

Hepatitis Awareness Month and Testing Day, May 2018

The United States commemorates National Hepatitis Awareness Month each May, and May 19 is designated as Hepatitis Testing Day. Viral hepatitis still persists as a major public health threat despite availability of preventive measures such as vaccines and therapies, including a curative treatment for hepatitis C virus (HCV) infection.

New cases of hepatitis B virus (HBV) and HCV infections are on the rise, largely among persons who inject drugs, with some attributed to the current U.S. opioid epidemic (1). Recent hepatitis A outbreaks have also occurred among unvaccinated injection drug users and homeless persons (2). Since August 2016, CDC has responded to hepatitis A outbreaks with high HBV/HCV co-infection, hospitalization, and mortality rates in multiple states (<https://www.cdc.gov/hepatitis/outbreaks/2017March-HepatitisA.htm>). New cases of perinatal HBV infection also continue (1); recently, CDC updated recommendations to strengthen vaccination among newborns and manage pregnant women (3).

This issue of *MMWR* includes an article about the promising outcomes of three HBV programs that implemented community-based services to improve HBV testing, linkage to care, and treatment among persons born in intermediate-high prevalence countries (4).

References

1. CDC. Viral hepatitis surveillance—United States, 2016. Atlanta, GA: US Department of Health and Human Services; 2016. <https://www.cdc.gov/hepatitis/statistics/2016surveillance/pdfs/2016HepSurveillanceRpt.pdf>
2. Williams WW, Lu PJ, O'Halloran A, et al. Surveillance of vaccination coverage among adult populations—United States, 2015. *MMWR Surveill Summ* 2017;66(No. SS-11). <https://doi.org/10.15585/mmwr.ss6611a1>
3. Schillie S, Vellozzi C, Reingold A, et al. Prevention of hepatitis B virus infection in the United States: recommendations of the Advisory Committee on Immunization Practices. *MMWR Recomm Rep* 2018;67(No. RR-1). <https://doi.org/10.15585/mmwr.rr6701a1>
4. Harris AM, Link-Gelles R, Kim K, et al. Community-based services to improve testing and linkage to care among non-U.S.-born persons with chronic hepatitis B virus infection—three U.S. programs, October 2014–September 2017. *MMWR Morb Mortal Wkly Rep* 2018;67:541–6.

Community-Based Services to Improve Testing and Linkage to Care Among Non-U.S.-Born Persons with Chronic Hepatitis B Virus Infection — Three U.S. Programs, October 2014–September 2017

Aaron M. Harris, MD^{1,6}; Ruth Link-Gelles, PhD^{1,6}; Karen Kim, MD²; Edwin Chandrasekar, MBA²; Su Wang, MD³; Nicole Bannister, MPH³; Perry Pong, MD⁴; Eric Chak, MD⁵; Moon S. Chen, Jr., PhD⁵; Christopher Bowlus, MD⁵; Noele P. Nelson, MD, PhD^{1,6}

Among an estimated 850,000 to 2.2 million persons with chronic hepatitis B virus (HBV) infection in the United States, 70% are non-U.S.-born (1,2). All patients require linkage to care, and approximately 20%–40% require antiviral treatment (3).

INSIDE

- 547 Outbreaks Associated with Treated Recreational Water — United States, 2000–2014
- 552 Trends in Antiretroviral Therapy Eligibility and Coverage Among Children Aged <15 Years with HIV Infection — 20 PEPFAR-Supported Sub-Saharan African Countries, 2012–2016
- 556 Cholera Epidemic — Lusaka, Zambia, October 2017–May 2018
- 560 Notes from the Field: Outbreak of *Vibrio cholerae* Associated with Attending a Funeral — Chegutu District, Zimbabwe, 2018
- 562 Notes from the Field: Investigation of an Outbreak of *Salmonella* Paratyphi B Variant L(+) tartrate + (Java) Associated with Ball Python Exposure — United States, 2017
- 565 QuickStats

Continuing Education examination available at https://www.cdc.gov/mmwr/cme/conted_info.html#weekly.



Without treatment, one in four persons chronically infected with HBV will die prematurely from liver failure, liver cirrhosis, or hepatocellular carcinoma (4). To mitigate morbidity and mortality, CDC funded a cooperative agreement to develop hepatitis B testing and linkage-to-care programs serving non-U.S.-born persons during October 2014–September 2017. This report describes each program's operational services and partnerships with primary care centers, community-based organizations, and public health departments to recruit non-U.S.-born persons for HBV testing using the hepatitis B surface antigen (HBsAg) and link those whose test results were positive to HBV-directed care (medical visit attendance with monitoring of HBV DNA and liver enzyme tests). Among 10,152 program participants, 757 (7.5%) were HBsAg-positive, indicative of chronic HBV infection; among these, 643 (85%) attended ≥ 1 medical visit, 587 (78%) received HBV-directed care, and 137 (18%) were prescribed antiviral treatment. Among 273 household contacts of HBsAg-positive persons, 39 (14%) had positive test results for HBsAg. Prevalence of current HBV infection was high in this non-U.S.-born population and among household and sexual contacts of HBV-infected persons. HBV testing and linkage to care can be achieved through partnerships with community organizations, health centers, and public health departments.

HBV testing and linkage-to-care programs serving non-U.S.-born populations were located at a nongovernmental agency in Chicago, Illinois; community health centers in Livingston, New Jersey and New York City, New York; and an

academic health center in Sacramento, California. Programs partnered with community-based organizations (CBOs), medical clinics (federally qualified health centers, primary care/specialists) and public health departments to implement various community-based services (Supplementary Table; <https://stacks.cdc.gov/view/cdc/53787>). Programs performed HBV screening by testing for HBsAg; persons whose test results were positive received a second HBsAg test 6 months later to confirm chronic HBV infection. Testing for antibody (total or immunoglobulin G [IgG]) to hepatitis B core antigen (anti-HBc) and antibody to hepatitis B surface antigen (anti-HBs) was performed when feasible. Linkage to care was defined as documentation of at least one medical visit. Community-based services used to facilitate linkage to care were qualitatively assessed and included community screening events, clinical decision support tools in the electronic medical record (EMR), including flagging of charts of patients who were potentially at high risk for infection, provider education and feedback, and patient navigation, which was defined as individualized efforts to assist patients in accessing health care services (5).

Two programs (Chicago and Livingston/New York City) participated in HBV testing and vaccination of household contacts of persons who tested positive for HBsAg. These household contacts were offered HBV testing, and those whose test results were HBsAg-positive were linked to care; persons whose test results were HBsAg-negative with positive anti-HBs results (indicative of immunity through immunization or resolved infection) were reassured; and persons whose test

The *MMWR* series of publications is published by the Center for Surveillance, Epidemiology, and Laboratory Services, Centers for Disease Control and Prevention (CDC), U.S. Department of Health and Human Services, Atlanta, GA 30329-4027.

Suggested citation: [Author names; first three, then et al., if more than six.] [Report title]. *MMWR Morb Mortal Wkly Rep* 2018;67:[inclusive page numbers].

Centers for Disease Control and Prevention

Robert R. Redfield, MD, *Director*
 Anne Schuchat, MD, *Principal Deputy Director*
 Leslie Dauphin, PhD, *Acting Associate Director for Science*
 Joanne Cono, MD, ScM, *Director, Office of Science Quality*
 Chesley L. Richards, MD, MPH, *Deputy Director for Public Health Scientific Services*
 Michael F. Iademarco, MD, MPH, *Director, Center for Surveillance, Epidemiology, and Laboratory Services*

MMWR Editorial and Production Staff (Weekly)

Charlotte K. Kent, PhD, MPH, *Acting Editor in Chief, Executive Editor*
 Jacqueline Gindler, MD, *Editor*
 Mary Dott, MD, MPH, *Online Editor*
 Teresa F. Rutledge, *Managing Editor*
 Douglas W. Weatherwax, *Lead Technical Writer-Editor*
 Glenn Damon, Soumya Dunworth, PhD, Teresa M. Hood, MS,
Technical Writer-Editors

Martha F. Boyd, *Lead Visual Information Specialist*
 Maureen A. Leahy, Julia C. Martinroe,
 Stephen R. Spriggs, Tong Yang,
Visual Information Specialists
 Quang M. Doan, MBA, Phyllis H. King,
 Terraye M. Starr, Moua Yang,
Information Technology Specialists

MMWR Editorial Board

Timothy F. Jones, MD, *Chairman*
 Matthew L. Boulton, MD, MPH
 Virginia A. Caine, MD
 Katherine Lyon Daniel, PhD
 Jonathan E. Fielding, MD, MPH, MBA
 David W. Fleming, MD

William E. Halperin, MD, DrPH, MPH
 King K. Holmes, MD, PhD
 Robin Ikeda, MD, MPH
 Rima F. Khabbaz, MD
 Phyllis Meadows, PhD, MSN, RN
 Jewel Mullen, MD, MPH, MPA

Jeff Niederdeppe, PhD
 Patricia Quinlisk, MD, MPH
 Patrick L. Remington, MD, MPH
 Carlos Roig, MS, MA
 William L. Roper, MD, MPH
 William Schaffner, MD

results were negative for all three HBV seromarkers (susceptible to infection) were offered hepatitis B vaccination (3-dose series over 6 months).

Among persons whose test results were positive for HBsAg, demographic characteristics, including sex, year of birth, race/ethnicity, health insurance status, and country of birth were collected, as were HBV-specific linkage-to-care indicators, including documentation of two medical visits (retention in care), and HBV-directed care, including monitoring HBV DNA, alanine aminotransferase, and hepatitis B e antigen (engaged in care). Information on diagnosis of hepatocellular carcinoma and liver cirrhosis was collected. Risk factor data were collected through voluntary questionnaires. A descriptive analysis was performed, and odds ratios with 95% confidence intervals were calculated using logistic regression.

Among 10,152 program participants, 757 (7.5%) had test results that were positive for HBsAg, indicating the presence of chronic HBV infection. The median age of these patients was 40 years (interquartile range 32–53 years); 344 (45%) were female, 602 (80%) were Asian, and 122 (16%) were black (Table). The most frequently reported countries of origin of participants were China (32%), Vietnam (16%), Myanmar (8%), Taiwan (7%), and Laos (3%). Among the 757 persons whose test results were positive for HBsAg, 634 (84%) attended ≥ 1 medical visit, 587 (78%) received HBV-directed care, 430 (57%) attended ≥ 2 medical visits, and 137 (18%) were prescribed antiviral therapy (Figure). Among HBsAg-positive participants, 123 (22%) were not linked to care, either because they received care in a different health system or were lost to follow-up. Nine (1.2%) persons received a diagnosis of hepatocellular carcinoma, and liver cirrhosis was diagnosed in 17 (2.2%). Among 8,837 participants who received anti-HBc testing, 2,832 (32%) tested positive, and among 7,421 tested for anti-HBs, 4,284 (58%) tested positive.

All three programs implemented community screening events, patient navigation, and EMR strategies. Chicago developed a patient navigation program; Livingston/New York City implemented a provider education and feedback curriculum; and Sacramento used the EMR to flag patients by Asian surname for HBV testing and to link HBsAg-positive patients identified in the EMR to care management to facilitate linkage to care.

HBsAg-positive persons who had health insurance were more likely to receive HBV-directed care than were those who were uninsured (Table). Antiviral treatment was more likely to be prescribed for those HBsAg-positive persons who were men, aged ≥ 50 years, who had liver cirrhosis or hepatocellular carcinoma, or who had a family history of HBV infection or hepatocellular carcinoma (Table).

Among 273 household contacts of HBsAg-positive participants, 39 (14%) had positive test results for HBsAg, 83 (30%) had negative test results for HBsAg and positive results for anti-HBc (immune because of resolved infection), and 101 (37%) were anti-HBs-positive and anti-HBc-negative (immune because of vaccination). Fifty (18%) household contacts had negative test results for all three HBV seromarkers, indicating susceptibility; among these persons, 1, 2, and 3 doses of hepatitis B vaccine were received by the end of the project by 37 (74%), 32 (64%), and 25 (50%) participants, respectively.

Discussion

In this analysis of community-based services used by three HBV testing and linkage-to-care programs that implement CDC's HBV testing recommendations (6) and link persons with chronic HBV infection to care, the overall prevalence of HBV infection among participants was 7.5%. Services used to link 78% of patients to HBV-directed care included community screening events, patient navigation, use of the EMR, and provider education and feedback. A 14% HBV infection rate was observed among household contacts of persons with HBV infection.

HBV testing and linkage to care was accomplished through targeted public health interventions, including partnerships with public health, CBOs, and health centers. Chicago developed partnerships with 11 CBOs, two health centers (a network of federally qualified health centers and a refugee health center), and two public health departments; each site implemented a clinic-based patient navigation program to facilitate access to care for persons with HBV infection. The Livingston/New York City program held HBV testing events in collaboration with community partners, local health departments, and its hospital; the program reported that combining community screening events with general health fairs led to more persons receiving HBV screening. Livingston developed a free HBV testing coupon for testing at the affiliated laboratory; HBsAg-positive patients received care at a primary care center (Livingston) and a federally qualified health center (New York City). Clinics offered trainings in HBV testing and linkage to care, followed by provider feedback to assess performance. Partnerships with local health departments improved HBV case reporting and contact testing. The program in Sacramento implemented community services, including HBV testing events at health fairs and faith-based centers; HBsAg-positive persons with insurance received HBV care within the health system, and those without insurance received care at student-run clinics.

