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Effectiveness of 2024–2025 COVID-19 Vaccines in Children in the United States — VISION, August 29, 2024–September 2, 2025

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Abstract

During September 2023–August 2024, approximately 38,000 COVID-19–associated hospitalizations occurred among children and adolescents aged <18 years in the United States, a rate of approximately 53 per 100,000 children, ranging from 600 per 100,000 children aged <6 months to 21 per 100,000 children and adolescents aged 5–17 years. On June 27, 2024, the Advisory Committee on Immunization Practices recommended that all persons aged ≥6 months receive a 2024–2025 COVID-19 vaccine, which targeted Omicron JN.1 and JN.1-derived sublineages. Investigators used a test-negative case-control design to estimate vaccine effectiveness (VE) of 2024–2025 COVID-19 vaccines against COVID-19–associated emergency department or urgent care (ED/UC) visits during August 29, 2024–September 2, 2025, among immunocompetent children aged 9 months–4 years and children and adolescents aged 5–17 years in the CDC-funded Virtual SARS-CoV-2, Influenza, and Other respiratory viruses Network (VISION), a multisite electronic health record–based network in nine states. Among children aged 9 months–4 years, VE against COVID-19–associated ED/UC visits was estimated at 76% (95% CI = 58%–87%) during the first 7–179 days after vaccination. Among children and adolescents aged 5–17 years, VE against COVID-19–associated ED/UC visits was an estimated 56% (95% CI = 35%–70%) during the first 7–179 days after vaccination. These findings suggest that vaccination with a 2024–2025 COVID-19 vaccine dose provided children with additional protection against COVID-19–associated ED/UC encounters compared with no 2024–2025 dose.

Introduction

Since 2020, COVID-19 has accounted for thousands of hospitalizations and hundreds of deaths in the United States each season, including approximately 38,000 hospitalizations among children and adolescents aged <18 years during September 2023–August 2024 (*1*). During 2024, the SARS-CoV-2 Omicron JN.1 and JN.1-derived lineages predominated and were genomically divergent from the XBB lineages on which the 2023–2024 COVID-19 vaccines were based.* On June 27, 2024, the CDC's Advisory Committee on Immunization Practices (ACIP) recommended 2024–2025 COVID-19 vaccines for persons aged ≥6 months (*2*); 2024–2025 COVID-19 vaccines became available on August 22, 2024.† For previously unvaccinated immunocompetent children aged 6 months–4 years, a multidose

* Variants and Genomic Surveillance | COVID-19 | CDC (Accessed November 14, 2025).
† FDA Approves and Authorizes Updated mRNA COVID-19 Vaccines to Better Protect Against Currently Circulating Variants | FDA

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initial series (including 3 doses of Pfizer-BioNTech vaccine or 2 doses of Moderna vaccine) was recommended; a single 2024–2025 dose was recommended for those who completed an initial series. For immunocompetent children aged ≥5 years, a single 2024–2025 dose was recommended, regardless of vaccination history[§] (*2*). Per an announcement from the Secretary of the U.S. Department of Health and Human Services, the Child and Adolescent Immunization Schedule was updated in May 2025 to indicate shared clinical decision-making[¶] for COVID-19 vaccination for healthy children and adolescents aged 6 months–17 years.[**]

This analysis estimated 2024–2025 COVID-19 vaccine effectiveness (VE) against COVID-19–associated emergency department or urgent care (ED/UC) encounters in children aged 9 months–4 years and children and adolescents aged 5–17 years during August 29, 2024–September 2, 2025. Age 9 months rather than 6 months was the youngest age included to allow time for completion of the Pfizer-BioNTech initial series in children aged 6 months.[††]

[§] The recommendation for unvaccinated children and adolescents aged ≥12 years receiving the Novavax COVID-19 vaccine is 2 doses.
[¶] ACIP Shared Clinical Decision-Making Recommendations | ACIP | CDC
[**] Child Immunization Schedule Notes | Vaccines & Immunizations | CDC
[††] Minimum age of 6 months at first dose and a minimum of 11 weeks between doses 1 and 3.

Methods

Data Source

The Virtual SARS-CoV-2, Influenza, and Other respiratory viruses Network (VISION) is a multisite electronic health record (EHR)–based network including ED/UCs and hospitals in nine states used to estimate VE. Methods for VE analyses in both adult and pediatric populations within VISION have been described (*3*–*6*). In VISION VE analyses, eligible encounters at participating health care systems are those among patients who have received molecular testing (e.g., real-time reverse transcription–polymerase chain reaction) or antigen testing for SARS-CoV-2 during the 10 days before or ≤72 hours after an eligible ED/UC encounter or hospital admission for COVID-19–like illness.[§§] This analysis included encounters among eligible immunocompetent children and adolescents aged 9 months–17 years who visited a participating ED/UC during August 29, 2024–September 2, 2025. COVID-19 vaccination history is ascertained from state or jurisdictional registries, EHRs, and, in a subset of sites, medical claims data.[¶¶]

Data Analysis

Eligible encounters from seven participating health care systems, including 256 ED/UCs, during August 29, 2024–September 2, 2025, were included. Case-patients were those with an ED/UC encounter for COVID-19–like illness and receipt of a positive SARS-CoV-2 molecular or antigen test result; control patients were those with an ED/UC

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encounter for COVID-19–like illness and receipt of a negative SARS-CoV-2 molecular test result.***

Children were excluded from analyses if they received a 2024–2025 COVID-19 vaccine dose <7 days before their index date††† or received a 2024–2025 COVID-19 vaccine dose <2 months after receiving any previous COVID-19 vaccine dose, unless part of an initial series. COVID-19 case-patients were also excluded if they received a positive test result for influenza virus or respiratory syncytial virus at the time of their SARS-CoV-2 ED/UC encounter. To reduce bias from overlapping vaccination patterns, control patients who received a positive or indeterminant influenza test result were excluded from the primary analysis (*7*). Previous SARS-CoV-2 infections are incompletely documented in medical records; therefore, children were included regardless of previous SARS-CoV-2 infections.

Primary VE analyses were conducted by age groups 9 months–4 years and 5–17 years due to differences in the recommended COVID-19 vaccination schedule. In primary VE analyses, children aged 9 months–4 years were considered vaccinated if they completed an initial series with at least 1 2024–2025 dose as part of that series or completed an initial series and then received a 2024–2025 dose as an additional vaccine. The 9 months–4 years comparator group comprised children who had completed the initial COVID-19 vaccine series but had not received a 2024–2025 dose or had no recorded COVID-19 vaccination. Children aged 9 months–4 years with an incomplete initial series were excluded from the primary analysis to assess the ACIP-recommended schedule for this age group. A sensitivity analysis among children aged 9 months–4 years compared children who received at least 1 2024–2025 COVID-19 vaccine dose with children who did not, regardless of COVID-19 vaccination history. Among children and adolescents aged 5–17 years, primary VE analyses compared those who received a 2024–2025 COVID-19 vaccine dose with those who did not, regardless of COVID-19 vaccination history. Results were also stratified by age groups of 5–11 years and 12–17 years.

Odds ratios (ORs) and 95% CIs were estimated using multivariable logistic regression, comparing persons who received a 2024–2025 COVID-19 vaccine dose with those who did not among case-patients and control patients, as described in this report. Models were adjusted a priori for age in years, race and ethnicity, sex, calendar day (days since August 29, 2024, to account for variability in COVID-19 circulation), and geographic region with age and calendar day included as natural splines.§§§ VE was calculated as (1 – adjusted OR) x 100% during the first 7–179 days since receipt of the most recent 2024–2025 COVID-19 vaccine dose. Sensitivity analyses in both the 9 months–4 years and 5–17 years age groups examined VE during the 7–299 days since receipt of a 2024–2025 COVID-19 vaccine dose.

