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Legionnaires Disease Associated with a Private-Use Hot Tub in a Vacation Rental Property — New York, October 2024–April 2025

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Abstract

In mid-October 2024, the New York State Department of Health (NYSDOH) was notified of two cases of Legionnaires disease in persons who stayed at the same short-term vacation rental property and had both used the rental property's hot tub. The diagnoses were confirmed by urine antigen tests, and NYSDOH successfully isolated *Legionella pneumophila* serogroup 1 from the sputum of one patient. Local health department staff members collected three samples from three sinks and two samples from two showers to assess the rental property's potable water system, which was supplied by a private well. Three samples were also collected from the rental property's hot tub. Whole genome sequencing of isolates from the hot tub samples and the sputum specimen were closely related, suggesting that the hot tub was the likely source of exposure. Hot tubs create aerosols and typically maintain water temperatures of approximately 100°F–104°F (38°C–40°C). This temperature is within the most favorable range for *Legionella* growth and also accelerates the decay of disinfectants. Guidance from NYSDOH and CDC regarding proper operation, disinfection, and remediation of hot tubs was provided to the rental property owner. NYSDOH recommended that the owner close the hot tub until proper remediation was performed and postremediation samples without detection of any *Legionella* bacteria were collected by NYSDOH staff members. The rental property owner did not initially comply with NYSDOH recommendations, and a public nuisance law was used to ensure that proper measures were taken to disinfect the hot tub before use by future guests. Activities to raise awareness among short-term rental and vacation rental property owners regarding the risks associated with an improperly managed hot tub are needed to decrease the likelihood that rental property hot tubs are in a condition that is conducive to *Legionella* growth and reduce the risk for Legionnaires disease associated with vacation rental stays. Travelers staying in vacation rental properties should be aware that use of hot tubs might pose a risk for Legionnaires disease and exercise caution when using hot tubs, particularly those travelers with underlying medical conditions.

Introduction

In mid-October 2024, the New York State Department of Health (NYSDOH) was notified of an increase in in the number of reported cases incidence of Legionnaires disease in a western New York county (county A). Five patients in the same city (city A) had received positive urine antigen test (UAT) results, indicating recent exposure to *Legionella pneumophila* serogroup 1 (during 2022–2024, county A averaged 22 cases

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per year. Two of these patients were family members who had spent several nights together at a short-term vacation rental property in city B, 40 miles south of city A. NYSDOH began an investigation of the rental property in an effort to ascertain the extent of this outbreak, identify any additional cases, and investigate any potential sources of exposures so that proper remedial and preventive action could be taken.

Investigations and Results

Epidemiologic Investigation

Initial investigation. Epidemiology staff members from the local health department interviewed five persons (patients A, B, C, D, and E) who received positive UAT results using the NYSDOH Legionnaires Disease Questionnaire (part of the standard case report form developed based on CDC's *Legionella* case report form) (Table 1). Two family members (patients A and B) who had stayed together at the rental property and had both used the hot tub, sauna, and shower reported similar symptom onset dates during the first week of October 2024. This outbreak investigation work represents standard public health practice by NYSDOH, and institutional review board review was not required.

Investigation of the rental property (patients A and B). After identification of the common exposures of patients A and B, and because Legionnaires disease has been associated with hot tub use (*1*,*2*), an investigation of the rental property was conducted. A confirmed case of Legionnaires disease associated with the rental property was defined as receipt of a positive UAT or *Legionella* species culture result in a person with a clinically compatible illness who reported a stay at the rental property in October 2024. Patient A and patient B experienced cough, fever, and chills. Patient A, who had comorbid conditions, was hospitalized and received antibiotics and invasive mechanical ventilation (Clinical Guidance for Legionella Infections | CDC) (Table 1). Patient A survived but the hospital discharge date is not known. Patient B visited an emergency department and was prescribed antibiotics but was not admitted. The results from a sputum sample collected from patient A were initially negative at a commercial laboratory. NYSDOH requested that the specimen be forwarded to the Wadsworth Center David Axelrod Institute (WC-DAI), a public health laboratory operated by NYSDOH, for further testing. No clinical specimen was collected from patient B. A line list of patients with Legionnaires disease associated with the rental property was developed by NYSDOH, which included demographic characteristics, signs and symptoms, underlying medical conditions, symptom onset date, travel and exposure history, and diagnostic testing results. Retrospective and prospective reviews of case exposure histories did not identify any additional cases associated with the rental property.*

* Interviews revealed that five additional guests stayed at the rental property and might have used the hot tub. These additional guests did not report any symptoms and therefore were not interviewed or part of any investigative process. Patients C, D, and E were investigated as a separate cluster. No additional exposures sources were identified.

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TABLE 1. Age, month of symptom onset, exposure history, and test results among five persons with Legionnaires disease,* including two who used a hot tub at the same vacation rental property — New York, 2024

Patient	Part of rental property investigation†	Age, yrs	Month of symptom onset	Sputum *Legionella* species culture result§	Exposure history	Test results
A¶	Yes	68	Oct	*Legionella pneumophila* serogroup 1 isolated**	Use of hot tub and sauna; shower at rental property	WGS from clinical sample closely related to environmental samples from rental property hot tub
B	Yes	33	Oct	No sputum sample collected	Use of hot tub and sauna; shower at rental property	No clinical sample collected, but environmental and epidemiologic evidence suggest infection caused by rental property hot tub exposure
C	No	48	Sep	Negative	Use of private residential hot tub and possible occupational exposure	Possible occupational exposure investigated; no exposure source confirmed
D	No	94	Oct	No sputum sample collected	Outpatient medical appointments and local restaurant visits	Patient unable to produce sputum; exposure source not identified
E	No	72	Sep	*L. pneumophila* isolated	Outpatient medical appointment visits, single night stay at local hotel, and use of private residential hot tub	No match between WGS results from clinical sample and anything in the database; exposure source not identified

Abbreviation: WGS = whole genome sequencing.

* Confirmed by urine antigen testing.

† Although the initial cluster notification included five confirmed cases in persons living within the same county, interviews identified common exposures of patients A and B at the rental property in a neighboring county, leading to a separate outbreak investigation. Interviews also revealed that five additional guests stayed at the rental property and might have used the hot tub. These additional guests did not report any symptoms and therefore were not interviewed or part of any investigative process. Patients C, D, and E were investigated as a separate cluster. No additional exposures sources were identified.

§ For a sputum sample to be collected and analyzed, the sample must be ordered by a physician, the ill persons must be able to produce sputum, and *Legionella* organisms must be isolated from the sample via culture before the species can be sequenced. Administering antibiotics before collecting the sample might reduce the likelihood of isolating *Legionella* species from a sputum sample.

¶ Patient A had preexisting hypertension and cardiovascular disease, was hospitalized, and received antibiotics and invasive mechanical ventilation. The patient survived, but the hospital discharge date is not known.

** Test results from a commercial laboratory for a sputum sample from patient A initially were negative, but *L. pneumophila* serogroup 1 was isolated by the New York State Department of Health public health laboratory by culture.

Investigation of patients C, D, and E. A separate cluster investigation was conducted for patients C, D, and E; no common exposures were identified among these patients (Table 1). A potential occupational exposure was investigated for patient C, but no source was identified.

Rental Property Environmental Health and Laboratory Investigation

Collection of samples. Eight samples were collected from the rental property (Table 2): five potable water samples from the sinks and showers, two swabs of hot tub surfaces, and one nonpotable water sample collected directly from the hot tub basin. Each water sample was initially collected into a sterile 34-oz (1-L) bottle and subsequently divided into 4-oz (120-mL) and 10-oz (290-mL) sterile plastic bottles containing sodium thiosulfate, which was used to neutralize chlorine in the sample and prevent further disinfection during transport to the laboratory and to ensure preservation of any viable *Legionella* species present in the sample.†

Analysis of water samples. All eight collected water samples were submitted to the Wadsworth Center Environmental Biggs Laboratory for analysis both by IDEXX's Legiolert and by standard culture (International Organization for Standardization [ISO] 11731:2017) (*3*). Legiolert is a culture-based method that can be conducted more quickly (7 days) than standard culture (10–14 days).§ Use of both methods increases the chances of recovering an organism and increases the likelihood of detecting any *Legionella* species in the sample.

Analysis of swab samples. Because the Legiolert test is only intended for use with water samples, the laboratory created a modified protocol for use with swabs. Swabs were prepared according to ISO 11731:2017 (*3*), generating 1:10 and 1:100 serial dilutions in phosphate-buffered saline. A 0.03-oz (1-mL) aliquot of each dilution was added to 3 oz (99 mL) of reagent water (highly purified water with no detectable concentration of the compound or element to be analyzed) and processed according to the manufacturer's instructions for potable water.

Identification of *L. pneumophila* from hot tub samples. Legiolert detected *L. pneumophila* in all three hot tub samples,

† Sterile plastic sample collection bottles were purchased from IDEXX for *Legionella* sample collection. These bottles are pretreated with sodium thiosulfate that can neutralize up to 15 mg/L of chlorine.

§ IDEXX's Legiolert is designed to detect viable *L. pneumophila* only.