EMR strategies have previously been documented to increase HBV testing rates (7); the program in Chicago included EMR prompts to identify populations at high risk, the program

TABLE. Percentage of HBsAg-positive persons participating in three programs to increase hepatitis B testing and linkage to care are who received HBV-directed care* and treatment, by demographic characteristics — Sacramento, California; Livingston, New Jersey and New York City, New York; and Chicago, Illinois, October 2014–September 2017

Demographic characteristic	HBsAg-positive	Received HBV-directed care*		Prescribed antiviral	
	No. (% of total)	No. (%)	Unadjusted OR (95% CI)	No. (%)	Unadjusted OR (95% CI)
Total	757 (100)	587 (78)	N/A	137 (18)	N/A
Sex					
Female	344 (45)	276 (80)	Referent	50 (15)	Referent
Male	413 (55)	349 (85)	1.3 (0.9–1.8)	87 (21)	1.6 (1.1–2.4)
Age group (yrs)					
<50	518 (68)	423 (82)	Referent	83 (16)	Referent
≥50	239 (32)	164 (69)	0.5 (0.3–0.7)	54 (23)	2.0 (1.4–3.0)
Race					
White	17 (2)	14 (82)	Referent	2 (12)	Referent
Black/African	122 (16)	83 (68)	0.5 (0.1–1.7)	7 (6)	2.3 (0.5–10.4)
Asian	602 (80)	474 (79)	0.8 (0.2–2.8)	122 (20)	0.5 (0.1–2.4)
Native American/Pacific Islander	3 (0)	3 (100)	—†	1 (33)	3.8 (0.2–62.8)
Other/Unknown	13 (2)	13 (100)	—†	5 (38)	—†
Health insurance					
None	121 (16)	68 (56)	0.3 (0.2–0.4)	19 (16)	0.9 (0.5–1.7)
Private	210 (28)	174 (83)	Referent	41 (20)	Referent
Public	334 (44)	289 (87)	1.3 (0.8–2.1)	56 (17)	0.8 (0.5–1.3)
Missing	92 (12)	56 (61)	N/A	21 (23)	N/A
Primary language					
English	229 (30)	178 (78)	1.0 (0.7–1.4)	52 (23)	1.4 (0.9–2.0)
Not English (yes to any other language)	520 (69)	406 (78)	Referent	84 (16)	Referent
Missing	8 (1)	3 (38)	N/A	1 (13)	N/A
Country of origin					
U.S.-born	16 (2)	13 (81)	1.3 (0.4–4.5)	3 (19)	1.2 (0.3–4.3)
Non-U.S.-born	732 (97)	567 (77)	Referent	133 (18)	Referent
Missing	9 (1)	7 (78)	N/A	1 (11)	N/A
Liver disease					
Cirrhosis (vs. no cirrhosis)	18 (2)	17 (94)	1.3 (0.1–9.9)	14 (78)	13.1 (4.2–40.6)
HCC (vs. no HCC)	9 (1)	9 (100)	—†	7 (78)	24.6 (3.0–202.4)
Neither cirrhosis nor HCC	469 (62)	439 (94)	N/A	98 (21)	N/A
Missing	264 (35)	128 (48)	N/A	24 (9)	N/A
Family history					
Family history of HBV (vs. no family history of HBV)	190 (25)	158 (83)	1.1 (0.7–1.7)	45 (24)	1.7 (1.1–2.7)
Family history of HCC (vs. no family history of HCC)	66 (9)	53 (80)	0.9 (0.5–1.7)	20 (30)	2.2 (1.2–4.0)
No family history of HBV/HCC	364 (48)	303 (83)	N/A	59 (16)	N/A
Missing	182 (24)	111 (61)	N/A	29 (16)	N/A
Risk factors (other than non-U.S.-born)					
No risk factors reported	485 (64)	409 (84)	Referent	82 (17)	Referent
At least one risk factor [§] reported	139 (18)	124 (89)	1.5 (0.9–2.8)	37 (27)	1.8 (1.1–2.7)
No risk factor data available	133 (18)	54 (41)	N/A	18 (14)	N/A

Abbreviations: CI = confidence interval; HBsAg = hepatitis B surface antigen; HBV = hepatitis B virus; HCC = hepatocellular carcinoma; N/A = not applicable; OR = odds ratio.

* Received testing for hepatitis B e antigen, hepatitis B virus DNA, and alanine transaminase.

† Insufficient cell size to calculate OR.

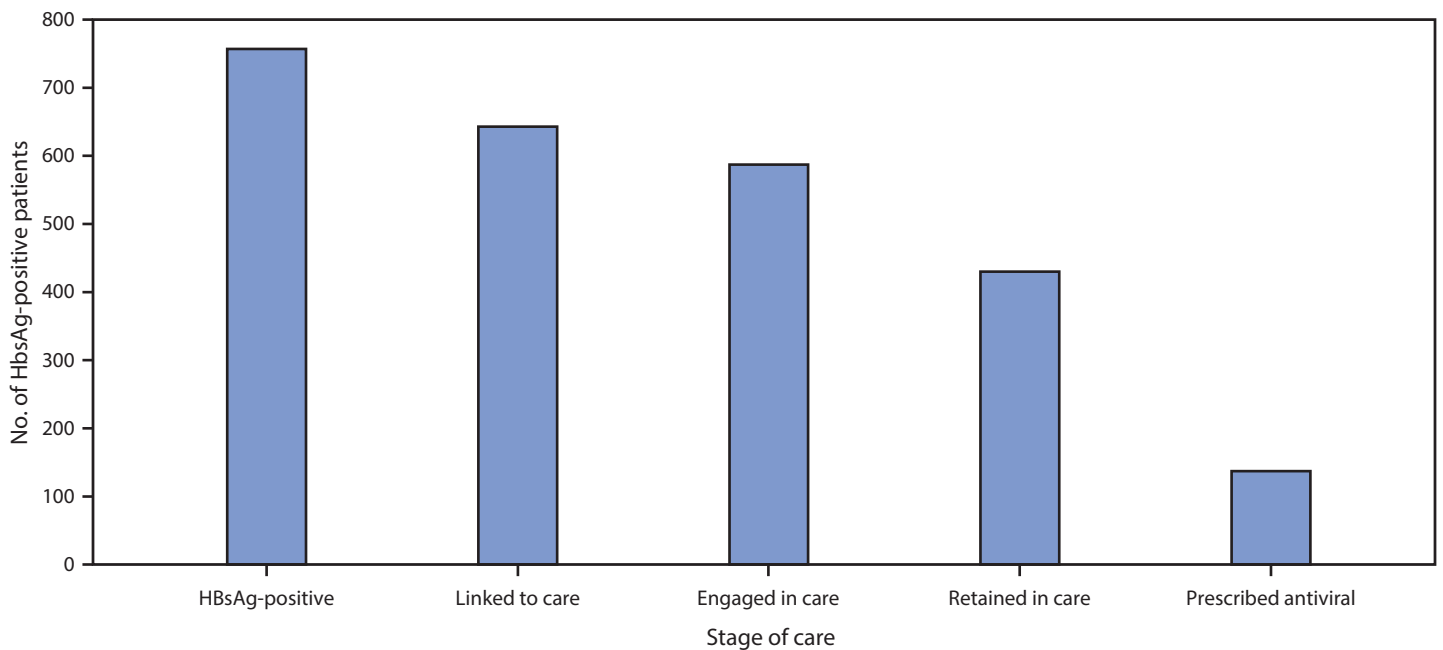
§ Injection drug use, men who have sex with men, household contact, sexual contact, multiple sex partners, human immunodeficiency virus-positive.

in Livingston modified their EMR to include HBV testing order sets (clinical decision support tools that include laboratory tests recommended for evaluating patients with chronic HBV infection), and the program in Sacramento developed an algorithm to flag charts of Asian persons to recommend testing as well as monthly EMR querying of HBsAg-positive patients to identify those not currently in care. A critical linkage-to-care strategy was the use of patient navigators at all sites (5,8). Patient navigators received training about HBV disease effects,

cultural competency, insurance evaluation, the marketplace insurance application process, development of bilingual education materials, and scheduling medical appointments and patients' guidance through health systems (5).

An estimated 20%–40% of HBsAg-positive persons require antiviral treatment (3), and this initiative demonstrated that 18% of identified HBsAg-positive patients received antiviral treatment. Reasons for not treating might include cost, access to care, patient preferences, or variation in clinical guidelines used (9,10).

FIGURE. Hepatitis B linkage-to-care continuum* — three U.S. programs, October 2014–September 2017



Abbreviation: HbsAg = hepatitis B surface antigen.

* Stages in care continuum are the following: linked to care = attended ≥ 1 medical visit; engaged in care = received hepatitis B e antigen, hepatitis B virus DNA, and alanine transaminase testing; retained in care = attended ≥ 2 medical visits; prescribed antiviral = given hepatitis B antiviral treatment (approximately 20%-40% of patients with chronic hepatitis B virus infection require treatment).

Summary

What is already known about this topic?

Among the 850,000 to 2.2 million U.S. residents with chronic hepatitis B virus (HBV) infection, approximately 70% are non-U.S.-born; nearly two thirds are unaware of their infection status, and <30% are linked to care and treatment.

What is added by this report?

CDC funded three programs to develop hepatitis B testing and linkage-to-care programs serving non-U.S.-born persons during 2014–2017; 78% of persons with chronic HBV infection were linked to care using community-based services. HBV infection rate among household contacts of HbsAg-positive persons was 14%.

What are the implications for public health practice?

HBV testing and linkage to care can be achieved among hard-to-reach populations through partnerships with community organizations, health centers, and public health departments.

The 14% HBV infection rate among household contacts in this population is higher than the 0.3% reported in the general population (2), highlighting the importance of screening household contacts of persons with HBV infection. Persons who are not immune are at risk for infection, and in these programs, 74% of susceptible household contacts received at least 1 dose of hepatitis B vaccine.

The findings in this report are subject to at least four limitations. First, each program used services specific to their catchment population, which limits generalizability. Second, linkage-to-care indicators might be underestimated because some participants had pending appointments that were not included at the end of the project period. Third, ascertainment of factors associated with progression in the care continuum is limited because of missing data (not all characteristics were documented). Finally, the proportion of treatment-eligible persons determined by clinical guidelines was not assessed.

HBV testing and linkage to care can be achieved among hard-to-reach populations through partnerships with community organizations, health centers, and public health departments. Household and sexual contacts of HBV-infected persons should be tested and linked to care.

Acknowledgements

Geoff Beckett, Natalie Blackburn, Gilberto Ramirez, Division of Viral Hepatitis, CDC; Fornessa Randall, Alia Ryan, Matt Johnson, Chicago, Illinois; Ruth Brogden, Wen-chi Chen, Judy Yuen, Livingston, New Jersey; Amy Tang, Janice Lyu, New York, New York; Duke Letran, Ann Sanchez, Julie Ha Thi Dang, Sacramento, California; all programs and staff members.

Conflict of Interest

Su Wang reports a FOCUS grant from Gilead Sciences, outside the submitted work. Moon Chen, Jr. reports personal fees from Gilead Sciences, outside the submitted work. No other conflicts of interest were reported.

¹Division of Viral Hepatitis, CDC; ²Asian Health Coalition, Chicago, Illinois; ³Saint Barnabas Medical Center, Center for Asian Health, Livingston, New Jersey; ⁴Charles B. Wang Community Health Center, New York, New York; ⁵Davis School of Medicine, University of California, Sacramento, California; ⁶United States Public Health Service, Rockville, Maryland.

Corresponding author: Aaron M. Harris, amharris@cdc.gov, 404-718-8541.