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.¶¶¶

Results

2024–2025 COVID-19 VE Against COVID-19–Associated ED/UC Visits in Children Aged 9 Months–4 Years

Among children aged 9 months–4 years, 44,541 ED/UC encounters met criteria for inclusion in the analyses, including 1,292 (3%) case-patients and 43,249 (97%) control patients (Table 1). Twelve (<1%) case-patients and 1,847 (4%) control patients had received a 2024–2025 COVID-19 vaccine dose. Effectiveness of a 2024–2025 COVID-19 vaccination against a COVID-19–associated ED/UC visit was 76% (95% CI = 58%–87%) during the first 7–179 days after vaccination and 77% (95% CI = 62%–86%) during the first 7–299 days after vaccination (Table 2). VE point estimates were lower

§§ Eligible ED/UC encounters or hospital admissions were those for COVID-19–like illness, obtained using *International Classification of Diseases, Tenth Revision* (ICD-10) discharge codes. The specific codes used were COVID-19 pneumonia: J12.81 and J12.82; influenza pneumonia: J09.X1, J10.0*, J11.0*, and 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; acute asthma 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*, R09.2, and J96.9*; other acute lower respiratory tract infections: B97.4, J20*, J21*, J22, J40, J44.0, J41*, J42, J43*, J47*, J85*, 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, R50.9, and R68.83; acute nonrespiratory illness signs and symptoms: M79.10, M79.18, R10.0, R10.1*, R10.2, R10.3*, R10.81*, R10.84, R10.9, R11.0, R11.10, R11.11, R11.15, R11.2, R19.7, R21*, R40.0, R40.1, R41.82, R43*, R51.9, R53.1, R53.81, R53.83, R57.9, and R65*; 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.

¶¶ National pharmacy chains were required to establish bidirectional linkage with jurisdictional immunization information systems (IISs) to support vaccine distribution early in the COVID-19 pandemic; thus, doses administered at pharmacies should be reported to IISs.

*** Antigen tests generally have lower sensitivity and specificity than molecular tests. In the test-negative design, small reductions in test specificity can cause greater bias in VE estimates than more substantial reductions in test sensitivity.

††† Earlier of ED/UC encounter or respective SARS-CoV-2 testing date.

§§§ Geographic region was included in the model based on site of the final discharge facility of the encounter.

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

TABLE 1. Patient characteristics of children and adolescents aged 9 months–17 years with COVID-19–associated emergency department or urgent care encounters, by age group — VISION, August 29, 2024–September 2, 2025

Characteristic	No. (column %)		
	Total encounters	COVID-19 case-patients	COVID-19 control patients
Aged 9 mos–4 yrs	**44,541 (100)**	1,292 (100)	43,249 (100)
HHS region*			
2	**5,208 (12)**	113 (9)	5,095 (12)
5	**15,589 (35)**	469 (36)	15,120 (35)
8	**6,613 (15)**	194 (15)	6,419 (15)
9	**15,575 (35)**	461 (36)	15,114 (35)
10	**1,556 (3)**	55 (4)	1,501 (3)
Female sex	**19,648 (44)**	564 (44)	19,084 (44)
Race and ethnicity			
Black or African American, non-Hispanic	**6,008 (13)**	139 (11)	5,869 (14)
White, non-Hispanic	**15,855 (36)**	476 (37)	15,379 (36)
Hispanic or Latino, any race	**14,199 (32)**	391 (30)	13,808 (32)
Other, non-Hispanic†	**7,390 (17)**	247 (19)	7,143 (17)
Unknown§	**1,089 (2)**	39 (3)	1,050 (2)
2024–2025 COVID-19 vaccine receipt¶	**1,859 (4)**	12 (1)	1,847 (4)
Moderna	**396 (21)**	2 (17)	394 (21)
Pfizer-BioNTech	**1,463 (79)**	10 (83)	1,453 (79)
Aged 5–17 yrs	**53,467 (100)**	**1,325 (100)**	**52,142 (100)**
HHS region*			
2	**4,857 (9)**	77 (6)	4,780 (9)
5	**18,833 (35)**	484 (37)	18,349 (35)
8	**12,994 (24)**	424 (32)	12,570 (24)
9	**14,609 (27)**	291 (22)	14,318 (27)
10	**2,174 (4)**	49 (4)	2,125 (4)
Female sex	**26,561 (50)**	687 (52)	25,874 (50)
Race and ethnicity			
Black or African American, non-Hispanic	**7,290 (14)**	166 (13)	7,124 (14)
White, non-Hispanic	**22,896 (43)**	603 (46)	22,293 (43)
Hispanic or Latino, any race	**14,961 (28)**	346 (26)	14,615 (28)
Other, non-Hispanic†	**7,585 (14)**	193 (15)	7,392 (14)
Unknown§	**735 (1)**	17 (1)	718 (1)
2024–2025 COVID-19 vaccine receipt¶	**2,488 (5)**	26 (2)	2,462 (5)
Moderna	**434 (17)**	5 (19)	429 (17)
Novavax	**5 (0)**	0 (—)	5 (0)
Pfizer-BioNTech	**2,049 (82)**	21 (81)	2,028 (82)

Abbreviations: HHS = U.S. Department of Health and Human Services; VISION = Virtual SARS-CoV-2, Influenza, and Other respiratory viruses Network.

* In VISION, geographic region was included in the model based on site of the final discharge facility of the encounter. HHS regions are included to illustrate geographic spread across VISION; regions are defined by HHS. States included in each region are available at HHS Regional Offices | HHS.gov. Included VISION sites were: *Region 2:* Columbia University (New York); *Region 5:* HealthPartners (Minnesota and Wisconsin) and Regenstrief Institute (Indiana); *Region 8*: Intermountain Healthcare (Utah) and University of Colorado (Colorado); *Region 9*: Kaiser Permanente Northern California (California); and *Region 10*: Kaiser Permanente Northwest (Oregon and Washington).

† "Other, non-Hispanic" race includes persons reporting non-Hispanic ethnicity and any of the following for race: American Indian or Alaska Native, Asian, Middle Eastern or North African, Native Hawaiian or 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 record.

¶ Receipt of a 2024–2025 COVID-19 vaccine dose during the 7–179 days before the index date (defined as the emergency department or urgent care encounter or respective SARS-CoV-2 testing date, whichever came first).

at 66% when the comparator group was expanded to include children with an incomplete initial COVID-19 vaccination series, but CIs overlapped with those in the primary analysis (95% CI = 51%–76%).

2024–2025 COVID-19 VE Against COVID-19–Associated ED/UC Visits in Children and Adolescents Aged 5–17 Years

Among children and adolescents aged 5–17 years, 53,467 ED/UC encounters met criteria for inclusion in the analyses, including 1,325 (2%) case-patients and 52,142 (98%) control patients (Table 1). Twenty-six (2%) case-patients and 2,462 (5%) control patients had received a 2024–2025 COVID-19 vaccine dose. Effectiveness of a 2024–2025 COVID-19 vaccination against a COVID-19–associated ED/UC visit was 56% (95% CI = 35%–70%) during the first 7–179 days after vaccination, and 45% (95% CI = 25%–59%) during the first 7–299 days after vaccination (Table 3). Results were similar when stratified by age (51% among children aged 5–11 years and 61% among children and adolescents aged 12–17 years, with overlapping CIs).

TABLE 2. Vaccine effectiveness* against laboratory-confirmed COVID-19–associated emergency department or urgent care encounters among children aged 9 months–4 years — VISION, August 29, 2024–September 2, 2025

COVID-19 vaccination pattern	Total encounters, no.	Days since last dose among vaccinated persons, no.		Positive SARS-CoV-2 test results, no. (column %)	VE, % (95% CI)	
		Median (IQR)	Maximum		Unadjusted	Adjusted*
Primary VE estimates†						
No 2024–2025 COVID-19 dose (Ref)	**42,682**	407 (290–675)	1,474	1,280 (99)	Ref	Ref
≥ 1 2024–2025 COVID-19 dose, 7–179 days earlier	**1,859**	78 (42–118)	179	12 (1)	79 (63–88)	76 (58–87)
Sensitivity VE estimates						
Extended VE interval†,§						
No 2024–2025 COVID-19 dose (Ref)	**42,682**	407 (290–675)	1,474	1,280 (99)	Ref	Ref
≥ 1 2024–2025 COVID-19 dose, 7–299 days earlier	**2,207**	91 (49–147)	296	15 (1)	78 (63–87)	77 (62–86)
Relaxed vaccination history requirement¶						
No 2024–2025 COVID-19 dose (Ref)	**44,314**	422 (289–695)	1,575	1,312 (98)	Ref	Ref
≥ 1 2024–2025 COVID-19 dose, 7–179 days earlier	**3,029**	73 (38–112)	179	32 (2)	65 (50–75)	66 (51–76)

Abbreviations: Ref = referent group; VE = vaccine effectiveness.