TABLE 2. Location, source type, and test results for samples collected from a vacation rental property associated with two cases of Legionnaires disease — New York, 2024

Sample collection location	Source type	Legiolert (MPN/mL)*	Culture (CFU/mL)†	WGS (SNP difference)§
Kitchen bathroom sink (cold water)	Potable water	<0.01	Not detected	NA
Primary bathroom shower (first draw, hot water)	Potable water	<0.01	Not detected	NA
Primary bathroom sink (first draw, hot water)	Potable water	<0.01	Not detected	NA
Basement shower (first draw, hot water)	Potable water	<0.01	Not detected	NA
Basement sink (first draw, hot water)	Potable water	<0.01	Not detected	NA
Hot tub water	Nonpotable water	134.2	Not detected	2
Hot tub swab (air-water interface)	Nonpotable water, swab	13,677	3,700	2
Hot tub swab (filter)	Nonpotable water, swab	13,677	Not detected	3

Abbreviations: CFU = colony-forming unit; MPN = most probable number; NA = not applicable; SNP = single nucleotide polymorphism; WGS = whole genome sequencing.
* This culture-based method only detects *Legionella pneumophila*; MPN represents the most probable number of colonies of *L. pneumophila* detected per 1 mL of a sample. A liquid-based enzyme substrate is incubated with a sample; after 7 days, the number of positive wells is counted, and an MPN table is used to determine the concentration *of L. pneumophila* (MPN/mL) in the original sample.
† The number of CFUs of *Legionella* species detected per 1 mL of a sample. Potable water samples were invalid because free chlorine exceeded 10 mg/L.
§ The number of SNPs compared with the patient sample obtained from investigation.

ranging from 134 to 13,677 most probable number (MPN) of colonies per milliliter[¶] (Table 2). Legiolert did not detect *L. pneumophila* in the potable water system samples. Standard culture (ISO 11731:2017) confirmed the presence of *Legionella* species in one sample, the swab from the air-water interface of the hot tub (3,700 colony-forming units per milliliter). The potable water samples were found to contain a total and free chlorine residual >10 mg/L, and the sodium thiosulfate contained in the sterile plastic bottles used for sample collection can neutralize up to 15 mg/L of chlorine, suggesting the presence of >25 mg/L. The high residual chlorine level would normally result in rejection of a sample, but the laboratory agreed to analyze these samples at the request of NYSDOH even though isolation of viable *Legionella* organisms from the potable water samples was deemed highly unlikely.

Whole genome sequencing (WGS) of isolates. WC-DAI performed the analysis and WGS of clinical specimens and environmental samples. A sputum sample from patient A that initially tested negative by culture at a commercial laboratory was forwarded to WC-DAI, which isolated *L. pneumophila* serogroup 1 via culture. The isolates from the hot tub differed by two to three single nucleotide polymorphisms from patient A's clinical isolate, indicating that they were closely related.

Public Health Response

Recommendations to the Rental Property Owner

Discussion between NYSDOH and the property manager revealed that the owner had disinfected the private well with a large amount of liquid chlorine bleach the night before health department officials were scheduled to visit the site. NYSDOH staff members learned that the hot tub was not regularly disinfected and recommended the hot tub immediately be closed to guests until it was cleaned professionally, and a chemical treatment program was implemented. CDC guidance was provided to the property owner (*4*), who was instructed to notify NYSDOH when proper remediation of the hot tub was completed.

Follow-Up After Remediation Recommendations

Approximately 4 weeks after sample collection and recommendations were provided to the rental property owner, local health department officials informed NYSDOH that the hot tub was back in use; NYSDOH had not been notified by the property owner. The rental property owner had personally cleaned the hot tub (i.e., did not hire professionals), tested a sample using an unapproved method, and reopened the hot tub for guest use without consulting NYSDOH. NYSDOH staff members reiterated the importance of having the equipment cleaned professionally and allowing NYSDOH staff members to collect the samples for analysis by a laboratory certified by the New York Environmental Laboratory Approval Program (*5*). After an additional 4 weeks, NYSDOH staff members were notified that the rental listing still advertised the hot tub, and guests were leaving new reviews that mentioned hot tub use.

Use of the New York Public Nuisance Law

Because the hot tub had not been satisfactorily disinfected, and the rental property owner continued to allow its use by guests, local health department officials charged the owner with violation of the Erie County Sanitary Code, and the hot tub was deemed a public nuisance. The health department also issued a commissioner's order to close the hot tub until it was deemed safe to use.

[¶] MPN of *L. pneumophila* colonies is based on reaction of *L pneumophila* with the enzyme substrate in the Legiolert test; after counting the number of positive wells, an MPN table is used to determine the concentration in the original sample. The MPN method is considered scientifically equivalent to, or better than, the colony-forming unit plate method for determining concentration.

Subsequent Remediation and Testing Results

After the hot tub was cleaned and disinfected by a professional, two rounds of follow-up sampling were conducted by the local health department staff members. The commissioner's order was lifted on March 31, 2025, after two successive rounds of sampling from the hot tub did not identify any viable *Legionella* organisms. The professional hired by the rental property to clean the hot tub was subsequently hired to service it weekly.

Discussion

By positively matching an environmental source of *L. pneumophila* with Legionnaires disease cases (*6*), WGS determined that the clinical specimen collected from patient A was closely related to the environmental samples collected from the hot tub, thereby establishing it as likely source of infection. Rental property hot tub use is frequently associated with reports of Legionnaires disease, and NYSDOH has successfully matched clinical samples from persons with Legionnaires disease to environmental samples from hot tubs in recent years (*1*,*6*).

According to CDC's Supplementary Legionnaires Disease Surveillance System, during 2014–2021, one in seven patients with Legionnaires disease report having stayed overnight in a hotel or vacation rental property; among those, approximately one half report having used a hot tub (*1*). A 2021 NYSDOH investigation concluded that at least one case of Legionnaires disease was associated with shared use of a private property hot tub (*6*), and CDC recently reported that two Legionnaires disease outbreaks were associated with outdoor hot tubs intended for private use on cruise ships (*2*). NYSDOH staff members added guidance to the program website designed to raise awareness about the risks involved with the use of an improperly managed hot tub and included guidance for proper routine water treatment practices.** New York has regulations designed to prevent *Legionella* contamination in cooling towers and in certain health care facilities†† (*7*) and to ensure that proper sanitary practices are followed in public pools (*8*); however, residential spa pools, including those at homes rented for overnight occupancy, are exempt from both regulations.

** The NYSDOH program Protect Yourself from Legionnaires Disease at Home guidance was updated to include additional guidance for hot tub and rental property owners. CDC also offers guidance for vacation rental owners. Legionnaires Disease Prevention | Providing a Home for Guests, not *Legionella* | CDC

†† Facilities include buildings of general hospitals that provide inpatient services or buildings of residential health care facilities providing a health-related service, such as lodging, board, or physical care.

Summary

What is already known about this topic?

Legionnaires disease results from inhalation of aerosolized *Legionella* bacteria from contaminated water. Hot tubs create aerosols and maintain water temperatures within a favorable range for *Legionella* growth. Private short-term rental properties are not subject to the same public health regulations as commercial properties.

What is added by this report?

A 2024 New York Legionnaires disease investigation used whole genome sequencing to identify a rental property hot tub as the source of two cases of Legionnaires disease. Health department officials used a public nuisance law to ensure that the hot tub was properly remediated before reopening.

What are the implications for public health practice?

Efforts to raise awareness among vacation rental and other short-term rental property owners of the risks associated with improperly managed hot tubs could reduce the risk for Legionnaires disease. Travelers staying in vacation rental properties should be aware that use of hot tubs might pose a risk for Legionnaires disease, particularly those travelers with underlying medical conditions.

Implications for Public Health Practice

Health department officials who perform waterborne disease investigations should prioritize testing any identified hot tub as a potential source of exposure when Legionnaires disease cases meet CDC's outbreak definition (*9*). Public health officials should conduct on-site field visits, collect and test samples, and use all available tools, including public nuisance laws if needed, to protect public health. Regular postremediation follow-up samples should be collected to ensure long-term control. Vacation and other short-term rental property owners should be informed of the risks associated with improperly managed hot tubs, particularly for persons at increased risk for severe illness, including those with underlying medical conditions.

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Alcohol Consumption During Pregnancy Among Women Aged 18–49 Years — United States, 2021–2024

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Abstract

Alcohol consumption during pregnancy can cause adverse birth outcomes and fetal alcohol spectrum disorders. One U.S. study identified a slight increasing trend in alcohol consumption during pregnancy from 2011 to 2018. During 2018–2020, 13.5% of pregnant women reported current drinking; more recent estimates are unavailable. CDC analyzed 2021–2024 Behavioral Risk Factor Surveillance System data to estimate prevalence of self-reported current drinking (one or more alcoholic drinks during the past 30 days), binge drinking (four or more alcoholic drinks on at least one occasion during the past 30 days), and heavy drinking (eight or more alcoholic drinks within 1 week during the past 30 days) among U.S. pregnant women aged 18–49 years. Multivariable regression was used to estimate adjusted prevalence ratios and identify correlates of alcohol consumption during pregnancy. Among U.S. pregnant women, 15.2% reported current drinking, 4.9% reported binge drinking, and 2.2% reported heavy drinking during the past 30 days. Higher prevalences of alcohol consumption were observed among pregnant women who were not married and those with frequent mental distress. Alcohol consumption during pregnancy remains a public health concern. Both clinical and community interventions might help reduce alcohol consumption during pregnancy and its associated adverse health outcomes.

