompromising conditions, receipt of an updated COVID-19 vaccine provided increased protection against COVID-19–associated hospitalizations compared with not receiving an updated COVID-19 vaccine. Few persons (18%) in this high-risk study population had received updated COVID-19 vaccine.

What are the implications for public health practice?

All persons with immunocompromising conditions should receive updated COVID-19 vaccination and may get additional updated COVID-19 vaccine doses ≥2 months after the last recommended COVID-19 vaccine.

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