* VE was calculated as (1 − adjusted odds ratio) × 100%, estimated using a test-negative case-control design, and adjusted for age in years, race and ethnicity, sex, calendar day (days since August 29, 2024), and geographic region with age and calendar day included as natural splines.

† In the primary VE and extended VE analyses, the vaccinated group was children who completed an initial series with ≥1 2024–2025 dose as part of the series or who completed an initial series and then received a 2024–2025 dose as an additional vaccine. The comparator group was children who completed an initial COVID-19 vaccine series with no receipt of a 2024–2025 dose or with no recorded COVID-19 vaccinations. Children aged 9 months–4 years with an incomplete initial series were excluded from the primary analysis. Among vaccinated children aged 9 months–4 years, the initial series and 2024–2025 dose were not required to be from the same manufacturer.

§ The extended VE analysis included 44,889 total encounters, of which 1,295 (3%) involved case-patients.

¶ In this sensitivity VE analysis, the vaccinated group was children who received at least 1 2024–2025 dose, regardless of COVID-19 vaccination history; the comparator group was children with no receipt of a 2024–2025 dose, regardless of COVID-19 vaccination history. This analysis included 47,343 total encounters, of which 1,344 (3%) involved case-patients.

Discussion

The 2024–2025 COVID-19 vaccines provided protection against COVID-19–associated ED/UC encounters among children and adolescents aged 9 months–17 years. This evaluation included children and adolescents with varied COVID-19 vaccination and SARS-CoV-2 infection histories, and therefore, results should be interpreted as estimates of the additional protection provided by a 2024–2025 COVID-19 vaccine in a population with mixed preexisting immunity.

Infants aged 6–11 months have the highest rates of COVID-19–associated hospitalization of any COVID-19 vaccine–eligible pediatric age group, and COVID-19–associated hospitalization rates in the United States during the 2024–25 respiratory virus season were higher in this group than all adult age groups other than those aged ≥65 years (*8*), underscoring potential benefits of COVID-19 vaccination in eligible infants. In this analysis, VE was highest in children aged 9 months–4 years, although CIs overlapped with older age groups. The apparent higher VE in younger children might be due to lower rates of previous SARS-CoV-2 infection.**** The primary estimates for VE in this analysis were similar to or higher than 2024–2025 VE estimates for adults in the United States (*9*); estimates were also similar to or higher than those for 2023–2024 in children (35% [95% CI = 16%–49%] for children aged 9 months–4 years and 44% [95% CI = 29%–55%] for children and adolescents aged 5–17 years) (*6*). Higher estimates for the 2024–25 season might be due to different patterns of recent previous SARS-CoV-2 infection compared with the 2023–24 season or might be due to fewer changes in circulating SARS-CoV-2 variants during the 2024–25 season.

Vaccination based on shared clinical decision-making is individually based and guided by a decision process between the health care provider and the patient or parent/guardian; generally, ACIP recommendations adopted by CDC and listed on CDC immunization schedules, including those based on shared clinical decision-making, are covered by health insurance plans. The impact that shifting from universal to shared

**** COVID-19 Vaccine Effectiveness Update | CDC

TABLE 3. Vaccine effectiveness* against laboratory-confirmed COVID-19–associated emergency department or urgent care encounters among children and adolescents aged 5–17 years — VISION, August 29, 2024–September 2, 2025

COVID-19 vaccination pattern	Total encounters, no.	Days since last dose among vaccinated persons, no.		Positive SARS-CoV-2 results, no. (column %)	VE, % (95% CI)	
		Median (IQR)	Maximum		Unadjusted	Adjusted*
Primary VE estimates						
No 2024–2025 COVID-19 dose (Ref)	**50,979**	986 (722–1,135)	1,633	1,299 (98)	Ref	Ref
At least 1 2024–2025 COVID-19 dose, 7–179 days earlier	**2,488**	84 (44–124)	179	26 (2)	60 (40–73)	56 (35–70)
Sensitivity VE estimates†						
Extended VE interval						
No 2024–2025 COVID-19 dose (Ref)	**50,979**	986 (722–1,135)	1,633	1,299 (97)	Ref	Ref
At least 1 2024–2025 COVID-19 dose, 7–299 days earlier	**3,152**	105 (55–167)	299	44 (3)	46 (27–60)	45 (25–59)
Estimates by age group, yrs						
5–11						
No 2024–2025 COVID-19 dose (Ref)	**31,508**	883 (595–1,050)	1,633	645 (98)	Ref	Ref
At least 1 2024–2025 COVID-19 dose, 7–179 days earlier	**1,443**	85 (44–126)	179	13 (2)	57 (24–75)	51 (14–72)
12–17						
No 2024–2025 COVID-19 dose (Ref)	**19,471**	1,056 (835–1,191)	1,552	654 (98)	Ref	Ref
At least 1 2024–2025 COVID-19 dose, 7–179 days earlier	**1,045**	82 (44–122)	179	13 (2)	64 (37–79)	61 (31–78)

Abbreviations: Ref = referent group; VE = vaccine effectiveness.

* VE was calculated as (1 – adjusted odds ratio) × 100%, estimated using a test-negative case-control design, and age in years, race and ethnicity, sex, calendar day (days since August 29, 2024), and geographic region with age and calendar day included as natural splines. In each analysis, the vaccinated group was children who received at least 1 2024–2025 COVID-19 vaccine dose, regardless of previous COVID-19 vaccination history; the comparator group was children with no receipt of a 2024–2025 COVID-19 vaccine dose, regardless of previous COVID-19 vaccination history.

† The extended VE analysis included 54,131 total encounters, of which 1,343 (2%) involved case-patients.

clinical decision-making (otherwise known as individual-based decision-making) will have on COVID-19 vaccination coverage or effectiveness in children is unclear, underscoring the importance of continued monitoring of COVID-19 VE.

Limitations

The findings in this report are subject to at least five limitations. First, although case-patients met a COVID-19–like illness definition and received a positive SARS-CoV-2 test result, they might have visited ED/UCs for reasons other than COVID-19, potentially lowering VE estimates. Second, misclassification of vaccination status was possible, which would likely result in underestimation of VE if the misclassification was nondifferential. Previous estimates across networks including various COVID-19 vaccine history ascertainment methods (i.e., EHR, immunization information systems, self-report, and claims data) have yielded similar VE estimates (*9*). Third, children aged 9 months–4 years and children and adolescents aged 5–17 years account for a smaller fraction of the general population than adults in age groups frequently examined in VE analyses (i.e., 18–64 years and ≥65 years), decreasing the sample size available for estimating VE in children and adolescents compared with adults. In addition, because of relatively low COVID-19 vaccination coverage in children compared with adults and overall lower rates of medically attended COVID-19 during 2024–2025 compared with 2023–2024, this study did not have sufficient statistical power to measure VE by finer intervals of time since dose and for hospitalization. Fourth, although analyses were adjusted for some relevant confounders, residual confounding from other factors, such as behavioral modifications to prevent SARS-CoV-2 exposure and outpatient antiviral treatment for COVID-19, might remain. Finally, low COVID-19 vaccination coverage among children and adolescents might reduce the generalizability of results.

Implications for Public Health Practice

In this analysis, receipt of a 2024–2025 COVID-19 vaccine dose provided additional protection against COVID-19–associated ED/UC visits among children and adolescents aged 9 months–17 years in a population with preexisting levels of

Summary

What is already known about this topic?

In June 2024, CDC's Advisory Committee on Immunization Practices recommended 2024–2025 COVID-19 vaccination for all persons aged ≥6 months to provide additional protection against severe COVID-19.

What is added by this report?

During August 29, 2024–September 2, 2025, within a multisite network including nine states, vaccine effectiveness of 2024–2025 COVID-19 vaccination was an estimated 76% against COVID-19–associated emergency department or urgent care (ED/UC) visits among immunocompetent children aged 9 months–4 years and an estimated 56% among children and adolescents aged 5–17 years, compared with those who did not receive a 2024–2025 vaccine.

What are the implications for public health practice?