Introduction

Alcohol consumption during pregnancy can cause adverse pregnancy and birth outcomes, including miscarriage and stillbirth, and fetal alcohol spectrum disorders, a group of lifelong behavioral, intellectual, and physical conditions. No amount of alcohol consumption during pregnancy is known to be safe; higher frequency and intensity of alcohol consumption during pregnancy are linked with higher risk for adverse pregnancy and birth outcomes (*1*). One previous study found a slight increasing trend in the prevalence of current drinking and binge drinking during pregnancy from 2011 to 2018, although increases were not consistently observed throughout that period (*2*). A recent study found current drinking and binge drinking prevalences of 13.5% and 5.2%, respectively, during 2018–2020 (*3*); more recent prevalence estimates are not available. To provide more recent estimates of alcohol consumption among pregnant women, CDC analyzed Behavioral Risk Factor Surveillance System (BRFSS) data to assess prevalences and correlates of self-reported current drinking, binge drinking, and heavy drinking among pregnant women aged 18–49 years in the United States during 2021–2024.

Methods

Data Source

BRFSS is an annual, state-based, random-digit–dialed telephone survey of health-related behaviors among noninstitutionalized adults aged ≥18 years in the United States and participating territories. To generate reliable prevalence estimates for this analysis, 2021–2024 BRFSS data from 50 U.S. states* and the District of Columbia were pooled. Across jurisdictions, median BRFSS response rates were 44.0% (range = 23.5%–60.5%) in 2021, 45.0% (22.8%–66.8%) in 2022, 44.7% (21.7%–63.1%) in 2023, and 43.9% (30.7%–64.8%) in 2024.†

Survey Measures

Respondents who reported that their sex at birth was female were asked whether they were currently pregnant; information on trimester of pregnancy was not collected. Current drinking (one or more alcoholic drinks during the past 30 days) and binge drinking (four or more alcoholic drinks on at least one occasion during the past 30 days)§ were defined based on the 2020–2025 Dietary Guidelines for Americans; heavy drinking (eight or more alcoholic drinks in a 1-week period during the past 30 days)¶ was classified based on CDC definitions.

* Florida (2021), Kentucky (2023), Pennsylvania (2023), and Tennessee (2024) did not collect sufficient data to meet minimum requirements for inclusion in the BRFSS public use data set for those years.

† Response rates were calculated using standard definitions from the American Association for Public Opinion Research.

§ Current drinking was defined as a response of "one or more" to the question, "During the past 30 days, how many days per week or per month did you have at least one drink of any alcoholic beverage such as beer, wine, a malt beverage or liquor?" Binge drinking was defined as a response of "one or more" to the question, "Considering all types of alcoholic beverages, how many times during the past 30 days did you have four or more drinks on an occasion?"

¶ Heavy drinking (for women, eight or more alcoholic drinks in a 1-week period during the past 30 days) was calculated by BRFSS from responses to the questions, "During the past 30 days, how many days per week or per month did you have at least one drink of any alcoholic beverage such as beer, wine, a malt beverage or liquor" and, "During the past 30 days, on the days when you drank, about how many drinks did you drink on average?" Calculated Variables in the 2024 Data File of the Behavioral Risk Factor Surveillance System | CDC

Sociodemographic and health characteristics examined included age, race and ethnicity, education, employment status, marital status, having a usual health care provider,** and experiencing frequent mental distress.††

Statistical Analysis

Among pregnant women aged 18–49 years with complete data for current drinking (8,579, unweighted), binge drinking (8,546, unweighted), or heavy drinking (8,550, unweighted) prevalences and 95% CIs were estimated overall, by survey year, and by sociodemographic and health characteristics. Because of small sample sizes for binge drinking and heavy drinking, only current drinking could be examined by geographic region. Rao-Scott chi-square tests were used to identify differences by survey year and geographic region. p-values <0.05 were considered statistically significant. Multivariable modified Poisson regression models with log link and robust SEs were used to estimate adjusted prevalence ratios (aPRs) and 95% CIs for associations between sociodemographic and health characteristics and current drinking, binge drinking, and heavy drinking. Estimates were considered statistically significant when 95% CIs excluded 1.0 or were nonoverlapping. Respondents with missing values for sociodemographic or health characteristics were excluded from the respective analyses.§§ Data were weighted to state-level population estimates and pooled to represent regional and national estimates. Analyses used SAS statistical software (version 9.4; SAS Institute); sample weights and design variables were incorporated and adjusted as recommended by BRFSS to account for the complex survey design and pooling of multiple years. This activity was reviewed by CDC, deemed not research, and conducted consistent with applicable federal law and CDC policy.¶¶

** Having a usual health care provider was ascertained by a response to the question, "Do you have one person you think of as your personal doctor or health care provider?" Participants who answered "no" were asked, "Is there more than one, or is there no person who you think of as your personal doctor or health care provider?" Responses were dichotomized into one or more (yes) or none (no).

†† Frequent mental distress was defined as a response of ≥14 days to the question, "Now thinking about your mental health, which includes stress, depression, and problems with emotions, for how many days during the past 30 days was your mental health not good?" Measuring Healthy Days | CDC

§§ Among respondents with complete information on current drinking, the unweighted proportion of those with missing values for sociodemographic and health characteristics ranged from 0.4% for education to 1.7% for frequent mental distress.

¶¶ 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.

Results

Prevalence of Alcohol Consumption Among Pregnant Women

Among U.S. pregnant women aged 18–49 years during 2021–2024, 15.2% reported current drinking, 4.9% reported binge drinking, and 2.2% reported heavy drinking during the past 30 days (Table). Among those reporting current drinking, 33.2% also reported binge drinking and 14.7% also reported heavy drinking. Prevalences did not differ significantly by survey year (Table).

Characteristics Associated with Alcohol Consumption Among Pregnant Women

Several characteristics were statistically significantly associated with current drinking, binge drinking, or heavy drinking (Table). For example, pregnant women who were not married had approximately twice the prevalence of current drinking (aPR = 1.8), binge drinking (aPR = 2.2), and heavy drinking (aPR = 2.0) compared with those who were married. In addition, pregnant women reporting frequent mental distress had approximately twice the prevalence of current drinking (aPR = 1.8) and binge drinking (aPR = 1.8) and three times the prevalence of heavy drinking (aPR = 3.0) compared with those who did not report frequent mental distress. Significant differences existed by geographic region for current drinking (p = 0.04): pregnant women living in U.S. Department of Health and Human Services (HHS) Region 1 (19.9%) had a higher prevalence of current drinking than did those living in HHS Region 6 (10.4%), HHS Region 7 (11.8%), and HHS Region 8 (12.4%) (Figure).

Discussion

Alcohol consumption during pregnancy remains a public health concern in the United States. The estimated prevalence of current drinking among pregnant women during 2021–2024 (15.2%) appears to be higher than it was during 2018–2020 (13.5%) (*3*), suggesting an ongoing need for clinical and community-level interventions.

Regional differences in current drinking during pregnancy observed in this analysis are generally consistent with patterns of current drinking observed among the general U.S. population. Geographic differences highlight the importance of tailoring public health interventions to account for local context and cultural norms when addressing alcohol consumption during pregnancy. Community-level approaches that focus on pregnant women, such as point-of-sale signs with information about adverse outcomes known to be associated with alcohol

TABLE. Estimated prevalence* and adjusted prevalence ratios of current drinking, binge drinking, and heavy drinking reported by pregnant women aged 18–49 years, by selected characteristics — Behavioral Risk Factor Surveillance System, United States, 2021–2024†