References

1. Kowdley KV, Wang CC, Welch S, Roberts H, Brosgart CL. Prevalence of chronic hepatitis B among foreign-born persons living in the United States by country of origin. *Hepatology* 2012;56:422–33. <https://doi.org/10.1002/hep.24804>
2. Roberts H, Kruszon-Moran D, Ly KN, et al. Prevalence of chronic hepatitis B virus (HBV) infection in U.S. households: National Health and Nutrition Examination Survey (NHANES), 1988–2012. *Hepatology* 2016;63:388–97. <https://doi.org/10.1002/hep.28109>
3. Cohen C, Holmberg SD, McMahon BJ, et al. Is chronic hepatitis B being undertreated in the United States? *J Viral Hepat* 2011;18:377–83. <https://doi.org/10.1111/j.1365-2893.2010.01401.x>
4. McMahon BJ. The natural history of chronic hepatitis B virus infection. *Hepatology* 2009;49(Suppl):S45–55. <https://doi.org/10.1002/hep.22898>
5. Asian Health Coalition. Hepatitis B patient navigator manual. Chicago, Illinois: Asian Health Coalition; 2015. <http://www.asianhealth.org/resources/ahc-publications/hep-b-navigator-guide-2015/>
6. Weinbaum CM, Williams I, Mast EE, et al. Recommendations for identification and public health management of persons with chronic hepatitis B virus infection. *MMWR Recomm Rep* 2008;57(No. RR-8).
7. Hsu L, Bowlus CL, Stewart SL, et al. Electronic messages increase hepatitis B screening in at-risk Asian American patients: a randomized, controlled trial. *Dig Dis Sci* 2013;58:807–14. <https://doi.org/10.1007/s10620-012-2396-9>
8. Chandrasekar E, Song S, Johnson M, et al. A novel strategy to increase identification of African-born people with chronic hepatitis B virus infection in the Chicago metropolitan area, 2012–2014. *Prev Chronic Dis* 2016;13:E118. <https://doi.org/10.5888/pcd13.160162>
9. Uribe LA, Nguyen N, Kim L, et al. Rates of treatment eligibility in follow-up of patients with chronic hepatitis B (CHB) across various clinical settings who were initially ineligible at presentation. *Dig Dis Sci* 2016;61:618–25. <https://doi.org/10.1007/s10620-015-3982-4>
10. Nguyen VG, Wan K, Trinh HN, Li J, Zhang JQ, Nguyen MH. Chronic hepatitis B treatment eligibility and actual treatment rates in patients in community gastroenterology and primary care settings. *J Clin Gastroenterol* 2015;49:145–9. <https://doi.org/10.1097/MCG.000000000000132>

Outbreaks Associated with Treated Recreational Water — United States, 2000–2014

Michele C. Hlavsa, MPH¹; Bryanna L. Cikesh, MPH^{1,2}; Virginia A. Roberts, MSPH¹; Amy M. Kahler, MS¹; Marissa Vigar, MPH^{1,2}; Elizabeth D. Hilborn, DVM³; Timothy J. Wade, PhD³; Dawn M. Roellig, PhD¹; Jennifer L. Murphy, PhD¹; Lihua Xiao, DVM, PhD¹; Kirsten M. Yates, MPH¹; Jasen M. Kunz, MPH⁴; Matthew J. Arduino, DrPH⁵; Sujan C. Reddy, MD⁵; Kathleen E. Fullerton, MPH¹; Laura A. Cooley, MD⁶; Michael J. Beach, PhD¹; Vincent R. Hill, PhD¹; Jonathan S. Yoder, MPH¹

Outbreaks associated with exposure to treated recreational water can be caused by pathogens or chemicals in venues such as pools, hot tubs/spas, and interactive water play venues (i.e., water playgrounds). During 2000–2014, public health officials from 46 states and Puerto Rico reported 493 outbreaks associated with treated recreational water. These outbreaks resulted in at least 27,219 cases and eight deaths. Among the 363 outbreaks with a confirmed infectious etiology, 212 (58%) were caused by *Cryptosporidium* (which causes predominantly gastrointestinal illness), 57 (16%) by *Legionella* (which causes Legionnaires' disease, a severe pneumonia, and Pontiac fever, a milder illness with flu-like symptoms), and 47 (13%) by *Pseudomonas* (which causes folliculitis ["hot tub rash"] and otitis externa ["swimmers' ear"]). Investigations of the 363 outbreaks identified 24,453 cases; 21,766 (89%) were caused by *Cryptosporidium*, 920 (4%) by *Pseudomonas*, and 624 (3%) by *Legionella*. At least six of the eight reported deaths occurred in persons affected by outbreaks caused by *Legionella*. Hotels were the leading setting, associated with 157 (32%) of the 493 outbreaks. Overall, the outbreaks had a bimodal temporal distribution: 275 (56%) outbreaks started during June–August and 46 (9%) in March. Assessment of trends in the annual counts of outbreaks caused by *Cryptosporidium*, *Legionella*, or *Pseudomonas* indicate mixed progress in preventing transmission. Pathogens able to evade chlorine inactivation have become leading outbreak etiologies. The consequent outbreak and case counts and mortality underscore the utility of CDC's Model Aquatic Health Code (<https://www.cdc.gov/mahc>) to prevent outbreaks associated with treated recreational water.

An outbreak associated with recreational water is the occurrence of similar illnesses in two or more persons, epidemiologically linked by location and time of exposure to recreational water or to pathogens or chemicals aerosolized or volatilized from recreational water into the surrounding air. Public health officials in the 50 states, the District of Columbia, U.S. territories, and Freely Associated States* voluntarily report outbreaks associated with recreational water to CDC. This report focuses on data in two groups of outbreaks associated with treated recreational water: 1) those that started during 2000–2012 and were previously summarized (1) and 2) those that started during 2013–2014 and were

electronically reported to the Waterborne Disease and Outbreak Surveillance System (WBDOSS)[†] by December 31, 2015 (<https://www.cdc.gov/healthywater/surveillance/rec-water-tables-figures.html>). Data on each outbreak included case count,[§] number of deaths, etiology, setting (e.g., hotel) and venue (e.g., pool, hot tub/spa) where the exposure occurred, and earliest illness onset date. Poisson regression analysis was conducted to assess the trend in the annual counts of outbreaks, except when overdispersion required the use of negative binomial regression analysis.

During 2000–2014, public health officials from 46 states and Puerto Rico reported 493 outbreaks associated with treated recreational water, which resulted in at least 27,219 cases (Table) and eight deaths. Etiology was confirmed for 385 (78%) outbreaks. Among these, 363 (94%) were caused by pathogens (including four caused by both *Cryptosporidium* and *Giardia*) and resulted in at least 24,453 cases. Twenty-two (6%) outbreaks were caused by chemicals and resulted in at least 1,028 cases. Among the 363 outbreaks with a confirmed infectious etiology, 212 (58%) were caused by *Cryptosporidium*, 57 (16%) by *Legionella*, and 47 (13%) by *Pseudomonas*. Of the 24,453 cases, 21,766 (89%) were caused by *Cryptosporidium*, 920 (4%) by *Pseudomonas*, and 624 (3%) by *Legionella*. Of the 212 outbreaks caused by *Cryptosporidium*, 24 (11%) each affected >100 persons; four of these outbreaks each affected ≥2,000 persons. At least six of the eight deaths,[¶] which all occurred after 2004, were in persons affected by outbreaks caused by *Legionella*.

Hotels** (i.e., hotels, motels, lodges, or inns) were the leading setting associated with 157 (32%) of the 493 outbreaks. Of

[†] 2013–2014 were the last years for which finalized data were available. For more information on WBDOSS, visit <https://www.cdc.gov/healthywater/surveillance/index.html>; outbreaks resulting from recreational water exposures on cruise ships are not reported to WBDOSS.

[§] Based on the estimated number of primary cases. For outbreaks that started before 2009, if both the actual and estimated case counts were reported, the estimated case count was used if the population was sampled randomly or the estimated count was calculated by applying the attack rate to a standardized population.

[¶] The two remaining deaths were in persons affected by an outbreak caused by an etiology that was unidentified but suspected to be *Legionella*.

** Other settings: community/municipality/public park (115 [23%] outbreaks), club/recreational facility (68 [14%]), waterpark (54 [11%]), private residence (31 [6%]), subdivision/neighborhood (21 [4%]), school/college/university (14 [3%]), unidentified (13 [3%]), camp/cabin setting (nine [2%]), child care/daycare center/day camp (six [1%]), health care facility (three [1%]), and other (two [0%]). Categories were not consistently used or defined over the study period.

* Includes Federated States of Micronesia, Marshall Islands, and Republic of Palau.

the 157 hotel-related outbreaks, 94 (60%)^{††} had a confirmed infectious etiology, 40 (43%) were caused by *Pseudomonas*, 29 (31%) by *Legionella*, and 17 (18%) by *Cryptosporidium*.^{§§} Sixty-five (41%) hotel-related outbreaks were associated with hot tubs/spas, and 47 (30%) started during February–March. Among all 493 outbreaks, a bimodal temporal distribution was observed. The 275 (56%) outbreaks that started during June–August were predominantly caused by *Cryptosporidium*, whereas the 46 (9%) that started in March were predominantly caused by an unidentified etiology or pathogens other than *Cryptosporidium* (Figure 1). Negative binomial regression analysis indicated that during 2000–2007, the annual number of outbreaks caused by *Cryptosporidium* increased by an average of 25% (95% confidence interval [CI] = 7%–45%) per year (Figure 2). No significant trend was found after 2007.^{¶¶} Poisson regression analysis indicated that during 2000–2014 the annual number of outbreaks caused by *Legionella* increased by an average of 13% (95% CI = 6%–21%) per year, and the annual number of *Pseudomonas* folliculitis outbreaks (a total of 41 outbreaks during 2000–2014) decreased by an average of 22% (95% CI = 14%–29%) per year.^{***}

Discussion

Approximately 500 outbreaks associated with treated recreational water occurred in the United States during 2000–2014. The most frequently reported outbreak setting was hotels. Approximately half of the outbreaks started during June–August, followed by a smaller peak in March. The second peak might reflect swimming's transition from an only-summertime to a year-round activity, as the relative number of indoor versus outdoor treated recreational water venues increases. The aquatics sector and public health can voluntarily adopt CDC's Model Aquatic Health Code to improve the design, construction, operation, and maintenance of public (nonbackyard) treated recreational water venues to prevent illness and injury.

^{††} Approximately half (60 [56%]) of the 108 outbreaks with an unidentified etiology were associated with the hotel setting. Among the 60 outbreaks, 23 (38%) started during March–April; 41 (68%) were outbreaks of skin-related illness.

^{§§} The remaining eight outbreaks were caused by norovirus (five [5%] outbreaks), *Bacillus* (one [1%]), nontuberculous mycobacterium (one [1%]), and *Staphylococcus* (one [1%]).

^{¶¶} The 2007 number of outbreaks associated with treated recreational water and caused by *Cryptosporidium* (40), and thus, of outbreaks overall might be outliers. For 2007, Utah reported a statewide outbreak primarily associated with treated recreational water and caused by *Cryptosporidium*; neighboring states reported additional outbreaks associated with recreational water and caused by *Cryptosporidium*. All of these individual outbreaks might have been a single multistate outbreak. <https://www.cdc.gov/mmwr/preview/mmwrhtml/ss6012a1.htm>.

^{***} Because of concerns that folliculitis might not be cultured, which means the etiology cannot be identified, a Poisson regression analysis was conducted to assess the annual number of outbreaks of skin-related illness caused by *Pseudomonas* or an unidentified etiology. The annual number of outbreaks decreased by 5% (95% CI = 1%–9%).

TABLE. Number of outbreaks associated with treated recreational water, total and median number of cases, by etiology — United States, 2000–2014

Etiology	No. (%) of outbreaks	No. (%) of cases	Median no. (range) of cases per outbreak
Total	493 (100)	27,219 (100)	10 (2–5,697)
Bacterium	129 (26)	1,899 (7)	6 (2–119)
<i>Bacillus</i>	1 (0)	20 (0)	20 (—*)
<i>Campylobacter</i>	2 (0)	10 (0)	5 (4–6)
<i>Escherichia coli</i>	6 (1)	86 (0)	12.5 (2–31)
<i>Legionella</i>	57 (12)	624 (2)	3 (2–107)
MRSA	1 (0)	10 (0)	10 (—)
Nontuberculous mycobacteria	2 (0)	14 (0)	7 (3–11)
<i>Pseudomonas</i>	47 (10)	920 (3)	10 (2–119)
<i>Salmonella</i>	1 (0)	5 (0)	5 (—)
<i>Shigella</i>	11 (2)	207 (1)	12 (3–56)
<i>Staphylococcus</i>	1 (0)	3 (0)	3 (—)
Parasite	220 (45)	21,976 (81)	14 (2–5,697)
<i>Cryptosporidium</i>	208 (42)	21,626 (79)	14.5 (2–5,697)
<i>Giardia</i>	8 (2)	210 (1)	8.5 (3–149)
<i>Cryptosporidium, Giardia</i>	4 (1)	140 (1)	37 (3–63)
Virus	14 (3)	578 (2)	36 (6–140)
Echovirus	1 (0)	36 (0)	36 (—)
Norovirus	13 (3)	542 (2)	36 (6–140)
Chemical	22 (4)	1,028 (4)	17.5 (2–665)
Excess chlorine, disinfection by-product, or altered pool chemistry	22 (4)	1028 (4)	17.5 (2–665)
Unidentified	108 (22)	1,738 (6)	7.5 (2–280)

Abbreviation: MRSA = methicillin-resistant *Staphylococcus aureus*.

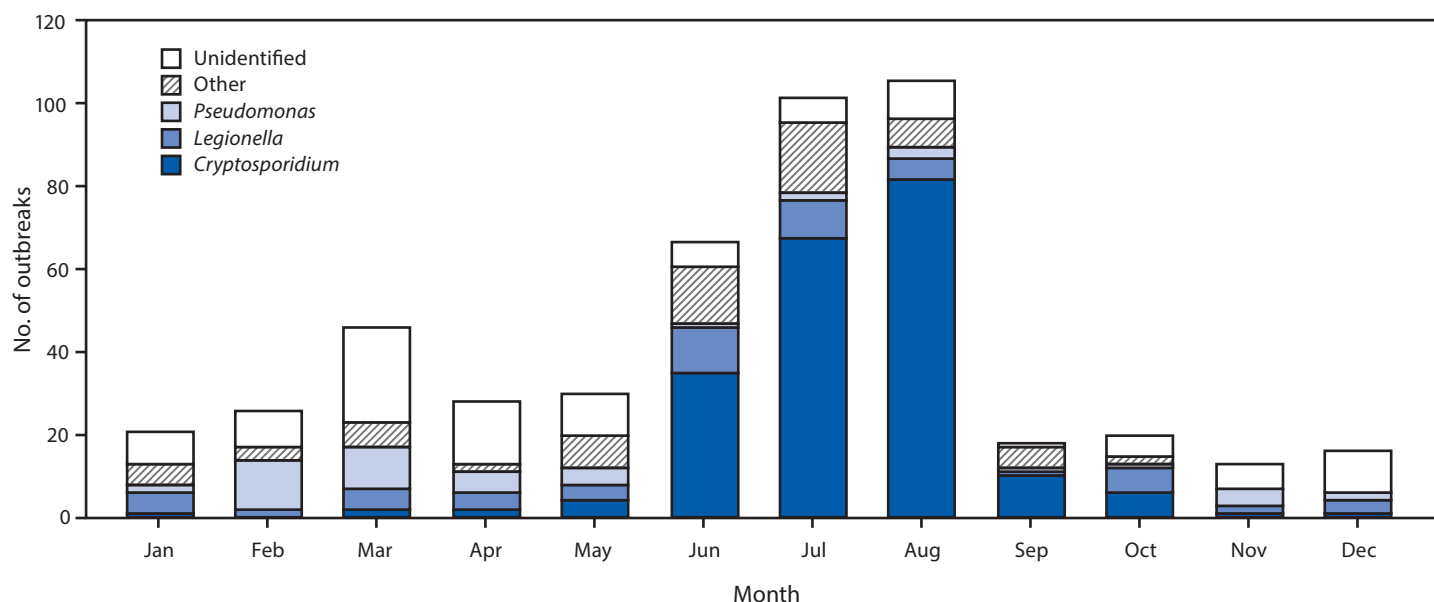
* Not applicable because only one outbreak was nationally reported for that etiology.