In a population with some persons having preexisting levels of protection from previous vaccination, previous infection, or both, 2024–2025 COVID-19 vaccination provided children with additional protection against COVID-19–associated ED/UC encounters compared with no 2024–2025 vaccination.

protection from previous vaccination, previous infection, or both. CDC continues to monitor VE of COVID-19 vaccines.

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Detection of *Paraburkholderia* in Clinical Specimens Associated with Use of Nonsterile Ultrasound Gel for Percutaneous Procedures — United States, Canada, and Israel, May 2023–April 2025

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Abstract

Contaminated nonsterile ultrasound gels have been implicated in outbreaks of *Burkholderia* infections associated with improper infection control practices before or during percutaneous procedures. In August 2024, the Minnesota Department of Health Public Health Laboratory noticed an increase in *Paraburkholderia fungorum* or *Paraburkholderia* species identified from referred clinical isolates. All isolates were recovered from blood cultures, and whole genome sequencing (WGS) confirmed that the isolates were genetically related. Because *P. fungorum* is not an established human pathogen and has rarely been reported in clinical specimens, an investigation was initiated, which was later joined by collaborators in Canada and Israel after similar observations in those countries. Forty-two patients from the United States, Canada, and Israel with genetically linked *P. fungorum* isolated from clinical specimens collected during May 2023–April 2025 were identified. Positive cultures were associated with the use of nonsterile ultrasound gel. Based on medical record review, treating clinicians deemed the isolate a culture contaminant in most cases; one patient had a confirmed invasive *P. fungorum* infection. WGS confirmed the relatedness of isolates from all three countries, including isolates cultured from clinical specimens as well as from nonsterile ultrasound gel products. Review of local practices revealed use of nonsterile ultrasound gel during point-of-care percutaneous procedures, including drawing blood, placing intravenous catheters, and paracentesis. This investigation underscores the continued importance of sterile gel use during percutaneous procedures and highlights the value of collaboration and shared WGS data for the investigation of international outbreaks.

Investigation and Results

Identification of *Paraburkholderia* spp. in Blood Cultures

In August 2024, the Minnesota Department of Health Public Health Laboratory (MDH-PHL) noted an increase in blood culture isolates referred from clinical laboratories in Minnesota that were identified as *Paraburkholderia fungorum* or *Paraburkholderia* spp. by 16S rRNA sequencing.[†] Seven isolates from patients hospitalized from January to August were submitted to MDH-PHL from three laboratories to rule out *Burkholderia mallei* and *Burkholderia pseudomallei*, Tier 1 select agents with bioterrorism potential.[§] *P. fungorum* is not an established human pathogen and has rarely been reported in clinical specimens (*1*–*3*), and MDH-PHL had not identified *P. fungorum* in any clinical specimens during the preceding decade. Whole genome sequencing (WGS) of the initial seven isolates found that they were closely genetically related. One laboratory reviewed previous test results, and *P. fungorum* was isolated from the blood cultures of eight additional patients who were identified dating back to September 2023. Because of the retrospective nature of the review and the length of time that had passed, isolates from these patients were not available for WGS. Medical record reviews of all 15 patients revealed that in several cases, the treating providers felt the likelihood of clinical infection was low and the positive blood culture represented a culture contaminant. In addition, for each patient, only a single culture bottle tested positive out of one or multiple sets of blood cultures, suggesting possible culture contamination rather than a true infection. This project was reviewed by the Minnesota Department of Health, classified as nonresearch public health surveillance, and was conducted consistent with applicable federal laws.

Identification of Additional Positive Cultures Through Statewide Review of Laboratory Records

On October 1, 2024, MDH-PHL notified clinical laboratories statewide, calling for a review of laboratory records of any clinical specimens collected after September 2023 with a positive *Paraburkholderia* spp. culture result. An additional 30 positive blood culture results were identified from 30 patients (one

[*] These authors contributed equally to this report.

[†] 16S rRNA sequencing is a method used to taxonomically classify cultured bacteria by analyzing sequence information from variable regions in the 16S rRNA gene that is present in all prokaryotes.

[§] MDH-PHL is a Laboratory Response Network Reference Laboratory and provides confirmatory testing for Tier 1 agents of potential bioterrorism, including *B. mallei* and *B. pseudomallei*.

isolate per patient), including four from Minnesota, one from North Dakota, and 25 sent to a national clinical reference laboratory for further identification from clinical laboratories in 11 other states. Only the isolate from North Dakota was available for analysis.

Initially, intrinsic contamination of blood culture bottles during manufacture was suspected, because all positive cultures identified until that time involved the same blood culture system manufacturer. Among the 30 positive cultures identified during the statewide review, MDH-PHL was initially able to obtain the isolate from North Dakota for WGS. As the investigation continued into December 2024, MDH-PHL obtained five additional isolates from Minnesota laboratories from patients hospitalized from August to December 2024 that were added to the WGS analysis, for a total of 12 isolates from Minnesota (including the original seven). The additional five isolates exhibited the same genetic relatedness to one another and to the seven original isolates. MDH notified CDC, the Food and Drug Administration (FDA), and the blood culture system manufacturer of these findings.

Identification of Positive Cultures from North Carolina, Canada, and Israel

Concurrent with this investigation, *Paraburkholderia* spp. were identified in clinical cultures processed by laboratories in North Carolina (21 cultures), Canada (four), and Israel (10); these three jurisdictions joined the investigation in late 2024 and early 2025. Microbiologists in Canada and Israel reached out to MDH-PHL after noticing the October 1 publicly posted online laboratory alert when searching for information on *P. fungorum*. North Carolina joined the investigation following personal communication between MDH-PHL and laboratory staff members from two clinical laboratories in North Carolina. North Carolina joined the investigation following personal communication between MDH-PHL and laboratory staff members from two clinical laboratories in North Carolina. Among the 21 positive cultures identified in North Carolina, 19 isolates were sent to MDH-PHL (Supplementary Table). These included nine that were identified on the initial list of 25 positive cultures from 11 other states (whose original isolates remained available from the originating laboratory) and sent to the reference laboratory in Minnesota. Among the 19 isolates, 16 were successfully sequenced and added to the WGS analysis, including two isolates from cultures obtained on two different dates from the same patient. Israel and Canada performed WGS on isolates from their jurisdictions and shared results with MDH-PHL. Thus, a total of 43 isolates from 42 patients were included in the WGS analysis (12 from Minnesota, 15 from North Carolina [including one patient with two isolates], one from North Dakota, four from Canada, and 10 from Israel) (Figure 1). All isolates were recovered from blood with the exception of three from Israel, which were recovered from ascitic fluid cultured in blood culture bottles.¶

Identification of Nonsterile Ultrasound Gel as a Potential Contamination Source

Whereas all positive cultures identified by MDH-PHL in the United States until October 1, 2024, involved the same blood culture system manufacturer, isolates from Israel involved a different blood culture system manufacturer, significantly decreasing the likelihood that intrinsic contamination of blood culture bottles with *P. fungorum* was the outbreak source. Investigation of cases in Israel with positive cultures from ascitic fluid obtained via paracentesis identified the use of nonsterile ultrasound gel (ClearImage brand) for point-of-care ultrasound (POCUS) for percutaneous procedures as a potential source of contamination. *P. fungorum* was subsequently cultured in Israel from six containers of the same ultrasound gel product, and WGS of these six isolates demonstrated genetic relatedness to clinical isolates from the United States, Canada, and Israel. Additional cultures from two different brands of nonsterile ultrasound gels in the United States (ClearImage and MediChoice) and Canada (ClearImage) both yielded genetically similar *P. fungorum*, including the same product that grew *P. fungorum* in Israel (ClearImage). In total, *P. fungorum* was isolated from six lots of nonsterile ultrasound gel from two different commercial brands (MediChoice and ClearImage) manufactured by a single company (NEXT Medical Products Company).