Characteristic	Current drinking§		Binge drinking¶		Heavy drinking**	
	% (95% CI)	aPR†† (95% CI)	% (95% CI)	aPR†† (95% CI)	% (95% CI)	aPR†† (95% CI)
Total	**15.2 (13.6–16.8)**	—	**4.9 (4.0–5.8)**	—	**2.2 (1.6–2.7)**	—
Survey year						
2021	15.8 (12.6–19.1)	—	5.6 (3.0–8.2)§§	—	2.1 (1.0–3.1)§§	—
2022	15.4 (12.6–18.1)	—	5.0 (3.5–6.5)	—	2.6 (1.5–3.6)§§	—
2023	15.1 (12.0–18.3)	—	5.5 (3.7–7.3)	—	NA¶¶	—
2024	14.5 (11.1–17.8)	—	3.5 (2.3–4.8)	—	1.2 (0.7–1.8)§§	—
Age group, yrs						
18–24	18.0 (14.3–21.7)	0.9 (0.7–1.1)	7.7 (4.9–10.4)	1.2 (0.7–2.0)	3.1 (1.7–4.4)§§	0.8 (0.4–1.5)
25–29	12.0 (9.7–14.2)	0.6 (0.5–0.8)	3.7 (2.4–4.9)	0.6 (0.4–1.1)	1.5 (0.6–2.3)§§	0.5 (0.2–1.1)
30–34	10.5 (8.3–12.8)	0.5 (0.4–0.7)	2.3 (1.6–3.1)	0.4 (0.2–0.6)	NA¶¶	NA¶¶
35–49	21.4 (17.6–25.2)	Ref	6.1 (4.3–8.0)	Ref	2.8 (1.6–4.0)§§	Ref
Race and ethnicity***						
Black or African American	17.9 (13.0–22.8)	1.1 (0.7–1.6)	7.6 (4.8–10.5)	1.4 (0.8–2.5)	3.7 (1.7–5.6)§§	1.9 (0.9–4.0)
White	15.0 (13.2–16.9)	1.1 (0.8–1.5)	4.1 (3.3–5.0)	1.0 (0.6–1.9)	2.1 (1.2–2.9)§§	1.6 (0.8–3.2)
Hispanic or Latino	12.5 (9.4–15.7)	Ref	4.2 (2.5–6.0)††	Ref	1.5 (0.8–2.2)§§	Ref
Other	19.9 (14.2–25.7)	1.4 (0.9–2.1)	NA¶¶	NA¶¶	NA¶¶	NA¶¶
Education						
High school diploma or less	12.9 (10.3–15.5)	Ref	4.9 (3.1–6.6)	Ref	1.8 (1.1–2.6)§§	Ref
Some college	15.8 (12.7–19.0)	1.2 (0.9–1.6)	5.1 (3.7–6.5)	1.1 (0.7–1.8)	3.0 (1.6–4.4)§§	1.6 (0.8–3.0)
College degree	18.0 (15.7–20.3)	1.5 (1.2–2.0)	4.8 (3.5–6.1)	1.4 (0.8–2.3)	1.8 (1.0–2.6)§§	1.2 (0.5–2.5)
Employment status						
Employed	17.1 (15.1–19.1)	1.2 (1.0–1.6)	5.0 (3.9–6.1)	1.1 (0.7–1.7)	2.2 (1.5–3.0)	1.1 (0.6–1.9)
Not employed	12.8 (10.3–15.3)	Ref	4.8 (3.2–6.4)	Ref	2.2 (1.3–3.0)§§	Ref
Marital status						
Married	12.0 (10.1–13.9)	Ref	3.1 (2.1–4.2)	Ref	1.3 (0.6–2.0)§§	Ref
Not married	19.1 (16.5–21.7)	1.8 (1.4–2.2)	7.0 (5.4–8.6)	2.2 (1.3–3.7)	3.1 (2.2–4.0)	2.0 (1.1–3.6)
Has a usual health care provider						
Yes	16.0 (14.2–17.9)	Ref	5.0 (3.9–6.1)	Ref	2.2 (1.5–2.8)	Ref
No	12.2 (9.5–15.0)	0.8 (0.6–1.0)	4.2 (2.6–5.8)	0.7 (0.4–1.3)	2.1 (0.9–3.3)§§	1.0 (0.5–2.2)
Frequent mental distress†††						
Yes	26.0 (21.3–30.8)	1.8 (1.4–2.3)	9.0 (6.6–11.4)	1.8 (1.2–2.6)	5.7 (3.7–7.7)	3.0 (1.7–5.0)
No	13.3 (11.7–15.0)	Ref	4.1 (3.1–5.2)	Ref	1.6 (1.0–2.2)	Ref

Abbreviations: aPR = adjusted prevalence ratio; NA = not available; Ref = referent group.

* Percentages are weighted to represent national estimates of the noninstitutionalized U.S. adult population.

† Florida (2021), Kentucky (2023), Pennsylvania (2023), and Tennessee (2024) did not collect sufficient data to meet minimum requirements for inclusion in the Behavioral Risk Factor Surveillance System public use data set for those years.

§ Defined as self-reported consumption of one or more alcoholic drinks during the past 30 days.

¶ Defined as self-reported consumption of four or more alcoholic drinks on at least one occasion during the past 30 days.

** Defined as self-reported consumption of eight or more alcoholic drinks in 1 week during the past 30 days.

†† aPRs generated from complete-case multivariable modified Poisson regression models are adjusted for age, race and ethnicity, education, employment status, marital status, usual health care provider, and frequent mental distress.

§§ Prevalence estimate might be unstable because the relative SE is 0.2–0.3.

¶¶ Prevalence estimate or corresponding prevalence ratio is suppressed because the relative SE for the prevalence estimate is >0.3.

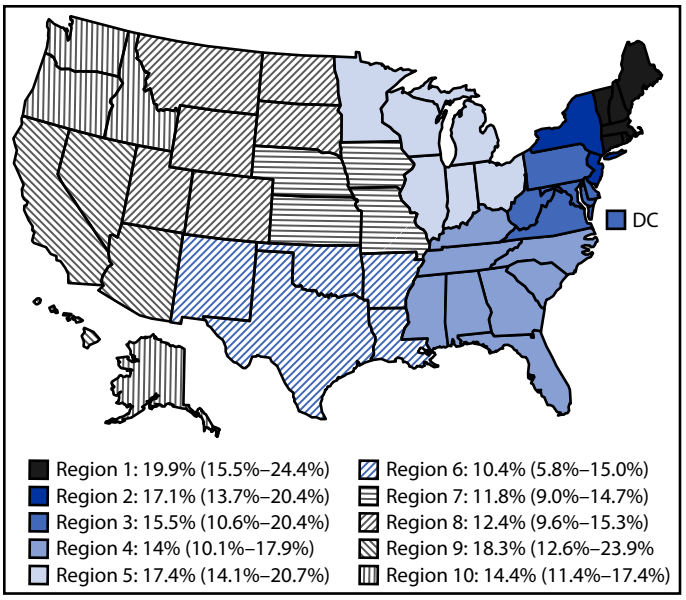
*** Persons of Hispanic or Latino (Hispanic) origin might be of any race but are categorized as Hispanic; all racial groups are non-Hispanic.

††† Defined as reporting ≥14 days of poor mental health during the past 30 days.

consumption during pregnancy (*4*) or that focus on the general population, such as sales taxes on alcoholic beverages (*5*), might help reduce prenatal alcohol exposure and its associated adverse health outcomes.

Pregnant women who were not married or who reported experiencing frequent mental distress had approximately two to three times the prevalence of current drinking, binge drinking, and heavy drinking compared with those who were married or did not experience frequent distress, consistent with findings from a previous study of current drinking and binge drinking during pregnancy (*3*). Studies suggest alcohol consumption might be used as a coping method to relieve stress and manage negative feelings, although alcohol consumption might alter or exacerbate stress pathways (*6*). Marital and other cohabitation statuses have been associated with reduced substance use, which might be explained in part by social support, although relationship quality and other factors might influence this association (*7*). These findings reinforce the importance of integrating behavioral health screening, treatment, and other support into prenatal care. The U.S. Preventive Services Task Force in

FIGURE. Estimated prevalence* of current drinking† during the past 30 days reported by pregnant women aged 18–49 years (N = 8,579), by U.S. Department of Health and Human Services region§ — Behavioral Risk Factor Surveillance System, United States, 2021–2024



Abbreviation: DC = District of Columbia.

* Percentages (with 95% CIs) are weighted to represent national estimates of the noninstitutionalized U.S. adult population. Estimate for region 6 might be unstable because the relative SE is 0.2–0.3. Florida (2021), Kentucky (2023), Pennsylvania (2023), and Tennessee (2024) did not collect sufficient data to meet minimum requirements for inclusion in the Behavioral Risk Factor Surveillance System public use data set for those years.

† Defined as self-reported consumption of one or more alcoholic drinks during the past 30 days.

§ U.S. Department of Health and Human Services regions

Summary

What is already known about this topic?

Alcohol consumption during pregnancy can increase the risk for adverse pregnancy and birth outcomes. No amount of alcohol consumption during pregnancy is known to be safe.

What is added by this report?

According to 2021–2024 data from the Behavioral Risk Factor Surveillance System, 15.2% of pregnant women in the United States reported current drinking, 4.9% reported binge drinking, and 2.2% reported heavy drinking during the past 30 days.

What are the implications for public health practice?

Clinical approaches, such as routine screening for alcohol consumption and mental health conditions during pregnancy, and community-level approaches, such as point-of-sale warning signs or alcohol sales taxes, might help reduce alcohol consumption during pregnancy and its associated adverse pregnancy and birth outcomes.

2018 recommended screening adults for unhealthy alcohol use, including alcohol use during pregnancy, and brief counseling to address unhealthy use (*8*). In addition, the American College of Obstetricians and Gynecologists recommends screening all pregnant women for anxiety and depression during prenatal care visits, emphasizing the importance of having systems in place, when needed, to ensure access to appropriate services (*9*).

Limitations

The findings in this report are subject to at least five limitations. First, some survey respondents who became pregnant within 30 days of survey administration might have reported alcohol use that occurred before, not during, pregnancy; this might have resulted in overestimates of alcohol consumption during pregnancy because studies conducted among women who delivered live infants have found alcohol consumption typically decreases when women realize they are pregnant (*10*). Second, self-reported alcohol consumption might be subject to misclassification related to social desirability and recall biases, which might have resulted in underestimates of consumption; in addition, because BRFSS questions do not capture all alcohol consumption patterns, heavy drinking results might be underestimates. Third, self-reported pregnancy status might be misclassified because early pregnancies might be unrecognized and unreported. Fourth, temporality is unknown for observed associations between health characteristics and alcohol consumption because data are cross-sectional. Finally, this analysis did not include an evaluation of patterns of alcohol consumption throughout pregnancy because information on trimester of pregnancy was not collected.