Chlorine is the primary barrier to the transmission of pathogens in treated recreational water. At CDC-recommended concentrations of at least 1 ppm,^{†††} free available chlorine inactivates most pathogens within minutes although extremely chlorine-tolerant *Cryptosporidium* can survive for >7 days (2,3). *Cryptosporidium* is transmitted when a diarrheal incident (i.e., a high-risk *Cryptosporidium* contamination event) occurs in the water and the contaminated water is ingested. The parasite's extreme chlorine tolerance enables it to persist in water, cause outbreaks that sicken thousands, and spread to multiple recreational water venues and other settings (e.g., child care settings). Rates of individual cases caused by *Cryptosporidium* peak in the summer, coinciding with the summer swim season (4).

In contrast, *Legionella* and *Pseudomonas* are effectively controlled by halogens (e.g., chlorine and bromine) in well-maintained treated venues. However, because these pathogens can persist in biofilm (where microbial cells inhabit a primarily polysaccharide matrix, the cells cannot be removed from a surface by gentle rinsing) (5), and they are protected from inactivation and amplify when disinfectant concentrations are not properly

^{†††} At water pH ≤7.5 and temperature ≥77°F (25°C).

FIGURE 1. Number of outbreaks associated with treated recreational water (N = 493), by etiology and month — United States, 2000–2014*



* Includes outbreaks with the following etiologies: *Bacillus*, *Campylobacter*, *Escherichia coli*, methicillin-resistant *Staphylococcus aureus*, nontuberculous mycobacteria, *Salmonella*, *Shigella*, *Staphylococcus*, *Giardia*, echovirus, norovirus, or excess chlorine/disinfection by-product/alterd pool chemistry.

maintained. Approximately 20% of 13,864 routine inspections of public hot tubs/spas conducted in 16 jurisdictions in 2013 identified improper disinfectant concentrations (6). *Legionella* is typically transmitted when aerosolized water droplets (e.g., produced by hot tub/spa jets) containing this bacterium are inhaled, whereas *Pseudomonas* is transmitted when skin comes in contact with contaminated water. Multiple factors contribute to *Legionella* and *Pseudomonas* growth in hot tubs/spas, including inadequate disinfectant concentration; warm (77°F–108°F [25°C–42°C]) water temperatures (which facilitate pathogen amplification and make it difficult to maintain adequate disinfectant concentration); water aeration (which depletes halogens); and the presence of biofilm on wet venue surfaces, scale, and sediment (7). The increasing annual rate of Legionnaires' disease cases (286% during 2000–2014) (8), and possibly, the significantly increasing annual number of outbreaks caused by *Legionella*, might be associated with increasing size of susceptible populations (persons aged ≥50 years or those with chronic disease [particularly chronic lung disease] or who are immunocompromised; current or former smokers; or cancer patients), and increased *Legionella* growth in the environment, as well as increased awareness of the disease with improved testing and reporting (8). The significantly decreasing number of annual *Pseudomonas* folliculitis outbreaks might reflect an actual decrease or possibly focusing on hot tub/spa remediation to prevent further transmission rather than outbreak investigation and reporting.

If a diarrheal incident occurs in treated recreational water or an outbreak at least suspected to be caused by *Cryptosporidium* occurs,

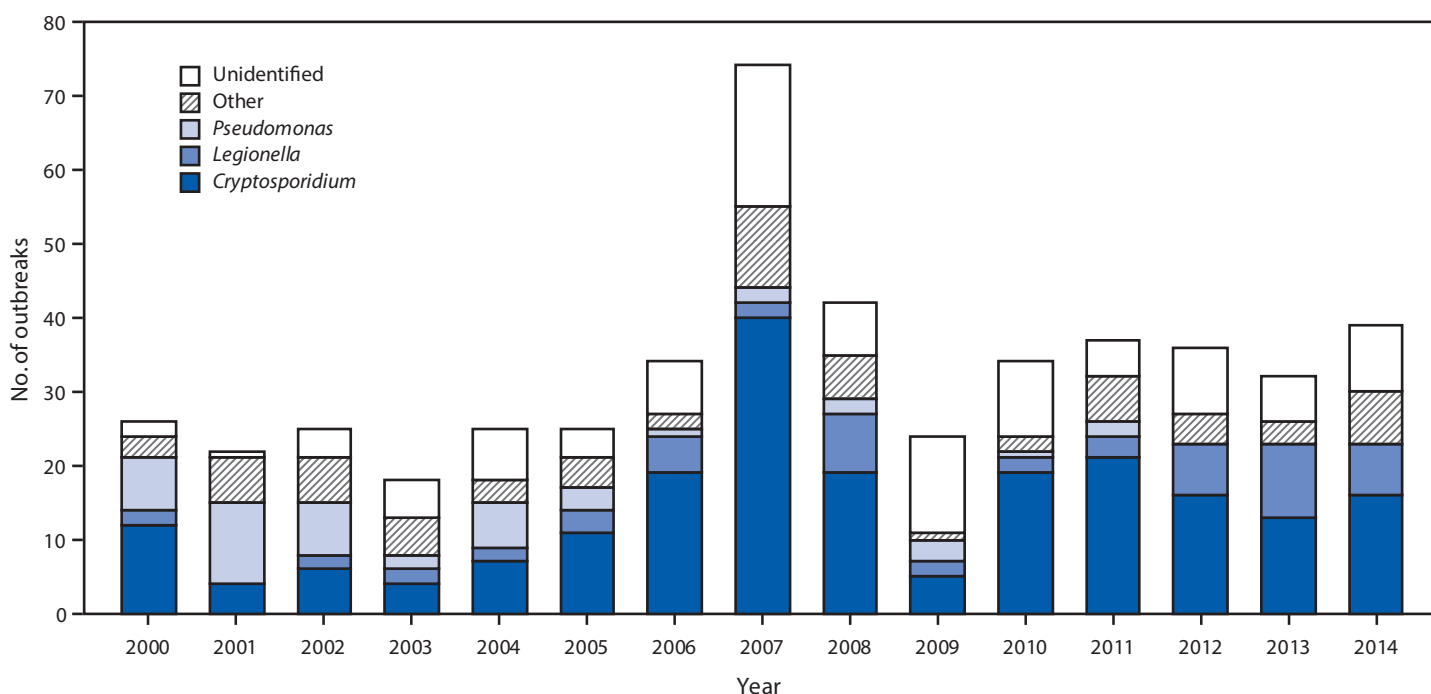
CDC recommends hyperchlorination, i.e., chlorinating water to achieve 3-log₁₀ (99.9%) *Cryptosporidium* inactivation^{§§§} (<https://www.cdc.gov/healthywater/swimming/aquatics-professionals/fec-alresponse.html>). Alternatively, ultraviolet light or ozone systems can be added to inactivate *Cryptosporidium*, particularly in venues at increased risk for contamination (e.g., those intended for children aged <5 years, who might have limited or no toileting skills). As in any public setting, treated venues in the hotel setting should be operated and maintained by a trained operator or responsible supervisor.^{¶¶¶} These and other recommendations can be found in CDC's Model Aquatic Health Code. CDC also provides specific recommendations for disinfecting hot tubs/spas contaminated with *Legionella* (<https://www.cdc.gov/legionella/downloads/hot-tub-disinfection.pdf>). Investigations of Legionnaires' disease outbreaks indicate that effective water management programs for buildings and treated recreational water venues (e.g., hot tubs/spas) at increased risk for *Legionella* growth and transmission can reduce the risk for Legionnaires' disease (8,9).

The findings in this report are subject to at least two limitations. First, the outbreak counts presented likely underestimate

^{§§§} At water pH ≤7.5 and temperature ≥77°F (25°C), 3-log₁₀ *Cryptosporidium* inactivation can be achieved in the absence of cyanuric acid (which prevents chlorine degradation by the sun's ultraviolet light but substantially delays pathogen inactivation) by maintaining free available chlorine at 20 ppm for 12.75 hours and in the presence of 1–15 ppm cyanuric acid by maintaining free available chlorine at 20 ppm for 28 hours.

^{¶¶¶} Trained operators are those who have successfully completed an approved operator training course; responsible supervisors are those who can conduct and record results of water quality testing, properly maintain water quality, perform general maintenance procedures, and identify when to close venues to protect public health.

FIGURE 2. Number of outbreaks associated with treated recreational water (N = 493), by etiology and year — United States, 2000–2014*



* Includes outbreaks with the following etiologies: *Bacillus*, *Campylobacter*, *Escherichia coli*, methicillin-resistant *Staphylococcus aureus*, nontuberculous mycobacteria, *Salmonella*, *Shigella*, *Staphylococcus*, *Giardia*, echovirus, norovirus, or excess chlorine/disinfection by-product/altering pool chemistry.

Summary

What is already known about this topic?

Outbreaks associated with treated recreational water can be caused by pathogens or chemicals.

What is added by this report?

During 2000–2014, 493 outbreaks associated with treated recreational water caused at least 27,219 cases and eight deaths. Outbreaks caused by *Cryptosporidium* increased 25% per year during 2000–2006; however, no significant trend occurred after 2007. The number of outbreaks caused by *Legionella* increased 14% per year.

What are the implications for public health practice?

The aquatics sector, public health officials, bathers, and parents of young bathers can take steps to minimize risk for outbreaks. The halting of the increase in outbreaks caused by *Cryptosporidium* might be attributable to Healthy and Safe Swimming Week campaigns.

the actual incidence, in part because of variation in public health capacity and reporting requirements across jurisdictions. Second, reporting and review procedures (e.g., increased completeness of data on outbreaks caused by *Legionella*) changed over time, which affects the ability to compare data across years.

Addressing the challenges presented by chlorine-tolerant and biofilm-associated pathogens require sustained attention to

improving design, construction, operation, and management of public treated recreational water venues. This includes educating the public. Preventing *Cryptosporidium* contamination is critical to preventing transmission. Thus, the key message to the public, particularly parents of young bathers, is “Don’t swim or let your kids swim if sick with diarrhea.” Preventing transmission of *Legionella*, *Pseudomonas*, and other chlorine-susceptible pathogens means educating bathers and parents of young bathers to check the inspection scores of public treated recreational water venues and conduct their own mini-inspection before getting into the water (e.g., measure bromine or free chlorine level and pH with test strips, which can be purchased at pool supply, hardware, and big-box stores). Potential hot tub/spa users should know whether they are at increased risk for Legionnaires’ disease, so they can choose to avoid hot tubs/spas, as indicated (<https://www.cdc.gov/legionella/downloads/fs-legionnaires.pdf>). The halting of the substantial increase in annual numbers of outbreaks caused by *Cryptosporidium* might, at least in part, be because of local, state, and federal Healthy and Safe Swimming Week (the week before Memorial Day) campaigns (10). Thus, the focus of these campaigns could regularly be expanded beyond preventing *Cryptosporidium* transmission in an effort to prevent other recreational water outbreaks.

Acknowledgments

State, territorial, local, and Freely Associated State waterborne disease coordinators, epidemiologists, and environmental health practitioners; Gordana Derado, Sarah A. Collier, Division of Foodborne, Waterborne, and Environmental Diseases, National Center for Emerging and Zoonotic Infectious Diseases, CDC.

Conflict of Interest

No conflicts of interest were reported.

¹Division of Foodborne, Waterborne, and Environmental Diseases, National Center for Emerging and Zoonotic Infectious Diseases, CDC; ²Oak Ridge Institute for Science and Education, Oak Ridge, Tennessee; ³Environmental Protection Agency, Washington, D.C.; ⁴Division of Emergency and Environmental Health Services, National Center for Environmental Health; ⁵Division of Healthcare Quality Promotion, National Center for Emerging and Zoonotic Infectious Diseases, CDC; ⁶Division of Bacterial Diseases, National Center for Immunization and Respiratory Diseases, CDC.

Corresponding author: Michele C. Hlavsa, mhlavsa@cdc.gov, 404-718-4695.