Whole Genome Sequencing

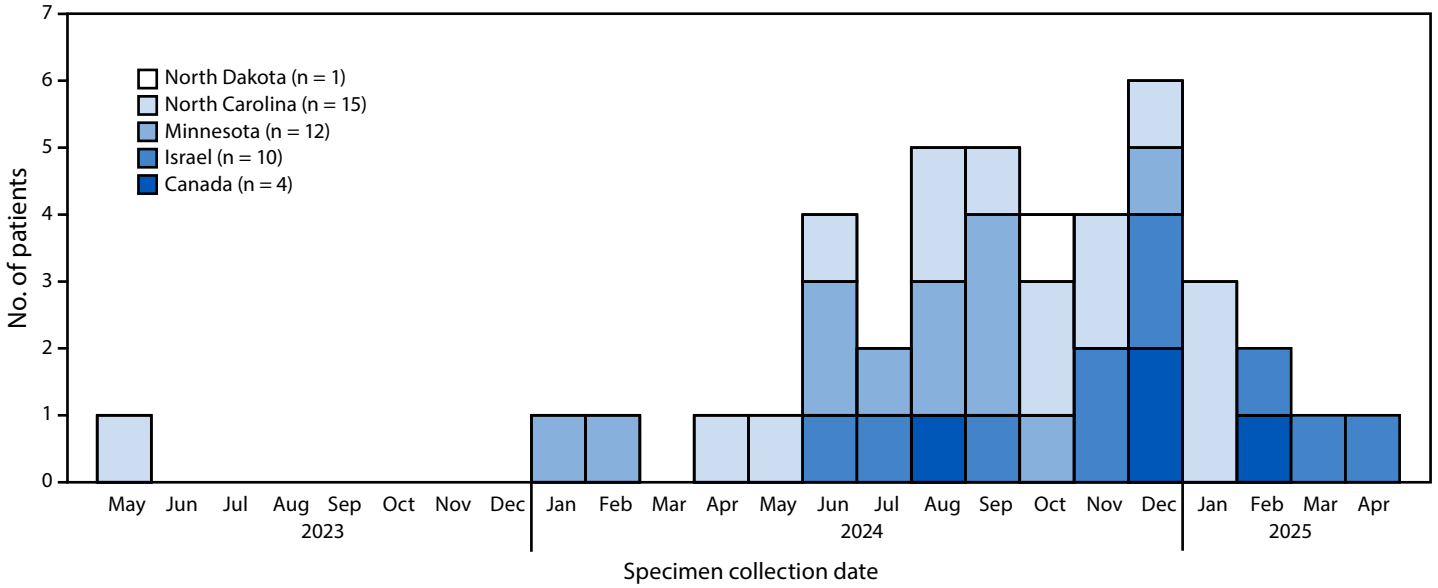
In total, WGS was performed on 43 clinical isolates from 42 patients,** nine ultrasound gel isolates (six from Israel, and one each from Canada, Minnesota, and North Carolina), and one historical clinical isolate from 2011.†† Sequence data were shared between Canada, Israel, and Minnesota, creating a joint genomic repository for real-time data analysis and cross-validation of results. WGS demonstrated that all clinical and gel isolates were closely related, exhibiting 0–10 single nucleotide polymorphism differences (Figure 2), confirming that all clinical and gel isolates belonged to a single clone of

¶ Time to culture positivity = 3–5 days.

** One patient in North Carolina had two isolates included in WGS. This patient had a central venous catheter and had three consecutive positive blood cultures for *P. fungorum* over 7 days, followed by a diagnosis of a central line–associated bloodstream infection (CLABSI).

†† WGS data were deposited under the BioProject ID: PRJNA1260949. A summary of short-read raw sequence and assembly data from isolates included in this analysis (including 52 isolates from this investigation, a historical clinical isolate from 2011, and 24 publicly available genome sequences), long-read sequence data (including three isolates), core genome multilocus sequence typing of *P. fungorum* cluster isolates compared with publicly available genomes, and detailed sequencing and bioinformatics methods are available at https://health.state.mn.us/diseases/idlab/mmwr.html.

FIGURE 1. Patients (N = 42) with genetically linked* *Paraburkholderia* spp. isolated from clinical cultures,† by date of initial specimen collection — Minnesota, North Carolina, North Dakota, Canada, and Israel, May 2023–April 2025



* All isolates underwent whole genome sequencing and were found to be genetically related.
† All isolates were recovered from blood cultures, except three isolates from Israel that were recovered from blood culture bottles inoculated with ascitic fluid.

P. fungorum. This clone appeared to be very distant from the 2011 historical isolate, implicating contaminated nonsterile ultrasound gel as the source of *P. fungorum*. Further genome analysis demonstrated that the cluster was unrelated to publicly available genomes.

Characteristics of Patients with Isolates Linked by WGS

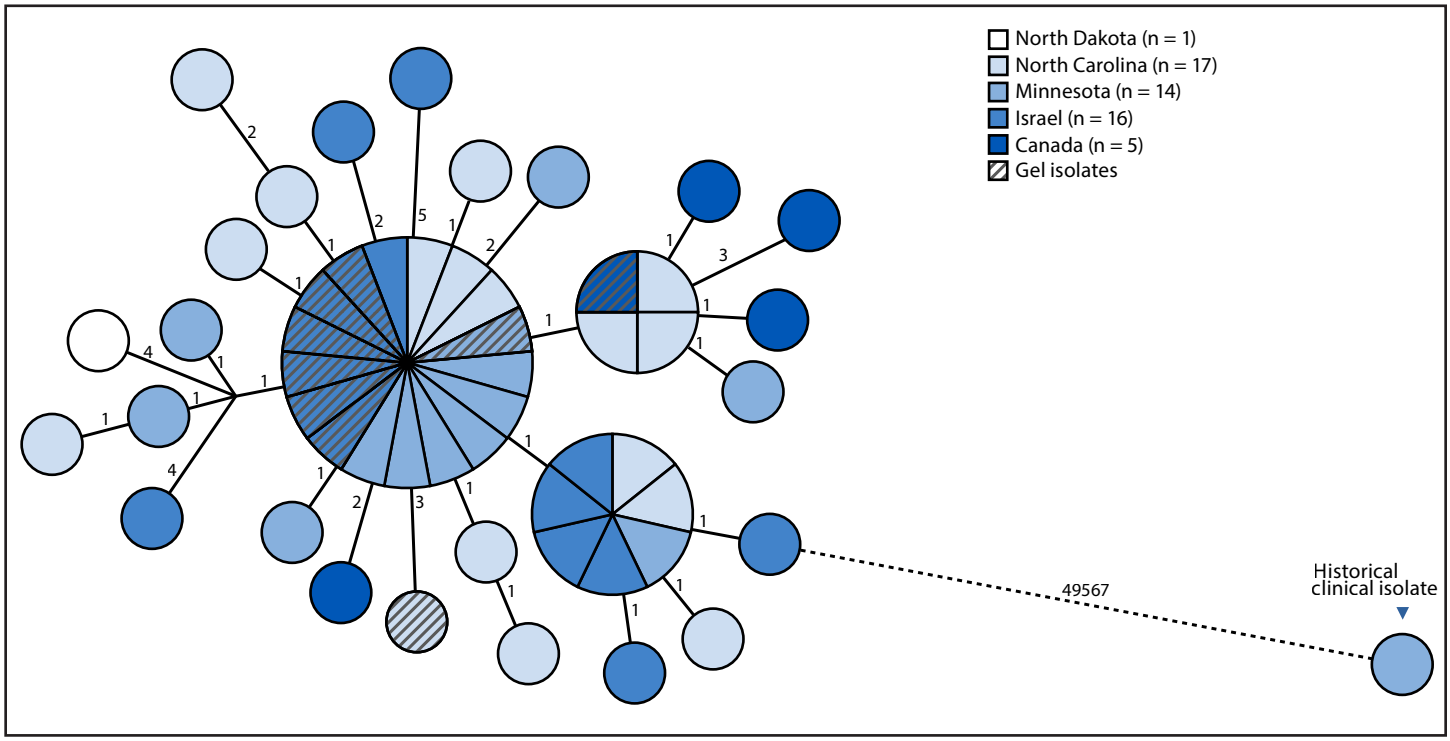
Medical records of patients in each jurisdiction were reviewed by members of the investigation team with clinical infectious disease expertise to obtain demographic and clinical characteristics. Where possible, health care providers who had performed an ultrasound-guided percutaneous procedure on the patient were interviewed on their use of ultrasound gel. Among 42 patients with positive cultures for *P. fungorum* genetically related by WGS in the United States, Canada, and Israel during May 2023–April 2025, 39 (93%) had positive blood culture results, the remaining three had positive cultures of ascitic fluid (Table). For one patient, three consecutive blood culture results were positive for *P. fungorum* over several days, and the patient received a diagnosis of a central-line–associated bloodstream infection (CLABSI)[§§]; no other patient had confirmed invasive *P. fungorum* infection based on the medical record review.[¶¶] Among 37 patients with available clinical information, antibiotic therapy was initiated, modified, or extended for 28 (76%) in response to the positive culture result (e.g., to provide empiric coverage for gram-negative bacteremia or to provide specific coverage for *Paraburkholderia* bacteremia). According to medical record review, providers ultimately deemed *Paraburkholderia* to be a culture contaminant in 25 (68%) cases. In three patients with *P. fungorum*–positive ascitic fluid cultures, peritonitis was ruled out through clinical and laboratory findings. Sixteen (38%) of the 42 patients had a documented ultrasound-guided percutaneous procedure before or during specimen collection, most commonly peripheral intravenous catheter placement and blood collection in an emergency department.[***] MediChoice or ClearImage nonsterile ultrasound gel use was confirmed in all facilities except one facility without information, with gel use confirmed for 15 (37%) patients, either through medical record documentation or health care provider interview.