Implications for Public Health Practice

The finding that during 2021–2024 more than one in seven (15.2%) U.S. pregnant women reported drinking alcohol during the past 30 days underscores the ongoing need for comprehensive strategies to reduce alcohol consumption during pregnancy. Recommended clinical interventions include routine screening for alcohol consumption and mental health conditions, brief behavioral counseling, and referral to specialized services (*8*,*9*). Community-level approaches that include providing information about outcomes associated with alcohol consumption during pregnancy or address alcohol consumption among the general population might also help reduce prenatal alcohol exposure and prevent its associated adverse health outcomes (*4*,*5*).

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Modeled Scenario Projections for the Ebola Disease Outbreak Caused by Bundibugyo Virus, 2026

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Abstract

On May 15, 2026, the Ministries of Health in the Democratic Republic of the Congo and Uganda declared outbreaks of Bundibugyo virus disease (BVD), a type of Ebola disease. In response to reports of high numbers of suspected cases and deaths in these outbreaks, CDC simulated scenario projections to understand possible future morbidity and mortality. A branching process model with the capacity to model transmission-reducing nonpharmaceutical interventions was calibrated to three putative cumulative death counts and projected for four possible intervention scenarios ranging from poor (20%) to extremely high (95%) levels of isolation and treatment of symptomatic persons. The analysis suggested a plausible spillover event (i.e., the transmission of a virus from its natural animal reservoir to humans) in mid to late February 2026. With poor isolation levels of patients with BVD (20%) and no other interventions, the likelihood of an outbreak that exceeds 20,000 cases within 3 months is 65%. If, however a high proportion of patients were to enter isolation (70%), only a one in 20 chance is projected for an outbreak with ≥10,000 cases within 3 months. These results underscore the importance of strong public health interventions, because the current outbreak is already the largest known BVD outbreak and has the potential to quickly become one of the largest Ebola disease outbreaks ever recorded.

Introduction

In May 2026, outbreaks of Bundibugyo virus disease (BVD) caused by species *Orthoebolavirus bundibugyoense*, a species of orthoebolavirus for which no approved vaccine or medication is currently available, were reported in the Ituri province in northeastern Democratic Republic of the Congo (DRC) and Uganda (*1*). As of June 2, 2026, a total of 378 confirmed cases (363 in DRC and 15 in Uganda) and 63 confirmed deaths (62 in DRC and one in Uganda) have been recorded (*2*). BVD causes a severe hemorrhagic fever. Bundibugyo virus is spread through direct contact with the body fluids of a person who is infected or has died from BVD. CDC modeled possible trajectories of the outbreak over 3 months. The models considered different assumptions about the cumulative number of deaths as of May 24, 2026, and different scenarios of public health intervention intensity, defined by the percentages of persons with BVD who are successfully isolated and therefore prevented from causing onward transmission.

Methods

Model Structure

CDC used a model to simulate BVD outbreaks. The model was adapted from one applied to previous viral hemorrhagic fever outbreaks, including a Marburg virus disease outbreak in Ethiopia in 2025. In this model, each simulated outbreak was initialized with one infected person, who represented the person first infected from a zoonotic source (a spillover event). This person infected a randomly generated number of additional persons based on assumptions about the basic reproductive number ([R_0], the average number of persons in a susceptible population infected by an infected person). Any infected persons were added to the simulation at times selected according to the distribution of intervals from one infection to the next and, in turn, were able to cause further infections. This simulation, called a branching process, continued until either 1) none of the infected persons in a generation caused any secondary infections, indicating termination of the outbreak or 2) the simulation reached 5,000 deaths, indicating a very large and exponentially growing outbreak.

Time Intervals

Intervals from infection to symptom onset, symptom onset to death, and symptom onset to recovery were held constant for all infections within each simulated outbreak but varied among simulated outbreaks. Simulated persons were never infectious before symptom onset or after recovery but could be infectious after death.

Assumptions about parameters were based on published estimates from previous Ebola outbreaks (Supplementary Box). Estimates specific to BVD were used when available.

Model Calibration to Assumed Number of Deaths

Assumptions for the cumulative number of BVD deaths as of May 24, 2026, were based on publicly available situation reports from DRC.* The model was calibrated to three

*The DRC national public health institute reported 10 confirmed deaths and 223 suspected deaths as of May 24, 2026. A subsequent report with data as of June 2, 2026, reported a cumulative total of 62 confirmed deaths in DRC.

different numbers of cumulative deaths (50, 100, and 200) to account for uncertainty in the current number of deaths caused by BVD.

A simulated outbreak was compatible with the real-world outbreak if it reached the assumed number of cumulative deaths by May 24, 2026, and if the first death occurred on or before April 24, 2026. Outbreaks were simulated until 500 simulations met these criteria. The accepted 500 simulated outbreaks were used to infer when the outbreak began and served as the basis for scenario projections of interventions for each model calibration.

Scenario Projections for Isolation

Four intervention scenarios were assessed for each calibration, each implementing a different level of isolation (i.e., percentage of symptomatic infected persons detected, isolated, and treated: 20% [poor], 50% [moderate], 70% [high], and 95% [extremely high]). The extremely high scenario was chosen to estimate a lower bound for transmission.

The intervention was assumed to start on May 24, 2026. On that day in each simulation, the designated percentage of symptomatic persons was selected to begin isolating, with an average delay of 2 days until isolation and treatment. The same percentage of persons who later developed signs or symptoms was selected to begin isolating, with an average delay of 2 days from symptom onset. Simulated persons in isolation were prevented from causing any onward transmission; the model implicitly assumed that isolated persons who died were safely buried (i.e., without washing or embalming and buried by trained teams using personal protective equipment).

Each simulation reported the cumulative number of cases and cumulative number of deaths from the date of spillover until August 22, which would be 90 days after interventions began. The percentages of simulations with <10,000, 10,000–19,999, and ≥20,000 cases and with <2,000, 2,000–3,999, and ≥4,000 deaths were calculated for all simulations in each scenario and separately for those with an R_0 less than or equal to and greater than the median R_0 value. The effective reproductive number (R_e, the average number of onward infections per infectious person, accounting for immunity and public health interventions) was calculated for the preintervention and postintervention periods.

The branching process model was written in Rust (version 1.95.0; The Rust Development Team), and the model calibration and scenario projection pipeline was written in Python (version 3.14.4; Python Software Foundation). This activity was reviewed by CDC, deemed not research, and conducted consistent with applicable federal law and CDC policy.[†]

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

Results

Outbreak Size Projections and Inferred Spillover Date by Assumed Number of Deaths

Assuming 50 deaths. The model calibrated to 50 deaths estimated that the spillover event that triggered this outbreak most likely occurred on approximately February 19, 2026 (interquartile interval [IQI] = February 1–March 8). Assuming that 20% of infected persons were successfully isolated beginning May 24, 2026, projections showed ≥20,000 cumulative cases in 65% of simulations, ≥10,000 cumulative cases in 85% of simulations, and ≥4,000 cumulative deaths in 69% of simulations (Figure). Even with 50% of infected persons isolated, many simulations still projected these numbers of cases but were less likely to occur (17% of simulations projected ≥20,000 cases and 22% projected ≥4,000 deaths). At 70% isolation, projected outbreaks were much more likely to be smaller, but still of substantial size, with 94% of simulations projecting <10,000 cases and only 1% projecting ≥20,000 cases; similarly, at this isolation level, 90% of simulations projected <2,000 deaths and only 3% projected ≥4,000 deaths. R_e declined proportional to the percentage of infected persons successfully isolated (Supplementary Figure 1).