References

1. CDC. Surveillance reports for recreational water-associated disease & outbreaks. Atlanta, GA: US Department of Health and Human Services, CDC; 2017. <https://www.cdc.gov/healthywater/surveillance/rec-water-surveillance-reports.html>
2. Shields JM, Hill VR, Arrowood MJ, Beach MJ. Inactivation of *Cryptosporidium parvum* under chlorinated recreational water conditions. *J Water Health* 2008; 6:513–20. <https://doi.org/10.2166/wh.2008.068>
3. Murphy JL, Arrowood MJ, Lu X, Hlavsa MC, Beach MJ, Hill VR. Effect of cyanuric acid on the inactivation of *Cryptosporidium parvum* under hyperchlorination conditions. *Environ Sci Technol* 2015;49:7348–55. <https://doi.org/10.1021/acs.est.5b00962>
4. Painter JE, Hlavsa MC, Collier SA, Xiao L, Yoder JS; CDC. Cryptosporidiosis surveillance—United States, 2011–2012. *MMWR Suppl* 2015;64(No. Suppl 3).
5. Donlan RM. Biofilms: microbial life on surfaces. *Emerg Infect Dis* 2002;8:881–90. <https://doi.org/10.3201/eid0809.020063>
6. Hlavsa MC, Gerth TR, Collier SA, et al. Immediate closures and violations identified during routine inspections of public aquatic facilities—Network for Aquatic Facility Inspection Surveillance, five states, 2013. *MMWR Surveill Summ* 2016;65(No. SS-5). <https://doi.org/10.15585/mmwr.ss6505a1>
7. American Society of Heating, Refrigerating and Air-Conditioning Engineers. Minimizing the risk of legionellosis associated with building water systems: ASHRAE guideline 12-2000. Atlanta, GA: American Society of Heating, Refrigerating and Air-Conditioning Engineers; 2000.
8. Garrison LE, Kunz JM, Cooley LA, et al. Vital signs: deficiencies in environmental control identified in outbreaks of Legionnaires' disease—North America, 2000–2014. *Mortal Wkly Rep* 2016;65:576–84. <https://doi.org/10.15585/mmwr.mm6522e1>
9. American Society of Heating, Refrigerating and Air-Conditioning Engineers. Legionellosis: risk management for building water systems: ANSI/ASHRAE standard 188–2015. Atlanta, GA: American Society of Heating, Refrigerating and Air-Conditioning Engineers; 2015.
10. CDC. Promotion of healthy swimming after a statewide outbreak of cryptosporidiosis associated with recreational water venues—Utah, 2008–2009. *MMWR Morb Mortal Wkly Rep* 2012;61:348–52.

Trends in Antiretroviral Therapy Eligibility and Coverage Among Children Aged <15 Years with HIV Infection — 20 PEPFAR-Supported Sub-Saharan African Countries, 2012–2016

Amanda Burrage, MD^{1,2}; Monita Patel, PhD²; Kelsey Mirkovic, PhD³; Eric Dziuban, MD²; Wondimu Teferi, MD⁴; Laura Broyles, MD²; Emilia Rivadeneira, MD²

Rapid disease progression and associated opportunistic infections contribute to high mortality rates among children aged <15 years with human immunodeficiency virus (HIV) infection (1). Antiretroviral therapy (ART) has decreased childhood HIV-associated morbidity and mortality rates over the past decade (2). As accumulating evidence revealed lower HIV-associated mortality with early ART initiation, the World Health Organization (WHO) guidelines broadened ART eligibility for children with HIV infection (2). Age at ART initiation for children with HIV infection expanded sequentially in the 2010, 2013, and 2016 WHO guidelines to include children aged <2, <5, and <15 years, respectively, regardless of clinical or immunologic status (3–5). The United States President's Emergency Plan for AIDS Relief (PEPFAR) has supported ART for children with HIV infection since 2003 and, informed by the WHO guidelines and a growing evidence base, PEPFAR-supported countries have adjusted their national pediatric guidelines. To understand the lag between guideline development and implementation, as well as the ART coverage gap, CDC assessed national pediatric HIV guidelines and analyzed Joint United Nations Programme on HIV and AIDS (acquired immunodeficiency syndrome; UNAIDS) data on children aged <15 years with HIV infection and the numbers of these children on ART. Timeliness of WHO pediatric ART guideline adoption varied by country; >50% of children with HIV infection are not receiving ART, underscoring the importance of strengthening case finding and linkage to HIV treatment in pediatric ART programs.

Pediatric ART eligibility criteria during 2012–2016 were abstracted from published national HIV treatment guidelines of 20 PEPFAR-supported countries in sub-Saharan Africa with the highest pediatric HIV burden.* Pediatric ART eligibility was defined as the recommended age for ART initiation, regardless of clinical or immunologic status, and was categorized by the following age categories: <1, <2, <5, or <15 years. Countries with “treat all” ART eligibility (i.e., immediate ART eligibility for all persons with HIV infection regardless of age, or clinical or immunologic status) for all persons living with

HIV were categorized as <15 years, because ages ≥15 were not included in this analysis. The year of the ART eligibility policy or the date of another published document that specified a change in pediatric ART eligibility guidelines was considered the national HIV guideline publication date.

UNAIDS data for the 20 countries were abstracted from the publicly available AIDSinfo website following the release of 2016 UNAIDS Spectrum model estimates in July 2017 (6). The Spectrum model, which is updated each year, calculates annual estimates of the HIV epidemic, including HIV prevalence and ART coverage, to monitor changes in national epidemics. UNAIDS data were analyzed by year during 2012–2016, comparing national estimates of number of children aged <15 years with HIV infection with number of those children on ART for each country. All Spectrum country data were finalized in the 2016 model, with the exception of Lesotho and Zimbabwe, for which 2015 Spectrum estimates were used for the 2016 time point because 2016 UNAIDS estimates were not available.

The age at eligibility for ART among the 20 countries increased during 2012–2016; in 2012, 95% of countries included children aged <2 years. By 2016, 35% of countries included children aged <5 years and 65% included all children aged <15 years (Table). The 2013 WHO guidelines

TABLE. Number and percentage of countries with age-specific pediatric ART eligibility, by year — 20 PEPFAR-supported sub-Saharan African countries,*,† 2012–2016

Age at ART eligibility (year recommended by WHO)	Year				
	2012	2013	2014	2015	2016
	No. (%)	No. (%)	No. (%)	No. (%)	No. (%)
<1 yr	6 (30)	3 (15)	— [§]	— [§]	— [§]
<2 yrs (2010)	13 (65)	11 (55)	4 (20)	— [§]	— [§]
<5 yrs (2013)	1 (5)	6 (30)	12 (60)	15 (75)	7 (35)
<15 yrs (2016)	— [§]	— [§]	4 (20)	5 (25)	13 (65)

Abbreviations: AIDS = acquired immunodeficiency syndrome; ART = antiretroviral therapy; PEPFAR = U.S. President's Emergency Plan for AIDS Relief; WHO = World Health Organization.

* Angola, Botswana, Cameroon, Côte d'Ivoire, Democratic Republic of the Congo, Ethiopia, Kenya, Lesotho, Malawi, Mozambique, Namibia, Nigeria, Rwanda, South Africa, South Sudan, Swaziland, Tanzania, Uganda, Zambia, and Zimbabwe.

† Kenya and Côte d'Ivoire adopted ART eligibility for children aged <10 years in 2014–2015 and 2015–2016, respectively; they were included in the <5 years category because they did not meet the more inclusive <15 years category criteria.

§ No country defined ART eligibility in that age range during that year.

* Angola, Botswana, Cameroon, Côte d'Ivoire, Democratic Republic of the Congo, Ethiopia, Kenya, Lesotho, Malawi, Mozambique, Namibia, Nigeria, Rwanda, South Africa, South Sudan, Swaziland, Tanzania, Uganda, Zambia, and Zimbabwe.

recommending ART eligibility for all children aged <5 years with HIV infection were adopted by six (30%) of the 20 countries in 2013; by 2014, 16 (80%) countries had adopted the guidelines, and by 2015, all 20 countries had implemented the policy. By the end of 2016, 13 (65%) of the 20 countries had adopted the 2016 WHO guidelines for ART eligibility for all children aged <15 years.

The percentage of children with HIV infection receiving ART increased from 24% in 2012 to 44% in 2016 (Figure 1). However, although the ART coverage gap decreased steadily during 2012–2016, there were still approximately 750,000 (56%) children with HIV infection not on ART as of 2016.

In 2016, national pediatric ART coverage ranged from 5% in South Sudan to 66% in Namibia; coverage estimates for 11 of the 18 countries with available data were <50% (Figure 2). During 2012–2016, ART coverage among children with HIV infection increased in all countries, with the exception of Namibia. In four countries (Angola, Botswana, Rwanda, and South Africa), pediatric ART coverage increased by 50% or less, in seven (Cameroon, Côte d'Ivoire, Ethiopia, Kenya, Nigeria, Swaziland, and Zambia), coverage increased by 51%–100%, and in six (Democratic Republic of the Congo, Malawi, Mozambique, South Sudan, Tanzania, and Uganda), coverage increased by >100%.

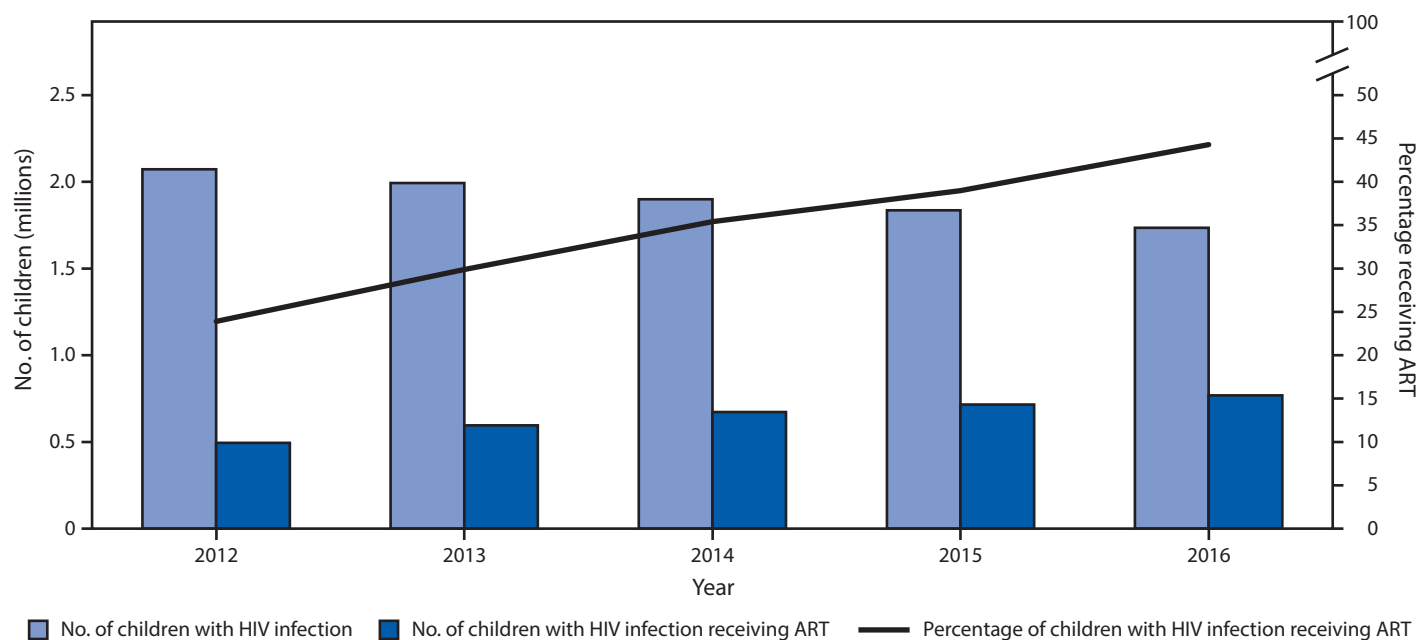
Discussion

As of 2015, all 20 PEPFAR-supported sub-Saharan African countries included in this analysis had adopted the 2013 WHO guidelines for ART eligibility for children with HIV infection aged <5 years. However, adoption of the 2013 guidelines in some countries did not occur until 2 years later, in 2015. Thirteen of the 20 countries expanded treatment eligibility at the end of 2016 to include all children aged <15 years, thus aligning with the most recent WHO guidelines published in 2016, which recommend a “treat all” approach.

Although the number of children on ART within these countries has risen steadily, a large coverage gap still exists between children with HIV infection and those who are receiving ART. Despite expanded ART eligibility guidelines, approximately 56% of children aged <15 years with HIV infection in these 20 PEPFAR-supported countries were not receiving life-saving ART in 2016. By country, the proportion of children with HIV infection on ART ranges from 5% to 66%.