[§§] Same North Carolina patient with CLABSI and two isolates were included in WGS. Cultures were cleared after removal of the catheter.

[¶¶] Examples of factors suggestive of contamination in these cases included 1) single positive culture only; 2) no signs or symptoms of infection at time of blood culture draw; 3) clear alternative infectious diagnosis; 4) alternative typical pathogen identified in culture; 5) longer time to culture positivity than that typically observed for an infectious pathogen (≥3 days); and 6) a treating clinician's determination of blood culture contamination. In many cases, it was not possible to determine with certainty on retrospective chart review whether the positive culture represented true infection.

[***] Although POCUS was not documented in the majority of patients' medical charts, all facilities reported that ultrasound guidance was common practice for many bedside procedures, including peripheral intravenous catheter placement and venipuncture.

FIGURE 2. Genetic relatedness of *Paraburkholderia fungorum* isolates using core-genome single nucleotide polymorphism analysis*,† — Minnesota, North Carolina, North Dakota, Canada, and Israel, May 2023–April 2025



Abbreviation: cgSNP = core-genome single nucleotide polymorphism.

* All 52 *P. fungorum* isolates from this cluster (43 clinical isolates [including two isolates from one patient] and nine isolates from ultrasound gel) were analyzed using cgSNP mapping alongside one historical clinical isolate from 2011, generating a 49,606 base cgSNP alignment displayed in a minimum-spanning phylogenetic tree. Labeled distances across connecting lines between nodes indicate the number of cgSNP differences. Nodes are illustrated with sizes proportional to the number of identical genomes. The three larger nodes represent clusters of isolates having zero cgSNP differences.

† Detailed sequencing and bioinformatics methods are available at https://www.health.state.mn.us/diseases/idlab/mmwr.html.

Public Health Response

Investigation findings were shared with infection prevention professionals at facilities reporting cases, and local practices for the use of ultrasound gel during percutaneous procedures were reviewed. State and local guidance was issued for infection prevention during POCUS procedures and implicated products were removed from those facilities. Information was reported to CDC, FDA, respective health authorities in Canada and Israel, and the gel manufacturer. On May 13, 2025, CDC posted an alert for clinicians describing preliminary findings from this investigation and reinforced its previous recommendation to always use sterile ultrasound gel for percutaneous procedures.

Discussion

Paraburkholderia fungorum (previously *Burkholderia fungorum*)††† is a gram-negative environmental bacterium commonly used as a beneficial microorganism in agriculture to improve crop yields (*4*). This bacterium has rarely been reported in human clinical specimens, and its significance as a pathogen is unclear (*1–3*). *P. fungorum* had not previously been reported in association with outbreaks or medical product contamination.

Burkholderia species contamination of ultrasound gel and resulting human infection has been previously reported (*5–7*). In this cluster, *P. fungorum* was likely introduced into culture specimens or blood during specimen collection, after the application and incomplete removal of contaminated gel from the skin. Culture collection through a peripheral intravenous catheter is also associated with a higher risk for contamination (*8*), although it was not clear for all cases in this investigation whether positive blood cultures represented contamination of specimens at the time of the procedure or true bacteremia resulting from inoculation of the organism into the patient's bloodstream. Examples of factors suggestive of culture contamination included instances in which patients had no signs or symptoms of infection at the time of the blood culture draw or had a clear alternative diagnosis or pathogen

††† The *Paraburkholderia* genus was proposed in 2015 as a distinct genus from *Burkholderia* to separate pathogenic species (such as *B. cepacia* complex) from other environmental species not commonly associated with disease.

TABLE. Characteristics and exposures of patients with genetically linked* *Paraburkholderia* spp. isolated from cultures of clinical specimens† (N = 42) — Minnesota, North Carolina, North Dakota, Canada, and Israel, May 2023–April 2025

Characteristic (no. of patients with available information)	No. (%)
Age group, yrs (42)	
<18	10 (23.8)
18–64	18 (42.9)
≥65	14 (33.3)
Median (range)	54 (2 mos–92 yrs)
Sex (42)	
Female	27 (64.3)
Male	15 (35.7)
Jurisdiction (42)	
Minnesota	12 (28.6)
North Dakota	1 (2.4)
North Carolina	15 (35.7)
Israel	10 (23.8)
Canada	4 (9.5)
Specimen source (42)	
Blood	39 (92.9)
Ascitic fluid	3 (7.1)
Specimen collection location (42)	
Emergency department	27 (64.3)
Intensive care unit	7 (16.7)
Hospital inpatient	6 (14.3)
Clinic	2 (4.8)
Number of positive culture bottles (42)	
Single bottle only	38 (90.5)
Both bottles in single set	3 (7.1)
One or more bottle in multiple sets	1 (2.4)
Received antibiotics for positive culture result§ (37)	
Yes	28 (75.7)
No	9 (24.3)
Positive culture ultimately deemed to be contaminant by treating provider¶ (37)	
Yes	25 (67.6)
No	6 (16.2)
Unknown	6 (16.2)
Ultrasound-guided percutaneous procedure performed before or during culture collection (42)**	
Peripheral intravenous catheter placement	8 (19.1)
Paracentesis	3 (7.1)
Venipuncture	4 (9.5)
Other††	1 (2.4)
Unknown	26 (61.9)
Exposure to MediChoice or ClearImage ultrasound gel (41)	
Patient known to have been exposed§§	15 (36.6)
Patient exposure unknown, but product known to have been used at facility	26 (63.4)

* By whole genome sequencing.
† All available isolates underwent whole genome sequencing and were found to be genetically related.
§ Includes initiation, modification, or extension of antibiotic therapy in response to the positive culture (e.g., to provide empiric coverage for gram-negative bacteremia or specific coverage for *Paraburkholderia* bacteremia).
¶ Includes patients identified during this investigation whose providers were advised of ultrasound gel contamination.
** Procedure documented in medical record as being performed with ultrasound guidance.
†† Intracardiac aspiration during resuscitation.
§§ Product use documented in medical record or determined during interview to have been used for the patient.

Summary

What is already known about this topic?

Contaminated nonsterile ultrasound gels have been implicated in outbreaks of *Burkholderia* infections associated with improper infection control practices before or during percutaneous procedures.

What is added by this report?

During May 2023–April 2025, use of contaminated nonsterile ultrasound gel before percutaneous procedures was associated with detection of genetically related *Paraburkholderia*, an environmental organism not typically associated with human infection, in 42 clinical specimens from the United States, Canada, and Israel. Based on medical record review, one patient had a confirmed invasive *Paraburkholderia* infection.

What are the implications for public health practice?