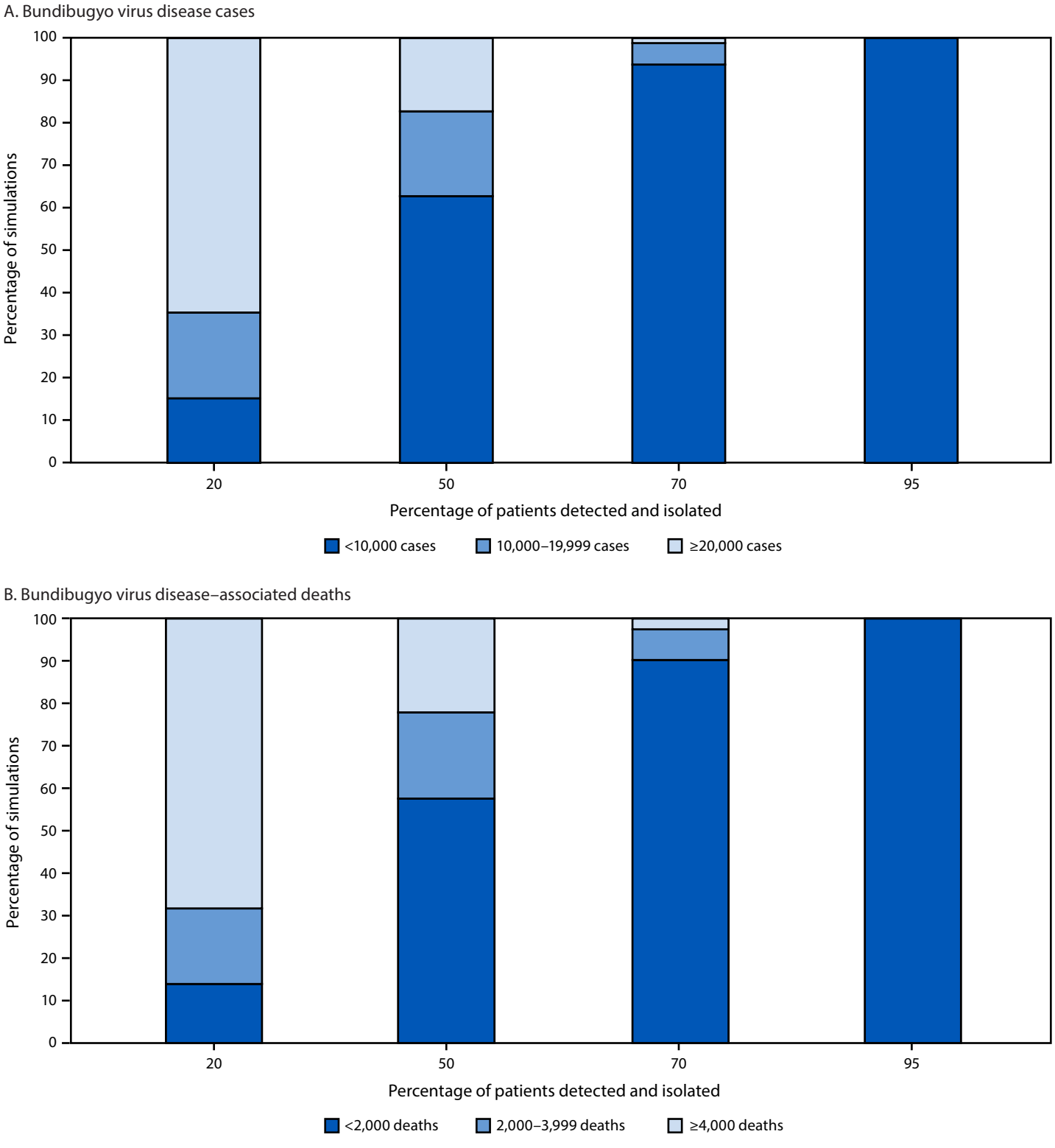
Assuming 100 deaths. Assuming 100 cumulative deaths as of May 24, 2026, the inferred median spillover date was February 8, 2026 (IQI = January 21–February 27). Very large outbreaks were likely in the scenario in which only 20% of patients were isolated (76% of simulations projected ≥20,000 cases and 87% projected ≥4,000 deaths). In the scenario in which 70% of infected persons were isolated, 73% of simulations projected <2,000 cumulative deaths by August 22, 2026, and 10% projected ≥4,000 deaths (Supplementary Figure 2).

Assuming 200 deaths. Assuming 200 deaths by May 24, 2026, the calibrated model inferred a median spillover date of January 29, 2026 (IQI = January 9–February 18). The earlier spillover date would have generated a larger outbreak by the time interventions began; thus, even with 70% of infected persons isolated, 42% of simulations projected ≥10,000 cases by August 22, 2026.

Sensitivity to Basic Reproductive Number

Simulated outbreaks with R_0 values higher than the median R_0 typically reached ≥10,000 cumulative cases and ≥2,000 cumulative deaths by August 22, 2026, in scenarios with ≤50% isolation, even assuming only 50 cumulative deaths by May 24. In the scenario with 70% of infected persons isolated and 50 assumed deaths by May 24, 2026, no simulations projected ≥2,000 deaths when R_0 values were lower than the median R_0, but 20% of simulations projected ≥2,000 deaths when R_0 values exceeded the median (Supplementary Figure 3).

FIGURE. Percentage of simulated Bundibugyo virus disease outbreaks, by cumulative outbreak size category on August 22, 2026, as measured by cases (A) and deaths (B), and by percentage of simulated patients detected and isolated, using a branching process model,* 2026



* A branching process model is a type of infectious disease transmission model that starts with a single infection and simulates a transmission tree that represents an expanding outbreak. Simulations (500 for each vertical bar) assume 50 Bundibugyo virus disease–associated deaths as of May 24, 2026, and that the isolation intervention began that day.

Discussion

Model-based scenario projections of the current BVD outbreak suggest that if large-scale and sustained public health interventions are not rapidly implemented to reduce disease transmission, this outbreak could become as large as the 2014–2016 West Africa Ebola virus disease outbreak, which resulted in more than 28,000 cases and more than 11,000 deaths (*2*). Although the worst outcomes (higher numbers of cases and associated deaths) in these projections were less likely when a larger proportion of patients were identified, isolated, and treated, this outbreak could, within 3 months and under low-isolation scenarios, become the second largest Ebola outbreak in history. In light of this projected risk for a very large outbreak even if reasonably effective control measures are implemented, the public health response to control this outbreak will likely need to be of similar magnitude to the response for the 2014–2016 West Africa Ebola outbreak (*3*).

Even among simulations calibrated to only 50 deaths or those with a lower R_0, very large outbreaks were still sometimes projected to occur, especially in scenarios without high levels of isolation. Calibrating the model to a larger number of deaths was approximately equivalent to assuming that interventions were implemented later in the outbreak. The results imply that intervening earlier in the outbreak would reduce the likelihood of worse outcomes.

The high probability of a large outbreak over a 3-month period primarily results from the large size of the outbreak at the time it was initially confirmed. This analysis did not provide evidence that R_0 for this outbreak is unusually large.[§] Time between Ebola outbreak onset and detection is positively correlated with overall outbreak size and duration (*4*).

CDC's assessment that the risk to the general U.S. population is low (*5*) is not changed by this analysis. Despite the unprecedented size of the 2014–2016 West Africa Ebola epidemic, only two Ebola transmission events occurred in the United States. Those two infected persons were health care workers caring for a patient with Ebola who had traveled to the United States before enhanced screening, risk assessment, and health education measures were implemented at U.S. ports of entry (*6*). Both persons infected in the United States recovered.

Limitations

The findings in this report are subject to at least five limitations. First, the true number of BVD deaths that occurred through May 24, 2026, is unknown. Some deaths from BVD might not have been confirmed; similarly, it is possible that other deaths might have been incorrectly attributed to BVD. Second, basic reproductive number estimates for Ebola disease vary widely across outbreaks. The true value of R_0 for this outbreak might be higher or lower than the values used in this analysis. High-quality data on changes in the number of cases and deaths over time are essential to more precisely estimate R_0. Third, changes in behavior that reduce risk for infection (e.g., avoiding contact with ill persons) were not included in the model and might help limit outbreak size. Fourth, the model did not account for transmission reductions attributable to an increase in the proportion of the population with infection-induced immunity. Given the population size of the communities where this outbreak is occurring, this limitation is unlikely to affect the validity of the projections over the time span and numerical ranges of cases presented in this analysis; however, the model could project unrealistically large outbreaks if applied to longer periods. Finally, the model did not include infection relapses after recovery (*7*). This limitation is unlikely to affect this analysis, but relapses could be important drivers of the course of the epidemic over a longer period.

Summary

What is already known about this topic?

An outbreak of Bundibugyo virus disease (BVD), a type of Ebola disease, is currently ongoing, centered in the Ituri province of the Democratic Republic of the Congo (DRC).

What is added by this report?

CDC used a transmission model to project outbreak growth over 3 months, by using different assumptions about the number of deaths as of May 24, 2026, and by varying the percentages of persons with BVD who are successfully identified and isolated to prevent ongoing transmission. Assuming 50 cumulative deaths as of May 24, 2026, if 70% of patients were to enter isolation, only approximately one in 20 simulations projected an outbreak exceeding 10,000 cases within 3 months.

What are the implications for public health practice?

Large-scale, rapid public health action is needed to control the current outbreak, already the largest known BVD outbreak, from becoming one of the largest Ebola epidemics in history.

Implications for Public Health Practice

The current BVD outbreak is already the largest known BVD outbreak, and in scenarios with low percentages of isolated patients, could become one of the largest Ebola outbreaks ever documented. Urgent and sustained public health action is needed to prevent the outbreak from becoming as large as or larger than the 2014–2016 West Africa Ebola epidemic. This effort could require resources comparable in magnitude to the

[§] The calibrated values for R_0 were nearly identical to the input assumption about R_0. The median basic reproductive number R_0 = 2.51 (IQI = 2.27–2.82) in the main analysis calibrated to 50 deaths.

2014–2016 Ebola response in West Africa. Rapid identification of cases, contact tracing, isolation and treatment of persons with BVD, community engagement, and use of safe and dignified burial for persons who die from BVD are necessary to control the outbreak.