Adoption of new guidelines requires review and approval by national experts and leaders, which often results in a lag between publication of WHO guidelines and country implementation of policy. Most low- and middle-income countries took almost 2 years to adopt the 2010 WHO ART guidelines (7). Limited data

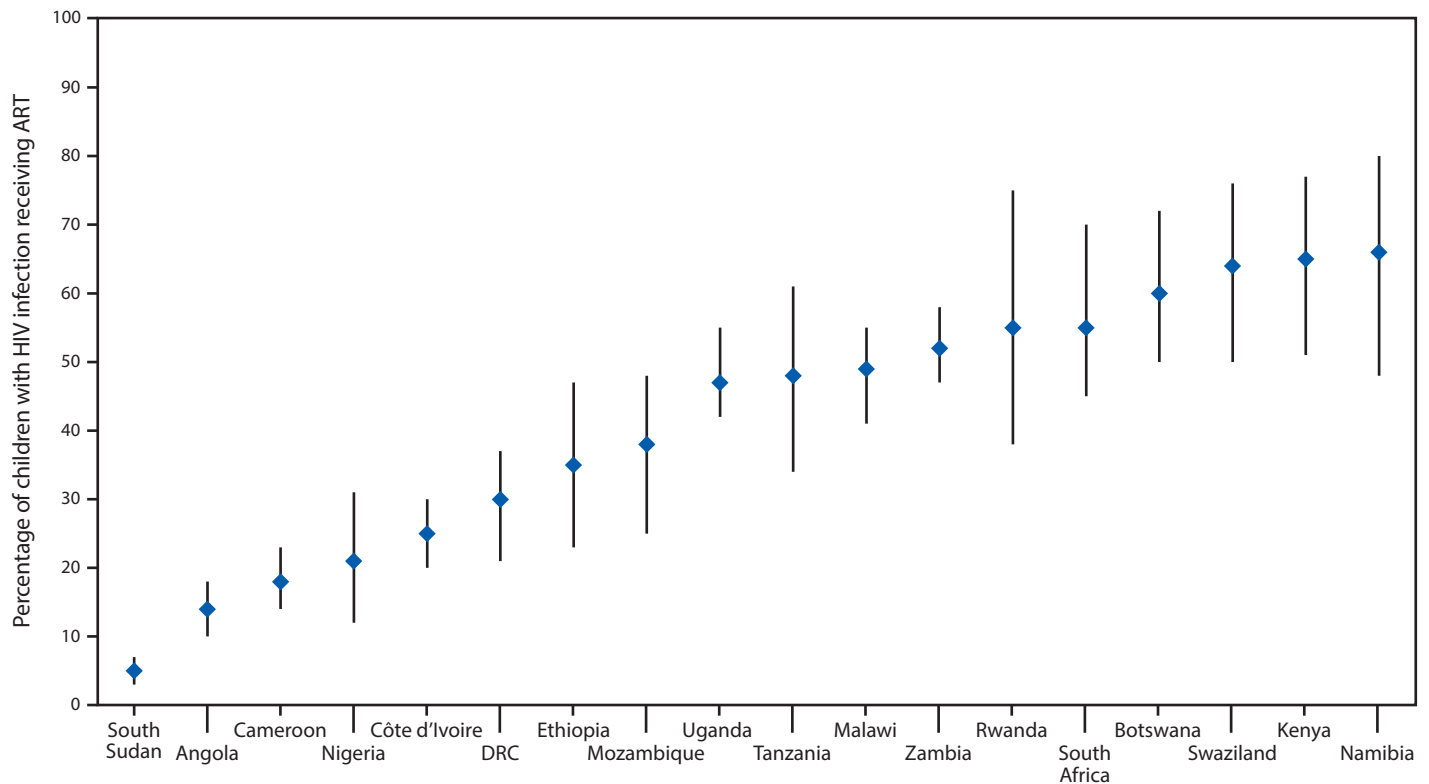
FIGURE 1. UNAIDS estimates for numbers of children with HIV infection and number and percentage receiving ART, by year — 20 PEPFAR-supported sub-Saharan African countries,*† 2012–2016



Abbreviations: AIDS = acquired immunodeficiency syndrome; ART = antiretroviral therapy; HIV = human immunodeficiency virus; PEPFAR = U.S. President’s Emergency Plan for AIDS Relief; UNAIDS = Joint United Nations Programme on HIV and AIDS.

* Angola, Botswana, Cameroon, Côte d’Ivoire, Democratic Republic of the Congo, Ethiopia, Kenya, Lesotho, Malawi, Mozambique, Namibia, Nigeria, Rwanda, South Africa, South Sudan, Swaziland, Tanzania, Uganda, Zambia, and Zimbabwe.

† Because 2016 UNAIDS estimates were not available for Lesotho and Zimbabwe, 2015 UNAIDS estimates were used for these two countries for the 2016 time point.

FIGURE 2. UNAIDS estimates of pediatric ART coverage — 18 PEPFAR-supported sub-Saharan African countries, 2016*[†]

Abbreviations: AIDS = acquired immunodeficiency syndrome; ART = antiretroviral therapy; DRC = Democratic Republic of the Congo; HIV = human immunodeficiency virus; PEPFAR = U.S. President's Emergency Plan for AIDS Relief; UNAIDS = Joint United Nations Programme on HIV and AIDS.

* Angola, Botswana, Cameroon, Côte d'Ivoire, DRC, Ethiopia, Kenya, Malawi, Mozambique, Namibia, Nigeria, Rwanda, South Africa, South Sudan, Swaziland, Tanzania, Uganda, and Zambia. Lesotho and Zimbabwe were not included in the 2016 individual country analysis because 2016 UNAIDS estimates were not available.

[†] The bars represent the ranges around the UNAIDS estimates and define the boundaries within which the actual numbers lie, according to UNAIDS.

on the impact of early ART initiation in older age groups might also delay adoption of new guidelines for pediatric ART eligibility (5). Whereas ample data show reduced mortality with early ART for children aged <1 year, evidence for reduced mortality with early ART for children aged ≥ 1 year are limited; however, benefits of early ART initiation in older children for growth, neurodevelopment, and retention in care have been identified (5,8).

Pediatric ART uptake challenges also include variable funding and procurement of pediatric ART formulations, ongoing need for training of clinical staff on current guidelines, and pediatric ART acceptance and administration by caregivers (7,9). Adoption of the most effective pediatric ART regimens and formulations requires additional agreement among national experts, guideline formulation, and implementation.

Although prompt adoption and implementation of expanded ART eligibility is required for improved pediatric ART coverage, attention to other key components of the HIV treatment cascade is critical. Identification of all children with HIV infection is fundamental; therefore, active case finding is essential to identify undiagnosed children with HIV infection included in the UNAIDS estimates. Prompt linkage to care (ideally, with

availability and initiation of same-day ART) is also required to initiate ART for patients with newly diagnosed HIV infection. Lastly, community-based retention and adherence support are necessary to help maintain children with HIV infection on ART; patient tracking might help initiate ART for previously ineligible children or those lost to follow-up (9).

The findings in this report are subject to at least two limitations. First, national guidelines were assessed based on the publication date, which might not match the date of policy implementation. Second, UNAIDS estimates for children with HIV infection and those on ART are derived from complex models. The most recent model estimates were used, but refinement occurs yearly, and estimates will continue to change. The Population-based HIV Impact Assessments, a collaboration between PEPFAR and ministries of health, are providing more accurate measures of HIV prevalence and incidence to incorporate into future UNAIDS models (10). Because 2016 UNAIDS estimates were not available for Zimbabwe and Lesotho, 2015 estimates were used, which likely slightly overestimated the number of children with HIV infection and underestimated the number on ART and ART coverage.

Summary**What is already known about this topic?**

World Health Organization (WHO) guidelines have expanded the recommended criteria for life-saving antiretroviral therapy (ART) eligibility among children with human immunodeficiency virus (HIV) infection.

What is added by this report?

All 20 sub-Saharan African countries included in this analysis adopted the 2013 WHO guidelines by 2015. In 2016, 13 of 20 countries adopted the 2016 guidelines to treat all children; however, approximately 56% of children aged <15 years with HIV infection in these countries were not receiving ART.

What are the implications for public health practice?

Closing the ART coverage gap requires prompt adoption of WHO guidelines, and strengthening ART programs to identify children with HIV infection, link them to HIV treatment programs, and ensure their retention in care.

This report highlights the continuing gaps in pediatric ART coverage in PEPFAR-supported sub-Saharan African countries with high HIV burden, despite expanded ART eligibility criteria. Robust pediatric HIV testing and comprehensive ART programs are needed to ensure that all children with HIV infection are identified and initiated on ART as early as possible. Further evaluation might identify challenges to implementation of ART guidelines and help rapidly address this gap in pediatric ART coverage to further reduce morbidity and mortality among children with HIV infection.

Acknowledgments

Sara Forhan, Surbhi Modi, Division of Global HIV and Tuberculosis, Center for Global Health, CDC.

Conflict of Interest

No conflicts of interest were reported.

¹Epidemic Intelligence Service, CDC; ²Division of Global HIV and Tuberculosis, CDC; ³Division of Global HIV and Tuberculosis, CDC Botswana; ⁴Division of Global HIV and Tuberculosis, CDC Ethiopia.

Corresponding author: Amanda Burrage, aburrage@cdc.gov, 404-718-5485.

References

1. Marston M, Becquet R, Zaba B, et al. Net survival of perinatally and postnatally HIV-infected children: a pooled analysis of individual data from sub-Saharan Africa. *Int J Epidemiol* 2011;40:385–96. <https://doi.org/10.1093/ije/dyq255>
2. Violari A, Cotton MF, Gibb DM, et al.; CHER Study Team. Early antiretroviral therapy and mortality among HIV-infected infants. *N Engl J Med* 2008;359:2233–44. <https://doi.org/10.1056/NEJMoa0800971>
3. World Health Organization. Antiretroviral therapy for HIV infection in infants and children: towards universal access. Geneva, Switzerland: World Health Organization; 2010. <http://www.who.int/hiv/pub/paediatric/infants2010/en/>
4. World Health Organization. Consolidated guidelines on the use of antiretroviral drugs for treating and preventing HIV infection. Geneva, Switzerland: World Health Organization; 2013. <http://www.who.int/hiv/pub/guidelines/arv2013/download/en/>
5. World Health Organization. Consolidated guidelines on the use of antiretroviral drugs for treating and preventing HIV infection. Geneva, Switzerland: World Health Organization; 2016. <http://www.who.int/hiv/pub/arv/arv-2016/en/>
6. Joint United Nations Programme on HIV/AIDS. AIDSinfo. Geneva, Switzerland: Joint United Nations Programme on HIV/AIDS; 2017. <http://aidsinfo.unaids.org/>
7. Nelson LJ, Beusenbergh M, Habiyambere V, et al. Adoption of national recommendations related to use of antiretroviral therapy before and shortly following the launch of the 2013 WHO consolidated guidelines. *AIDS* 2014;28(Suppl 2):S217–24. <https://doi.org/10.1097/QAD.0000000000000239>
8. Puthanakit T, Saphonn V, Ananworanich J, et al.; PREDICT Study Group. Early versus deferred antiretroviral therapy for children older than 1 year infected with HIV (PREDICT): a multicentre, randomised, open-label trial. *Lancet Infect Dis* 2012;12:933–41. [https://doi.org/10.1016/S1473-3099\(12\)70242-6](https://doi.org/10.1016/S1473-3099(12)70242-6)
9. Dziuban EJ, Rivadeneira ED. Universal antiretroviral treatment eligibility for children and adolescents living with HIV: a new era. *Pediatr Infect Dis J* 2016;35:1225–8. <https://doi.org/10.1097/INF.0000000000001276>
10. ICAP at Columbia University. PHIA project. New York, NY: ICAP at Columbia University; 2018. <http://phia.icap.columbia.edu/>

Cholera Epidemic — Lusaka, Zambia, October 2017–May 2018

Nyambe Sinyange, MBChB^{1,2,3}; Joan M. Brunkard, PhD⁴; Nathan Kapata, MBChB^{1,2}; Mazyanga Lucy Mazaba, MSc^{1,2}; Kunda G. Musonda, MBChB, MD^{1,2}; Raymond Hamoonga, MSc^{1,2}; Muzala Kapina, MBChB^{1,2}; Fred Kapaya, MBChB^{1,2,3}; Lwito Mutale¹; Ernest Kateule^{1,2,3}; Francis Nanzaluka¹; James Zulu, MBChB¹; Chileshe Lukwesa Musyani, MBChB¹; Alison V. Winstead, MD⁴; William W. Davis, DrPH⁴; Hammad S. N'cho, PhD⁴; Nelia L. Mulambya¹; Patrick Sakubita¹; Orbie Chewe¹; Sulani Nyimbili, MSc¹; Ezinne V.C. Onwuekwe⁵; Nedghie Adrien, MPH⁴; Anna J. Blackstock, PhD⁴; Travis W. Brown, MPH⁴; Gordana Derado, PhD⁴; Nancy Garrett⁴; Sunkyoung Kim, PhD⁴; Sydney Hubbard, MPH⁴; Amy M. Kahler, MS⁴; Warren Malambo, MSc⁴; Eric Mintz, MD⁴; Jennifer Murphy, PhD⁴; Rupa Narra, MD⁴; Gouthami G. Rao, MPH⁴; Margaret A. Riggs, PhD⁴; Nicole Weber, MPH⁴; Ellen Yard, PhD⁴; Khozoya D. Zyambo, MD¹; Nathan Bakyaite, MBChB⁶; Namani Monze, MBChB¹; Kennedy Malama, MBChB¹; Jabbin Mulwanda, MBChB¹; Victor M. Mukonka, MBChB, PhD^{1,2,7}

On October 6, 2017, an outbreak of cholera was declared in Zambia after laboratory confirmation of *Vibrio cholerae* O1, biotype El Tor, serotype Ogawa, from stool specimens from two patients with acute watery diarrhea. The two patients had gone to a clinic in Lusaka, the capital city, on October 4. Cholera cases increased rapidly, from several hundred cases in early December 2017 to approximately 2,000 by early January 2018 (Figure). In collaboration with partners, the Zambia Ministry of Health (MoH) launched a multifaceted public health response that included increased chlorination of the Lusaka municipal water supply, provision of emergency water supplies, water quality monitoring and testing, enhanced surveillance, epidemiologic investigations, a cholera vaccination campaign, aggressive case management and health care worker training, and laboratory testing of clinical samples. In late December 2017, a number of water-related preventive actions were initiated, including increasing chlorine levels throughout the city's water distribution system and placing emergency tanks of chlorinated water in the most affected neighborhoods; cholera cases declined sharply in January 2018. During January 10–February 14, 2018, approximately 2 million doses of oral cholera vaccine were administered to Lusaka residents aged ≥ 1 year. However, in mid-March, heavy flooding and widespread water shortages occurred, leading to a resurgence of cholera. As of May 12, 2018, the outbreak had affected seven of the 10 provinces in Zambia, with 5,905 suspected cases and a case fatality rate (CFR) of 1.9%. Among the suspected cases, 5,414 (91.7%), including 98 deaths (CFR = 1.8%), occurred in Lusaka residents.