Use of nonsterile ultrasound gel for percutaneous procedures is not recommended. Guidelines on appropriate ultrasound gel use recommend sterile gel for any applications before, during, or after a procedure that breaches the skin at the ultrasound site.

identified that was more consistent with their clinical presentation, but it was not possible to determine on retrospective chart review with certainty in each case whether the positive culture represented true infection. Unlike other outbreaks in which contaminated ultrasound gel has caused invasive infections, this investigation identified only one patient with confirmed invasive *P. fungorum* infection. It remains unclear whether this represents an intrinsic lack of *Paraburkholderia* virulence or whether cases of invasive infection are underreported. Although treating providers ultimately assessed *Paraburkholderia* to be a blood culture contaminant in two thirds (68%) of patients with available information, three fourths (76%) of patients received antibiotics to empirically treat gram-negative bacteremia or to specifically treat *Paraburkholderia* bacteremia. This finding is consistent with previous studies documenting the association between blood culture contamination and unnecessary antibiotic use (*9*) and might also reflect more conservative management because of the high mortality of gram-negative sepsis and the infrequency of gram-negative organisms as contaminants in blood cultures.

The findings from this investigation highlight the need for vigilance regarding best practices for ultrasonography around invasive procedures. Existing guidelines on the use of ultrasound gel are clear that health care personnel should always use only sterile, single-use ultrasound gel products for ultrasonography in preparation for, or during, percutaneous procedures (*10*). Health care personnel who perform percutaneous POCUS procedures, including peripheral intravenous catheter placement and venipuncture, should be trained in

the appropriate use of ultrasound gel. If nonsterile gel is inadvertently applied before percutaneous procedures, it should be thoroughly removed from the skin before performing skin antisepsis (*5*).

Limitations

The findings in this report are subject to at least two limitations. First, despite routine use, ultrasound gel and POCUS for percutaneous procedures (e.g., venipuncture) are often not documented; thus, a retrospective chart review was unable to confirm gel use for all patients. Second, identification of *P. fungorum* in clinical specimens is not reportable; thus, its incidence is likely underestimated.

Implications for Public Health Practice

Infections and contaminated clinical specimens due to contaminated ultrasound gel continue to occur (*5*–*7*) and might become a larger concern as POCUS use becomes more common in clinical care, especially in emergency and intensive care settings. It is important for health care personnel, health care facilities, infection prevention specialists, and manufacturers to be aware of this risk and consider additional infection prevention measures. For instance, this investigation determined that several facilities reported stocking single-use packets of nonsterile gel; this packaging format itself might have been misinterpreted as a marker of sterility and could have contributed to its inappropriate use for percutaneous procedures. Manufacturers and health care facilities should ensure that nonsterile gel, particularly in single-use packets, is clearly labeled as nonsterile. Quality improvement measures to reduce blood culture contamination, such as those developed by CDC to promote best practices in blood culture collection and reporting of possible skin contaminants, can also reduce the rate of false positive cultures and limit unnecessary antibiotic therapy. The multiple countries involved in this investigation highlight the value of WGS for international surveillance and outbreak response, which allowed rapid sequence data sharing to establish the outbreak scope and source.

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Rabies Cluster Among Steers on a Dairy Farm — Minnesota, 2024

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Abstract

Rabies clusters in domestic livestock are rare but can result in human exposure and economic loss for farmers. During a 4-week period in May 2024, five of 35 steers on a Minnesota dairy farm developed neurologic signs consistent with rabies. Three clinically ill steers were euthanized, and brain specimens were submitted for rabies testing. Direct fluorescent antibody testing and whole genome sequencing confirmed rabies virus (North Central Skunk variant) in all three steers. After identification of the first two rabid steers, the remaining animals were quarantined for 120 days and vaccinated against rabies; three additional steers became ill during quarantine and were euthanized. The Minnesota Department of Health and Minnesota Board of Animal Health investigated human and animal exposures through interviews and site visits. Five persons were recommended to receive rabies postexposure prophylaxis because of known or potential exposures. The outbreak likely resulted from a single rabid skunk biting multiple cattle housed in a small pen, although steer-to-steer transmission cannot be ruled out. In addition to the loss of livestock, direct medical and veterinary costs associated with this outbreak totaled approximately $35,000. Preventive vaccination of cattle should be considered in areas with high activity of terrestrial rabies (i.e., rabies in land-based animals), presence of high-value livestock, and potential for human exposure.

Introduction

Rabies is a vaccine-preventable, viral, zoonotic disease that affects the central nervous system of mammals (*1*). Rabies virus is typically transmitted through the bite of an infected mammal or mucous membrane exposure to the virus (*2*). In the United States, the wildlife reservoirs for rabies are bats (multiple species), raccoons, foxes, mongooses, and skunks (Rabies in the United States | CDC). Although rabies has an almost 100% fatality rate, prompt administration of rabies post exposure prophylaxis (PEP) after an exposure is highly effective at preventing disease (*2*,*3*). Rabies clusters in domestic livestock are rare but can result in human exposure and significant economic losses for farmers. Cattle are not routinely vaccinated against rabies.

Investigation and Findings

Identification of the First Rabies Cases

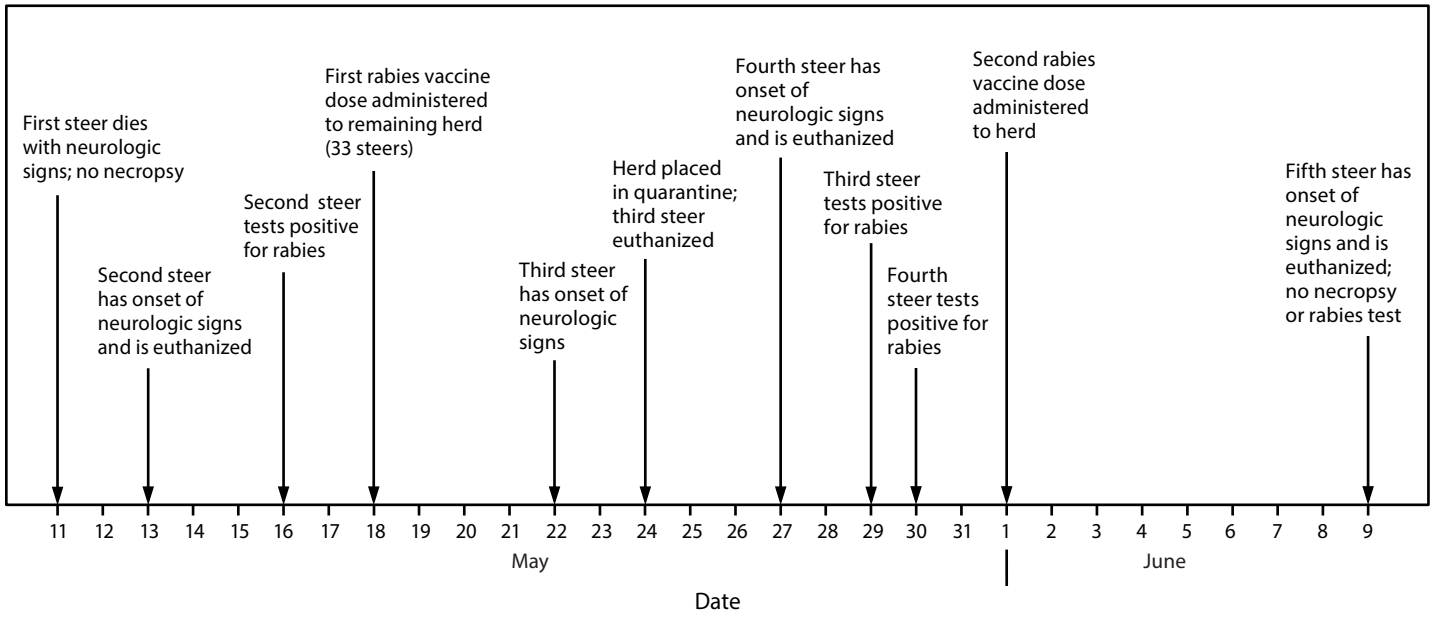
On May 11, 2024, a steer on a Minnesota dairy farm died a few days after the onset of neurologic signs including drooling, poor coordination, bellowing, and head thrashing; no necropsy was performed. On May 13, the farm owners sought veterinary care for a second steer exhibiting similar neurologic signs. The second steer was euthanized, and a sample of brain tissue was prepared at the University of Minnesota Veterinary Diagnostic Laboratory. Direct fluorescent antibody (DFA) testing of the brain tissue was performed at the Minnesota Department of Health (MDH) Public Health Laboratory and was positive for rabies on May 16. Whole genome sequencing (WGS) of the rabies virus was performed, which identified the North Central Skunk rabies virus variant. MDH and Minnesota Board of Animal Health (BAH) investigated to determine human and animal exposures. These activities were reviewed by CDC, deemed not research, and were conducted consistent with applicable federal law and CDC policy.*

Investigation and Management of Animals on the Farm

A BAH district veterinarian visited the farm premises to conduct an investigation, which included interviewing the farm owners, verifying animal vaccination histories, assessing potential rabies exposures among the animals, and establishing any necessary animal quarantines. During this investigation, the farm owners reported smelling a skunk several weeks before the onset of the first steer's illness, although no bite to the steer was identified. None of the animals in the herd had received rabies vaccination. To decrease the risk for rabies in additional steers in the herd and human exposure to rabid animals, the herd veterinarian initiated a 2-dose regimen of postexposure rabies vaccination for the remaining 33 steers, with the first dose administered on May 18 (Figure). Because two steers from the same pen had been infected, on May 24, BAH placed the 33 steers in a pen under a 45-day quarantine for rabies observation.