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Assessment of Risk to the U.S. Population from the Ebola Disease Outbreak Caused by Bundibugyo Virus, 2026

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On June 5, 2026, this report was posted as an MMWR *Early Release on the* MMWR *website (https://www.cdc.gov/mmwr).*

Abstract

On May 15, 2026, the ministries of health in the Democratic Republic of the Congo and Uganda declared outbreaks of Bundibugyo virus disease (BVD), a type of Ebola disease. In response to reports of high numbers of suspected cases and deaths in the affected countries, CDC assessed the risk posed by the BVD outbreak to the U.S. population during the next 3 months. This analysis used a standardized risk assessment approach that included epidemiologic data from the ongoing outbreak and historical data from previous Ebola outbreaks; the overall risk was determined by taking into account independent assessments of the likelihood of infection and the impact of infection. The assessment found that the overall risk to the U.S. population posed by the current BVD outbreak during the next 3 months is low, based on the extremely low likelihood of transmission, despite the high impact that potential infection could have and the resources that would be required to respond to the outbreak. Limitations to this assessment included uncertainties around the epidemiology of BVD as well as the current and future scope and geographic spread of the outbreak. CDC continues to monitor factors that could change this risk assessment.

Introduction

Bundibugyo virus disease (BVD), a type of Ebola disease, is a severe and often fatal viral hemorrhagic fever caused by Bundibugyo virus (species *Orthoebolavirus bundibugyoense*). No vaccines or medications have been approved for BVD. As of June 2, 2026, a total of 378 confirmed BVD cases and 63 deaths have been reported in the Democratic Republic of the Congo (DRC) and Uganda (*1*). CDC assessed the potential public health implications of this BVD outbreak to the U.S. population during the next 3 months. The purpose of this risk assessment was to guide the development and implementation of U.S. preparedness efforts, including risk communication.

Methods

CDC subject matter experts in risk assessment methodology, infectious disease modeling, global health, and Ebola disease and viral hemorrhagic fevers collaborated to develop this assessment. These experts used a standardized risk assessment approach that has been applied to previous viral hemorrhagic fever outbreaks (*2*). They considered available evidence including epidemiologic data from the ongoing BVD outbreak and historical data on Bundibugyo virus and other Ebola disease outbreaks.

Overall risk to the U.S. population was determined by independently assessing two factors: 1) the likelihood of infection and 2) the impact of infection[†] (*2*). The likelihood of infection refers to the probability that members of the U.S. population would acquire Bundibugyo virus infection during the next 3 months; this, in turn, depends on the likelihood of exposure, infectiousness of the virus, and susceptibility of the population. The impact of infection refers to the consequences of infection in this population. Factors include the severity of disease, level of population immunity to severe disease, availability of medications and vaccines, and necessary public health response resources. Risk was assessed only for the general U.S. population; however, subpopulations that might have different assessments of likelihood are noted, based on varying risk factors. Experts then assigned a degree of confidence to the assessment, taking into account evidence quality, extent, and corroboration of information. This activity was reviewed by CDC, deemed not research, and conducted consistent with applicable federal law and CDC policy.[§]

Results

CDC assessed the overall risk posed by the ongoing BVD outbreak to the U.S. population during the next 3 months as low. This assessment was made with moderate confidence, given the data available. This overall risk was determined based on a combination of extremely low likelihood of infection, but high impact of infection for the U.S. population, were it to occur.

Likelihood of Infection

The likelihood of Bundibugyo virus infection for the U.S. population was assessed as extremely low. The initial reported case numbers in this outbreak are larger than initial case reports from many recent Ebola disease outbreaks, suggesting that transmission

[*] These authors contributed equally to this report.

[†] Overall risk is assessed at a predefined level (extremely low, very low, low, moderate, high, and very high) with varying combinations of assessed likelihood and impact.

[§] 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.

might have been ongoing for an extended period before the outbreak was recognized (*3*). Despite the large number of cases identified at the time the outbreak was reported, the current likelihood for potential spread of BVD from DRC to the United States, via travelers from DRC who might be infected, is considered very low based on modeling results that consider population movement. These modeling results suggested that the relative risk of importation to the United States compared with other locations was 1.3% (*4*). In addition, on May 18, enhanced traveler screening and entry restrictions were established to further reduce the potential for importation of BVD into the United States.

If BVD were to be introduced into the United States, based on historical observation and the known epidemiology of BVD, secondary transmission would likely be minimal. The United States has the public health capacity to rapidly implement case identification, laboratory confirmation, isolation of patients, contact tracing, and infection prevention and control measures that can contain and control an outbreak. Although BVD symptoms can appear suddenly and might be nonspecific, these public health measures are highly effective against Ebola disease, in part because the average interval between cases is long (10–16 days), and because persons are not known to be infectious before the onset of symptoms (*5*). Only 11 persons infected with Ebola disease have ever been treated in the United States; all were associated with the 2014–2016 Ebola virus disease outbreak in West Africa (*6*). Despite two instances of secondary transmission to U.S. health care workers during that outbreak, no community spread occurred in the United States. Although the likelihood of infection for the general U.S. population is low, the likelihood of infection might be higher among U.S. health care workers practicing in or who have recently returned from affected regions in DRC and Uganda based on possible exposure risks.

Impact of Infection

The impact of infection, based on the standardized framework, was assessed as high, primarily based on the severity of the illness, lack of available medications and vaccines, and resources required to respond to the current outbreak. In the two previously identified outbreaks of BVD in Uganda in 2007 and DRC in 2012, case-fatality rates ranged from 25% to 50%. However, many of the deaths in these outbreaks occurred in locations where health resources are limited; clinical outcomes might improve with the specialized care available in the United States.

No approved vaccines or medications are currently available for BVD. A licensed vaccine and two licensed monoclonal antibody products have been used in previous outbreaks of Ebola disease caused by a different virus (species *Orthoebolavirus zairense*); whether these products are effective against BVD is unknown. While investigational medications are being evaluated, treatment for BVD is currently limited to supportive care.

Preventing spread of Bundibugyo virus requires considerable public health resources and risk communication. Public health interventions could include extensive contact tracing activities, quarantine of 21 days for persons with high-risk exposures, and stringent infection prevention and control measures for health care workers and laboratory personnel. Even very limited numbers of BVD cases in the United States might cause substantial concern among the public, possibly with some disruption of normal societal activities and to health care facilities.

Confidence Level

Confidence in this assessment of BVD risk to the U.S. population during the next 3 months was assessed as moderate, based on availability of credible information from reliable sources, requiring minimal assumptions to be made for the analysis. The United States is prepared to respond to imported cases, and the largest previous outbreaks of Ebola disease in other countries led to very few cases within the United States. However, this assessment also recognizes uncertainties about the epidemiology of BVD, the scope and geographic spread of the outbreak, and the potential timelines for implementation of interventions.

Discussion

CDC assessed the risk to the U.S. population posed by the current BVD outbreak as low during the next 3 months, based on the extremely low likelihood of infection, despite the high impact of infection, should it occur, and the resources required to respond to the outbreak. This assessment aligns with similar analyses conducted by other international public health organizations (*7*–*9*). Several factors could alter this assessment, including detection of any BVD cases in the United States; evidence suggesting increased transmissibility or changed clinical severity compared with previous outbreaks; or spread of the outbreak to urban, international hubs, which could increase the likelihood of importation into the United States. The emergence of additional evidence related to these factors could warrant an update to this assessment.

Limitations

The findings in this report are subject to at least three limitations related to key uncertainties about this outbreak. First, given that only two previous BVD outbreaks have occurred, less is known about Bundibugyo virus than other types of orthoebolaviruses that cause human illness (e.g., *O. zairense*, which was responsible for the 2014–2016 Ebola virus disease outbreak in West Africa). Second, limited confirmatory diagnostic testing and challenges in contact tracing that likely resulted in undetected transmission mean that the full scope of the current

Summary

What is already known about this topic?

An outbreak of Bundibugyo virus disease (BVD), a type of Ebola disease, is currently occurring, centered in the Ituri province of the Democratic Republic of the Congo (DRC).

What is added by this report?

CDC assessed the risk posed by this ongoing outbreak to the U.S. population during the next 3 months as low.

What are the implications for public health practice?

Ensuring sufficient public health resources to control the outbreak in DRC will be necessary for maintaining a low risk to the U.S. population. If cases arise in the United States, there is public health capacity to contain and control an outbreak, and CDC guidance for U.S. clinicians and public health practitioners can help prevent the potential spread.

outbreak is unclear, making it difficult to assess the potential geographic spread of the outbreak and the subsequent potential for spread to the United States. Nonetheless, even the largest previous outbreak of Ebola led to very few cases among U.S. persons (*6*). Finally, although DRC and neighboring countries have extensive experience responding to outbreaks of viral hemorrhagic fevers, several features of this outbreak pose challenges to assessing its future trajectory (*3*), including that the outbreak is occurring in a region with ongoing conflict and unpredictable infrastructure (*1*), and the initial large size of the outbreak combined with limited confirmatory diagnostic testing might lead to challenges in infection prevention and control efforts (*10*).