Investigation and Results

MoH worked with multiple organizations, including the Zambia National Public Health Institute (ZNPFI), the Zambia Field Epidemiology Training Program (ZFETP), CDC, the World Health Organization (WHO), and the Africa Centres for Disease Control and Prevention (Africa CDC) to investigate the cholera outbreak and guide targeted, timely response activities. A suspected cholera case was defined as the development of acute watery or “rice water” diarrhea (three or more events within a

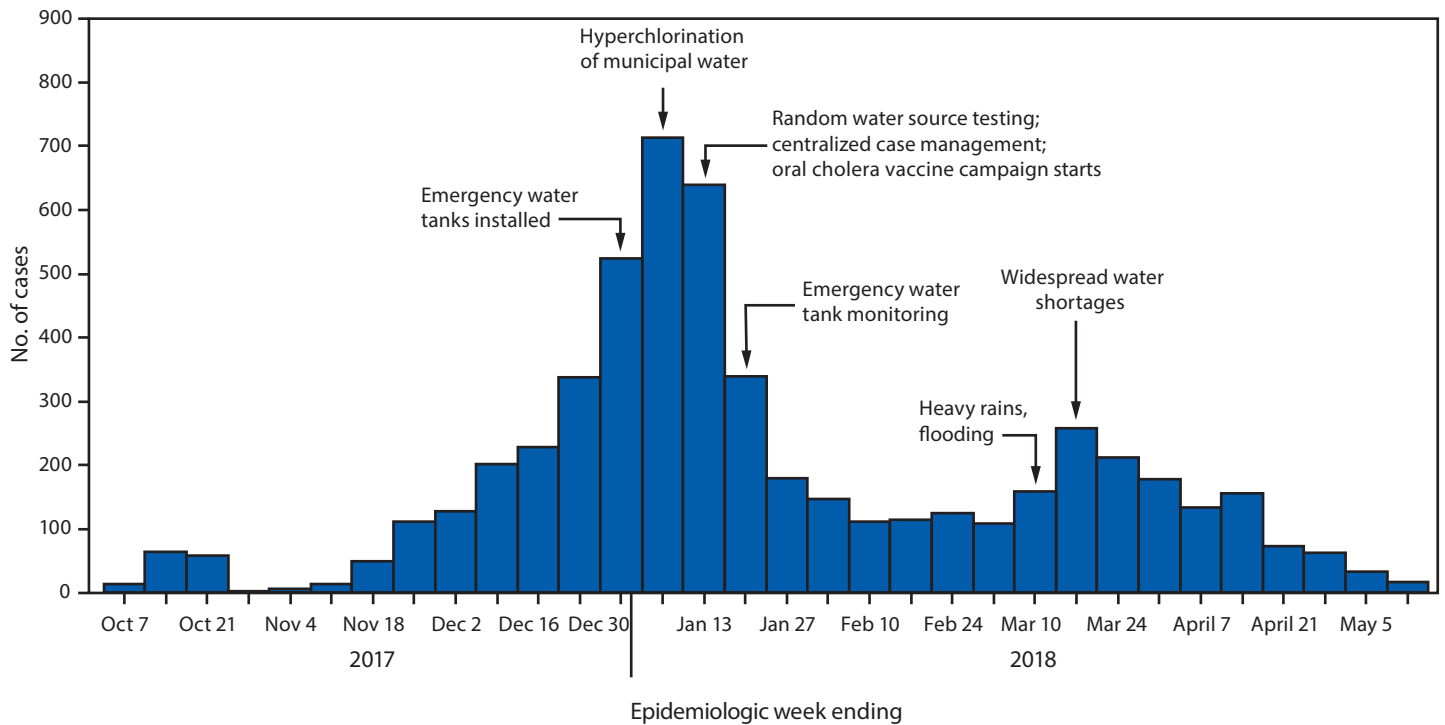
24-hour period) with or without vomiting or dehydration in any person of any age.* A confirmed case was defined as isolation of *V. cholerae* O1 from the stool of a person with suspected cholera.

Epidemiologic investigations. To assess knowledge, attitudes, and practices (KAP) regarding water, sanitation, and cholera, a cross-sectional survey was conducted in mid-December 2017 among 267 households in the most heavily affected neighborhoods of Lusaka. The KAP results indicated that most respondents (58%) believed poor hygiene to be the cause of cholera; 63% identified drinking contaminated water as a risk factor. To identify factors associated with transmission, a matched case-control study was conducted during December 18–21. Surveyors interviewed 81 case-patients with confirmed or suspected cholera and 130 controls. Preliminary results indicate that the odds of developing cholera were higher among those who had contact with a person with cholera (unadjusted odds ratio [OR] = 6.6; 95% confidence interval [CI] = 2.3–22.8) or who reported consumption of untreated water (OR = 3.6; 95% CI = 1.5–10.2) and were lower for females (OR = 0.3; 95% CI = 0.1–0.6). A total of 98 deaths occurred during October 4, 2017–May 12, 2018, in Lusaka; 40 (41%) deaths were reported by cholera treatment centers (CTCs), and 58 (59%) deaths occurred in the community. To identify risk factors associated with death from cholera, a case-control mortality study was conducted during January 12–March 26, 2018, with 32 cases (cholera deaths) and 64 controls (cholera survivors) matched by age and date of onset. Preliminary results indicated that the odds of dying from cholera were less among those who stayed an additional night at a CTC (OR = 0.30; 95% CI = 0.04–0.88), underscoring the importance of access to cholera treatment, including rehydration.

Case management training. Based on health care worker surveys and CTC assessments, ZNPFI, CDC, and the District Health Management Team organized cholera training for health care workers to help them address knowledge gaps. Training focused on cholera detection and clinical management and reached approximately 100 health care workers in Lusaka during January–February 2018.

* WHO updated cholera case definition: http://www.who.int/cholera/task_force/GTFCC-Laboratory-support-public-health-surveillance.pdf.

FIGURE. Number of reported cholera cases and related events, by week — Lusaka, Zambia, October 2017–May 2018



Water source testing and monitoring. MoH, ZNPHI, and CDC, in collaboration with the Lusaka Water and Sewerage Company (LWSC), implemented a water source monitoring program to test randomly selected drinking water sources for free chlorine residual and *Escherichia coli* (*E. coli*), an indicator of fecal contamination. Approximately 220 randomly selected water sources in areas across Lusaka affected by and not affected by cholera were tested in January 2018; results were provided daily to MoH, NPHI, and LWSC. In total, 160 (73%) of the 220 drinking water sources tested had inadequate levels of free chlorine residual (<0.2 mg/L); 41 (31%) of the 160 water sources with inadequate free chlorine residual were positive for *E. coli*. The most commonly contaminated water sources were shallow wells (91%) and boreholes (34%). On January 15, 2018, a daily monitoring program was begun for all emergency water tanks across Lusaka. Daily reports continue to be provided to LWSC and MoH regarding the locations of tanks that are empty and those that have free chlorine residual <1.0 mg/L[†] so that immediate corrective action can be taken to refill tanks or boost chlorination in water trucks at the filling reservoirs.

Clinical isolate characterization. Of 2,054 stool specimens tested during October 4, 2017–May 12, 2018, at the

University Teaching Hospital national reference laboratory in Zambia, 925 (45%) yielded *Vibrio cholerae* O1. The majority were serotype Ogawa; five isolates yielded *Vibrio cholerae* O1, serotype Inaba. Antibiotic susceptibility testing was conducted in mid-January 2018.[§] All 50 isolates tested were sensitive to cotrimoxazole, tetracycline, chloramphenicol, and azithromycin; 72% were sensitive and 28% had intermediate sensitivity (i.e., response rates might be lower) to ampicillin. The first-line treatment for cholera cases was doxycycline for adults and cotrimoxazole for children.

Public Health Response

In October 2017, MoH activated a national emergency operations center, using an incident management system to collaborate with other government ministries and partner organizations, including CDC, Africa CDC, the United Nations Children's Fund (UNICEF), WHO, Zambia Red Cross, Médecins Sans Frontières, and others. To improve safe water supply, 282 emergency chlorinated water tanks were installed beginning in December 2017. In addition, household water treatment products were distributed to approximately 1 million households in the most affected areas. To strengthen

[†] WHO recommends maintaining the following chlorine residuals during a cholera outbreak: 0.5 mg/L at all points in a piped supply, 1.0 mg/L at standposts and wells, and 2.0 mg/L in tanker trucks at filling.

[§] Antibiotic susceptibility testing was conducted using the Bauer-Kirby disc diffusion method, and minimum inhibitory concentration (MIC) for azithromycin using the E-test according to Clinical and Laboratory Standards Institute guidelines. <http://www.facm.ucl.ac.be/intranet/CLSI/CLSI-2017-M100-S27.pdf>.

surveillance, MoH disseminated information and trained staff members on standardized cholera case definitions and communication strategies and produced daily situation and outbreak reports. Cholera prevention and water treatment materials were developed and publicized through door-to-door campaigns, mass media, and by community health workers. A 2-dose oral cholera vaccine campaign was launched in cholera-affected subdistricts of Lusaka in January 2018. Approximately 1 million residents received 2 doses of oral cholera vaccine, representing approximately 80% of the targeted population and 50% of Lusaka's population.

Discussion

Cholera remains a global public health challenge, with an estimated 2.9 million cases occurring each year in countries with endemic disease and 1.3 billion persons at risk for infection (1). Large, rapidly escalating outbreaks of cholera are transmitted primarily through contaminated drinking water supplies. Cholera incidence can be reduced through increased access to safe water, sanitation, and hygiene (WASH) facilities and through behavioral changes resulting from community education and training; oral cholera vaccines are increasingly used as a temporizing measure. Since 1970, cholera has become endemic in many sub-Saharan African countries and remains a recurring major public health problem (2); recent outbreaks have occurred in Angola, the Democratic Republic of the Congo, Malawi, Tanzania, and Zimbabwe (3,4). Zambia's first cholera outbreak was reported during 1977–1978, and outbreaks with approximately 11,000 cases occurred in 1991, 1992, and 1999 (5). The current outbreak has been concentrated in peri-urban areas of Lusaka, which have limited access to municipal water supplies or sewer systems, and where approximately 60% of Lusaka's population resides (6).

Early case investigation indicated that consumption of contaminated water and contact with a person ill with cholera were likely risk factors for transmission, a hypothesis supported by findings from a case-control study and water source testing results. This information led to improvements in water supply and increases in chlorine levels throughout the municipal water distribution system, installation of emergency chlorinated water tanks in the communities at most risk, and widespread distribution of household water treatment products. Implementation of these activities was followed by a sharp reduction in cholera cases; however, the onset of a late rainy season and underlying WASH vulnerabilities, including water shortages resulting from emergency repairs of the city's primary water treatment plant, led to a resurgence of cases in March 2018. Most areas affected by flooding have a high concentration of pit latrines and shallow wells, a situation conducive to contamination of drinking water sources. Heavy rainfall has been associated with previous cholera outbreaks in Zambia and across Africa (7,8).

Summary

What is already known about this topic?

Approximately 2.9 million cholera cases occur each year worldwide, and 1.3 billion persons are at risk for infection, usually from contaminated drinking water.

What is added by this report?

A cholera outbreak that began in October 2017 in Zambia has resulted in approximately 5,900 cases and 114 deaths. The government improved the water supply and administered oral cholera vaccine, but flooding led to a resurgence of cholera. A multisectoral and well-coordinated response was key to the control of the outbreak.

What are the implications for public health practice?

Gains can be made in outbreak control with a robust public health response. However, cholera resurgence remains a risk unless access to safe drinking water and adequate sanitation are assured.

In the current outbreak, a higher percentage of deaths occurred in the community (59%) than in CTCs (41%). Delay in seeking care is a known risk factor for cholera mortality but is most often associated with outbreaks in rural areas where transportation and distance to care are limiting factors (9). Preliminary qualitative data and community reports indicate that stigma over concern about being associated with poor hygiene might have played a role in patients delaying seeking care in Lusaka; findings from the KAP survey indicated that residents associated cholera with poor hygiene.