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

FIGURE. Rabies cases among steers on a dairy farm — Minnesota, May 11–June 9, 2024*



* No additional cases were reported after June 9, 2024.

One dog, that was up-to-date on its rabies vaccine, lived on the farm and had access to the steer's carcass before burial. The dog received a rabies vaccine booster dose on May 17, and BAH placed the dog on a 45-day observation period, which consisted of the owners watching the dog closely for signs of illness, limiting contact to those inside the household, and contacting BAH if clinical signs developed. The dog remained healthy. Per National Association of State Public Health Veterinarians guidance (*4*), 12 unvaccinated farm cats that did not have clinical signs of rabies but might have been exposed to the rabid steers were euthanized.

On May 24 and 27, two additional steers displayed neurologic signs similar to those observed in the first two steers and were euthanized; DFA testing of brain specimens was positive for rabies virus for both animals. Because additional cases were identified after the index case, BAH extended the quarantine of the herd to 120 days to ensure that any possible steer-to-steer transmission was detected.

On June 1, the 31 remaining steers received the scheduled second rabies vaccine dose. On June 9, a fifth steer developed signs similar to those observed among the previous four steers and died; no tissue from this animal was submitted for rabies testing. WGS of rabies virus isolated from the three tested animals (steers 2, 3, and 4) (Figure) indicated that the detected North Central Skunk rabies virus variant differed by at least single nucleotide polymorphisms. No additional steers died.

Identification of Potentially Exposed Persons

MDH epidemiologists conducted interviews with six potentially exposed persons to determine whether rabies PEP was indicated. These included persons who might have had contact with saliva from or might have been bitten by a rabid steer and were not wearing appropriate personal protective equipment (i.e., gloves, eye protection, and face protection).

Five persons (one veterinarian, two farm owners, and two children) were determined to have had possible exposure to rabid steers. The veterinarian's glove and skin were punctured during removal of an infected steer's brain. The farm owners had extensive contact with all of the infected steers, including possible saliva contact. The children, aged <10 years, had unsupervised contact with the area where the steers were housed, and thus exposure could not be ruled out. All five persons received rabies PEP.† The four family members received the full PEP series, and the veterinarian, who had received rabies vaccine before the exposure, received 2 booster doses.

Public Health Response

On June 12, BAH published a rabies alert on its website providing details about the rabid steers, information on

† Rabies PEP consists of 1 dose of human rabies immune globulin (HRIG) (20 IU per kg of body weight), followed by 4 rabies vaccine doses on days 0, 3, 7, and 14. HRIG is administered on the same day as the first rabies vaccine dose and is only indicated for persons who have not previously been vaccinated against rabies (Rabies post-exposure prophylaxis | CDC).

Summary

What is already known about this topic?

Rabies is a viral disease that infects mammals and has an almost 100% fatality rate if postexposure prophylaxis is not administered before symptom onset. Outbreaks among cattle are rare but have been reported.

What is added by this report?

During a 4-week period in May 2024, five of 35 steers on a Minnesota dairy farm developed neurologic signs consistent with rabies. The cluster likely represents a point-source exposure to a rabid skunk; however, steer-to-steer transmission could not be ruled out.

What are the implications for public health practice?

Rabies in cattle can expose humans to the disease and result in economic loss for farmers. Preventive vaccination of cattle should be considered to prevent human exposure in areas where rabies is prevalent and the value of the livestock is high.

vaccinating pets and livestock, and recommendations for actions to take if an abnormally behaving skunk was identified. A press release summarizing the outbreak and providing educational resources and contact information to discuss potential rabies exposures was issued by MDH and published by select rural newspapers in Minnesota. The press release and subsequent articles informed residents of the increased number of rabid skunks and subsequent increased number of rabid cattle in Minnesota in 2024 (*5*). The press release and articles served as reminders to vaccinate pets, consider vaccinating livestock, and seek medical attention for any potential rabies exposures. Direct medical and veterinary costs for this outbreak included PEP for four persons ($32,000), booster vaccine doses for the veterinarian ($730), veterinary visits ($1,300), postexposure vaccination of steers ($889), rabies booster for the dog ($134), and specimen shipping and rabies testing ($218)[§] (*6*).

Discussion

An estimated 60,000 human exposures to rabies occur each year in the United States through exposure to wildlife and unvaccinated domestic animals (*7*). Striped skunks are the primary terrestrial (land-based) wildlife rabies reservoir in Minnesota. Forty-two percent of skunks submitted for rabies testing in Minnesota are confirmed positive (Animals tested for rabies | 2003–2024 | MDH); the rabies variant most commonly identified in infected domestic animals in Minnesota (including in cats, dogs, horses, and cattle) is the North Central Skunk rabies virus variant (MDH, unpublished data, 2015–2024).

[§] Cost information for rabies postexposure vaccination was obtained by interviewing the farm owners and the herd veterinarian. Veterinary costs to the farm owners were obtained from service bills provided by the herd veterinarian.

Temporal clustering of rabid animals on a farm is unusual but has been reported (*4*). The dairy steers on this farm were housed in a small pen, making it possible for a rabid skunk to bite multiple animals. The incubation period for rabies in domestic animals can vary depending on the location and severity of the bite, and the rabies virus variant. Combined with WGS results that indicated closely related viruses, findings from this investigation suggest that multiple steers were infected by a single rabid skunk. However, a cluster of five rabid steers (three laboratory-confirmed cases and two with compatible clinical signs) during a 4-week period on one farm is highly unusual, and steer-to-steer transmission cannot be ruled out.

Rabid livestock can result in exposures to humans and economic loss to farmers; such losses are not typically reimbursed by farm business insurance and are also not part of the Department of Agriculture's Livestock Indemnity Program, which provides benefits to livestock producers for deaths in excess of normal mortality. All associated veterinary costs, income loss from the five steers, and additional feed costs for the remaining herd were incurred by the owners. Although not routinely vaccinated against rabies, cattle are the livestock species most often infected (*8*). An economic analysis of rabies vaccination in cattle estimated U.S. losses associated with livestock rabies ranging from $9.7 million to $40.5 million during 2012–2021 (*8*). Preventive vaccination of cattle should be considered in areas where terrestrial rabies is prevalent, the value of the animals is high, and potential for human exposure exists (*8*).

Limitations

The findings in this report are subject to at least two limitations. First, MDH was unable to procure brain tissues samples for DFA testing from the first and last dairy steers that exhibited abnormal neurologic signs and died. However, based on the similar signs and timing of illness and the fact that they were housed in the same pen as the three steers with confirmed rabies infection, rabies is likely also the cause of their deaths. Second, the source of rabies exposure could not be confirmed. While there was evidence of skunk activity on the farm, no skunk was observed on the property or submitted for rabies testing, and it was not possible to confirm that steer-to-steer transmission did not occur.

Implications for Public Health Practice

Rabies is considered a fatal disease if PEP is not administered (Rabies | CDC; Minnesota's Rabies Facts | MNDOH). Temporal clustering of rabid animals on a farm is unusual but when it does occur it can result in potential human exposures and economic loss for the owners. In regions of the United States with a high level of rabies in terrestrial reservoirs, it might

be worth evaluation of the benefits and costs of preventive vaccination of high-value animals to prevent human rabies and to potentially save animal owners from economic loss.

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