Implications for Public Health Practice

To help ensure that the risk to the U.S. population remains low, efforts are underway to reduce the likelihood of importation to the United States and to respond quickly and effectively to any cases that might occur in the United States (*1*). Sustained public health actions are needed to slow the spread of this outbreak at its epicenter, prevent additional cases and deaths, and reduce the risk for spread to additional regions or countries (*3*). If a person in the United States is suspected to have BVD, early implementation of CDC guidance for U.S. clinicians and public health practitioners for Ebola diseases and viral hemorrhagic fevers can help prevent further transmission. Leveraging experience from past Ebola outbreaks, U.S. federal, state, tribal, local, and territorial public health, clinical, and laboratory partners will continue efforts to prevent and prepare for a possible BVD case in the United States.

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Notes from the Field

Outbreak of Ebola Disease Caused by Bundibugyo Virus — Democratic Republic of the Congo and Uganda, May 2026

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Bundibugyo virus disease (BVD) is a type of Ebola disease, a severe and often fatal viral hemorrhagic fever (*1*). Bundibugyo virus was first identified in 2007, when it caused an outbreak in Uganda with 149 suspected cases and 37 deaths (*2*). A 2012 BVD outbreak in DRC resulted in 56 laboratory-confirmed cases and 17 deaths (*3*). On May 15, 2026, the ministries of health in the Democratic Republic of the Congo (DRC) and Uganda declared outbreaks of BVD. As of June 2, a total of 378 confirmed cases and 63 confirmed deaths have been reported.

Investigation and Outcomes

Characteristics of Patients

The initial clusters of BVD cases were identified among health care workers in DRC, whose signs and symptoms included acute fever, vomiting, diarrhea, and, in some cases, bleeding (*4*). As of June 2, a total of 378 confirmed cases (363 in DRC and 15 in Uganda) and 63 confirmed deaths (62 in DRC and one in Uganda) have been reported, primarily among adults aged 18–49 years, with cases approximately evenly distributed between females and males. Uganda's outbreak has primarily involved travelers arriving from DRC, with secondary transmission to health care workers.

Laboratory Findings

Laboratory analysis by the DRC National Institute of Biomedical Research confirmed Bundibugyo virus (species *Orthoebolavirus bundibugyoense*). Initial genomic sequencing was consistent with a new spillover event (i.e., transmission of virus from its natural reservoir to an intermediate animal) from an unknown zoonotic host.

Transmission and Treatment

Based on evidence from other Ebola disease outbreaks, Bundibugyo virus is likely transmitted through direct contact with body fluids of an infected person (e.g., blood, vomitus, feces, urine, tears, sweat, saliva, breast milk, amniotic fluid, vaginal secretions, or semen). The incubation period is expected to range from 2 to 21 days, and patients are considered most infectious in the late stages of the disease and after death, when high concentrations of virus are present in body fluids (*1*). Treatment consists of supportive care; no medications or vaccines against BVD have been approved.

BVD Exposures Among U.S. Citizens

After developing symptoms, one U.S. health care worker in DRC received a positive test result for Bundibugyo virus and was transported to Germany for treatment. Six other U.S. citizens (health care workers and their close contacts) who had high-risk exposures to BVD in DRC were transported to Germany and Czechia for monitoring. No BVD cases have been reported in the United States. This activity was reviewed by CDC, deemed not research, and conducted consistent with applicable federal law and CDC policy.*

Preliminary Conclusions and Actions

On May 17, 2026, CDC initiated a public health emergency response to support U.S. preparedness, the international outbreak response, and U.S. public health response coordination. The same day, the World Health Organization determined this outbreak to be a public health emergency of international concern. On May 18, the U.S. Department of Homeland Security and CDC announced new public health measures that included temporary U.S. entry restrictions. On May 19, CDC released a health advisory, initiated enhanced airport screening, and issued interim guidance for U.S. health departments managing travelers in their jurisdictions. CDC also issued a Level 3 Travel Health Notice for DRC (reconsider nonessential travel to provinces with cases) and a Level 2 Travel Health Notice for Uganda (practice enhanced precautions).

To reduce the risk for Bundibugyo virus transmission in the United States, CDC is providing outreach and preparedness information for the public, clinical guidance for health care providers, and guidance for state, tribal, local, and territorial partners on public health management. In addition, CDC's Laboratory Response Network is supporting diagnostic testing capacity at more than 40 U.S. laboratories. When needed, CDC offers clinical consultation for suspected Ebola cases

*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.

Summary

What is already known about this topic?

Bundibugyo virus has caused two previous Ebola disease outbreaks in the Democratic Republic of the Congo (DRC) and Uganda.

What is added by this report?

In May 2026, a large outbreak of Bundibugyo virus disease was identified in DRC and Uganda. As of June 2, a total of 378 confirmed cases and 63 confirmed deaths have been reported. No cases have been reported in the United States.

What are the implications for public health practice?

To help reduce the risk for continued spread of Bundibugyo virus, including potential spread beyond DRC and Uganda or importation to the United States, ongoing collaboration between CDC and international partners and coordination among U.S. government agencies are essential.

and exposure risk assessments for U.S. citizens abroad who are returning to the United States.

To reduce the risk for spread to other countries and regions, CDC is collaborating with international partners and country offices in DRC and Uganda by providing assistance with epidemiologic investigations and contact tracing, laboratory testing, data management, infection prevention and control, border health surveillance, and risk communication and community engagement. In addition, CDC has worked with international partners to complete readiness assessments in bordering countries.

To support coordination among U.S. government agencies, CDC launched an Ebola dashboard within the Interagency Readiness and Response Hub, a secure collaboration platform, and is providing technical recommendations for BVD diagnostics to the U.S. Department of State. CDC is also collaborating with the Administration for Strategic Preparedness and Response and the National Institutes of Health to guide interagency recommendations on medical countermeasures for BVD.

This ongoing BVD outbreak is occurring in geographic areas that have limited public health infrastructure and are affected by armed conflict, frequent population displacement, and cross-border movement (*5*). The scope of the outbreak is likely larger than that represented by available data and might prove challenging to contain and control.

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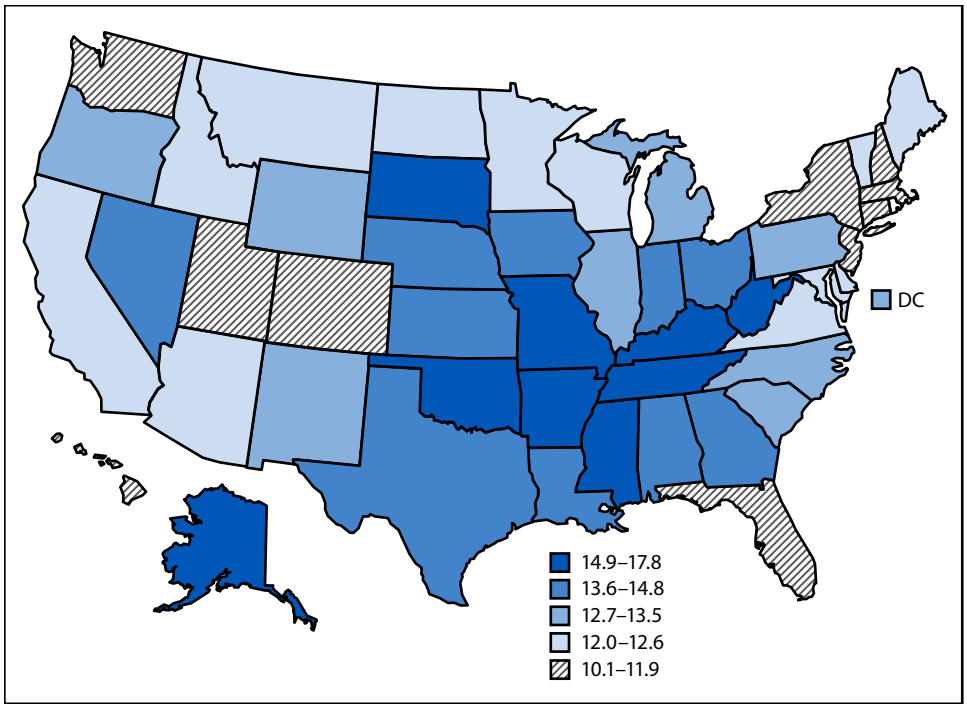
QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Age-Adjusted Colorectal Cancer Death Rates,* by State — United States, 2024



Abbreviation: DC = District of Columbia.

* Death rates per 100,000 standard population. Colorectal cancer deaths were identified using *International Classification of Diseases, Tenth Revision* underlying cause-of-death codes C18–C21. Age-adjusted colorectal cancer death rates were calculated using the direct method and the 2000 U.S. Census Bureau standard population.

In 2024, the U.S. colorectal cancer death rate was 12.9 deaths per 100,000 standard population. Rates were generally lower in the Northeast and higher in the South. Colorectal cancer death rates were highest in Oklahoma (17.8) and lowest in Rhode Island (10.1).

Supplementary Table: https://stacks.cdc.gov/view/cdc/256552#tabs-3

Source: National Center for Health Statistics, National Vital Statistics System, Mortality Data, 2024. Underlying Cause of Death, 2018–2024, Single Race Request

Reported by: Sibeso N. Joyner, MPH; Deepthi Kandi, MS; Arialdi Miniño, MPH.

For more information on this topic, CDC recommends the following link: Colorectal Cancer | CDC

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