The findings from this outbreak investigation demonstrate the need for a robust public health response during the initial stages of a cholera outbreak and the importance of enhanced surveillance and continual efforts to maintain an adequate, chlorinated drinking water supply to achieve sustained outbreak control. However, cholera resurgence remains a risk unless underlying WASH vulnerabilities, including lack of access to safe drinking water and adequate sanitation, are addressed. The Global Task Force for Cholera Control recently proposed a comprehensive, multisectoral approach to reducing cholera deaths and ending local cholera transmission through proactive investments in preparedness, WASH, and oral cholera vaccine in known areas of cholera transmission (10). A resolution to support this approach will be considered at the World Health Assembly during May 2018.

Acknowledgments

Lusaka provincial and district health teams; University Teaching Hospital bacteriological laboratory; World Health Organization; United Nations International Children's Emergency Fund; CDC Zambia; Medecins Sans Frontières; Zambia Red Cross; United States Agency for International Development (USAID) Discover; National Institute for Scientific and Industrial Research.

Conflict of Interest

No conflicts of interest were reported.

¹Ministry of Health, Lusaka, Zambia; ²Zambia National Public Health Institute, Lusaka; ³Zambia Field Epidemiology Training Program, Lusaka; ⁴CDC; ⁵Africa Centres for Disease Control and Prevention; ⁶World Health Organization; ⁷Copperbelt University, School of Medicine, Ndola, Zambia.

Corresponding author: Nyambe Sinyange, bsinyange@gmail.com, +260977430267.

References

1. Ali M, Nelson AR, Lopez AL, Sack DA. Updated global burden of cholera in endemic countries. *PLoS Negl Trop Dis* 2015;9:e0003832. <https://doi.org/10.1371/journal.pntd.0003832>
2. Mintz ED, Tauxe RV. Cholera in Africa: a closer look and a time for action. *J Infect Dis* 2013;208(Suppl 1):S4–7. <https://doi.org/10.1093/infdis/jit205>
3. World Health Organization. Weekly Bulletin on Outbreaks and Other Emergencies. 2018. <http://www.afro.who.int/health-topics/disease-outbreaks/outbreaks-and-other-emergencies-updates>
4. McAteer JB, Danda S, Nhende T, et al. Notes from the field: outbreak of *Vibrio cholerae* associated with attending a funeral—Chegutu District, Zimbabwe, 2018. *Morb Mortal Wkly Rep* 2018;67:560–1.
5. Global Task Force on Cholera Control, World Health Organization. Cholera country profile: Zambia. Geneva, Switzerland: World Health Organization, Global Task Force on Cholera Control; 2011. <http://www.who.int/cholera/countries/ZambiaCountryProfile2011.pdf>
6. Ministry of Local Government and Housing, Government of the Republic of Zambia. National urban and peri-urban sanitation strategy (2015–2030). Lusaka, Zambia: Government of the Republic of Zambia, Ministry of Local Government and Housing; 2015.
7. Luque Fernández MA, Bauernfeind A, Jiménez JD, Gil CL, El Omeiri N, Guibert DH. Influence of temperature and rainfall on the evolution of cholera epidemics in Lusaka, Zambia, 2003–2006: analysis of a time series. *Trans R Soc Trop Med Hyg* 2009;103:137–43. <https://doi.org/10.1016/j.trstmh.2008.07.017>
8. Moore SM, Azman AS, Zaitchik BF, et al. El Niño and the shifting geography of cholera in Africa. *Proc Natl Acad Sci USA* 2017;114:4436–41. <https://doi.org/10.1073/pnas.1617218114>
9. Djouma FN, Ateudjieu J, Ram M, Debes AK, Sack DA. Factors associated with fatal outcomes following cholera-like syndrome in far north region of Cameroon: a community-based survey. *Am J Trop Med Hyg* 2016;95:1287–91. <https://doi.org/10.4269/ajtmh.16-0300>
10. Global Task Force on Cholera Control, World Health Organization. Ending cholera: a global roadmap to 2030. Geneva, Switzerland: World Health Organization, Global Task Force on Cholera Control; 2017. <http://www.who.int/cholera/publications/global-roadmap/en/>

Notes from the Field:

Outbreak of *Vibrio cholerae* Associated with Attending a Funeral — Chegutu District, Zimbabwe, 2018

Jarred B. McAteer, MD^{1,2}; Sydney Danda, MSc³; Tonderai Nhende³; Paul Manamike³; Tonderai Parayiwa⁴; Andrew Tarupihwa⁵; Ottias Tapfumane⁶; Portia Manangazira, MPH⁶; Gibson Mhlanga, MD⁶; Daniela B. Garone, MD⁷; Andrea Martinsen, MPH⁸; Rachael D. Aubert, PhD²; William Davis, DrPH^{1,2}; Rupa Narra, MD²; Shirish Balachandra, MD⁹; Beth A. Tippet Barr, DrPH⁹; Eric Mintz, MD²

On January 16, 2018, the Zimbabwe Ministry of Health and Child Care (MoHCC) was notified of five adults with watery diarrhea and severe dehydration who were admitted to Chegutu District Hospital, Mashonaland West Province. Three of the five patients died within hours of admission. *Vibrio cholerae* O1 serotype Ogawa was isolated from the stool sample of one decedent, prompting an investigation. During 2008–2009, Zimbabwe experienced one of the largest and deadliest cholera outbreaks in recent history (98,585 cases and 4,287 [4.3%] deaths), during which Chegutu reported a case fatality rate (CFR) >5% (1,2). During 2012–2016, Zimbabwe reported 93 cholera cases and two deaths nationwide, but the increasing population density and aging water and sanitation infrastructure in Chegutu raised concern about the possibility of another widespread outbreak.

MoHCC identified the index patient as a woman aged 79 years who died on January 8 after 2 days of watery diarrhea. Before her death, she sought care at a private clinic, but cholera was not suspected at the time. In accordance with local practice, water was flushed through the woman's body to cleanse it in preparation for burial; the water was subsequently discarded into the municipal sewer network without further treatment. One person who had been involved in preparation of the body and who served traditional food at the multiday funeral reception at the index patient's home developed watery diarrhea 2 days after the funeral. Six other funeral attendees, including all three decedents, had reported developing acute watery diarrhea within 6 days of the funeral. Two of the patients who subsequently died had reported assisting with the burial.

Within 4 days of the index patient's funeral, the outbreak had spread to local residents who reported no epidemiologic links to the funeral (Figure). During this time, intermittent interruptions of the chlorinated municipal water supply and low pressure areas might have increased the use of unchlorinated boreholes and shallow wells that are vulnerable to contamination from adjacent, poorly maintained, sewer pipes, including those containing water used to wash the body. Microbiologic testing from a shallow well at the funeral reception location

yielded fecal coliform bacteria, suggesting conditions conducive to cholera transmission.

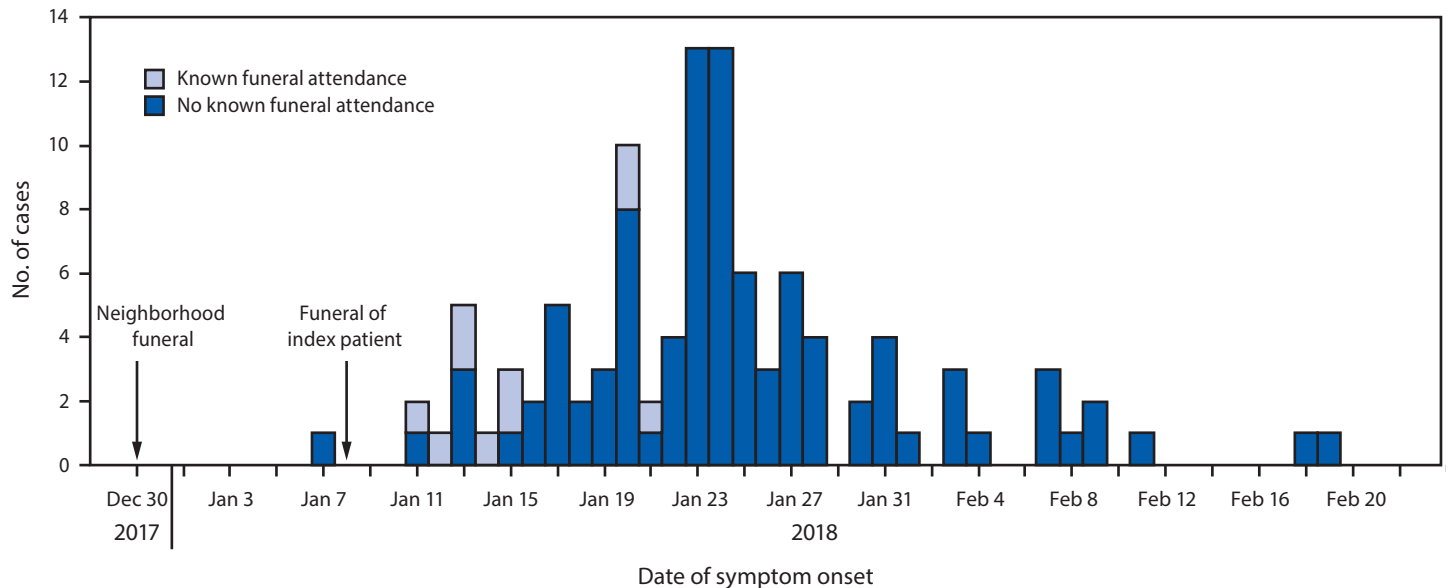
Although the index patient had not reported any travel, the epidemiologic investigation revealed that her home was less than a half mile from the site of a separate funeral that had taken place on December 30, 2017. Although that death was not associated with a diarrheal illness, two persons who attended the funeral had traveled 292 miles (470 km) from Lusaka, Zambia, where a cholera outbreak was ongoing (3). These attendees did not report diarrhea and were not tested for asymptomatic carriage of *V. cholerae*. It is not known how the index patient became infected; however, it is likely that funeral practices employed to prepare her body for burial and unsafe food preparation at the subsequent funeral potentiated the wider geographic distribution of this outbreak.

Following a coordinated rapid response effort including surveillance, health promotion, laboratory testing, case management training, and emergency water, sanitation, and hygiene (WASH) activities by MoHCC and international partners, the Zimbabwe outbreak was contained to urban and peri-urban areas of Chegutu. A single suspected case was identified along the major highway from Chegutu to the capital of Harare, 62 miles (100 km) away, but no cases were identified in Harare.

As of April 5, 2018, a total of 107 cases, including 51 hospitalizations and four deaths (CFR = 3.8%) had been reported in Zimbabwe; 9% of the cases occurred in children aged <5 years. The last case was reported on February 19. Approximately 60% of the cases occurred in three suburbs: Chegutu township (19; 17%), Pfupajena (31; 29%), and Kaguvi (13; 12%). Of 64 stool specimens tested from January 10 to February 21, nine (14.1%) yielded *V. cholerae* O1. Antimicrobial susceptibility testing by disk diffusion identified eight isolates with decreased susceptibility to cotrimoxazole, and two with decreased susceptibility to tetracycline. All isolates were susceptible to ciprofloxacin, considered first line therapy for severe cholera in accordance with Zimbabwe national guidelines.

In the setting of cholera epidemics, localized outbreaks have been associated with funeral gatherings, including transporting and washing or preparing a body for burial and contamination of shared meals at a funeral (4,5). However, outside of epidemics, cholera outbreaks rarely originate from funeral gatherings (6). Given the increase in regional travel to and from countries experiencing cholera outbreaks and those with endemic cholera transmission (7), the potential for cholera outbreaks should be considered an ever-present risk in areas that lack adequate WASH infrastructure. Early detection and promotion of safe

FIGURE. Number of reported cholera cases, by known date of symptom onset (N = 106*) and the patient's funeral attendance status — Zimbabwe, December 30, 2017–April 5, 2018



* Date of symptom onset was unknown for one additional patient.

handling of the dead are part of the routine recommendations during a cholera outbreak. This outbreak is a reminder that even in settings where cholera has been absent, public messaging about safe burial and safe food handling need to be provided at all times.

Conflict of Interest

No conflicts of interest were reported.

¹Epidemic Intelligence Service, CDC; ²Division of Foodborne, Waterborne, and Environmental Diseases, National Center for Emerging and Zoonotic Infectious Diseases, CDC; ³Chegutu District Hospital; ⁴Chegutu Municipality; ⁵National Microbiological Reference Laboratory; ⁶Ministry of Health and Child Care, Zimbabwe; ⁷Médecins Sans Frontières, Zimbabwe; ⁸Emergency Response and Recovery Branch, Division of Global Health Protection, Center for Global Health, CDC; ⁹CDC-Zimbabwe, Harare.

Corresponding author: Jarred McAteer, jmcaateer@cdc.gov, 404-718-5506.

References

- Mukandavire Z, Liao S, Wang J, Gaff H, Smith DL, Morris JG Jr. Estimating the reproductive numbers for the 2008–2009 cholera outbreaks in Zimbabwe. *Proc Natl Acad Sci U S A* 2011;108:8767–72. <https://doi.org/10.1073/pnas.1019712108>
- World Health Organization. Daily cholera update and alerts. July 30, 2009. Geneva, Switzerland: World Health Organization; 2009. http://www.who.int/hac/crises/zwe/sitreps/zimbabwe_cholera_update_30july2009.pdf?ua=1
- Sinyange N, Brunkard JM, Kapata N, et al. Cholera epidemic—Lusaka, Zambia, October 2017–May 2018. *Morb Mortal Wkly Rep* 2018;67:556–9.
- Acosta CJ, Galindo CM, Kimario J, et al. Cholera outbreak in southern Tanzania: risk factors and patterns of transmission. *Emerg Infect Dis* 2001;7(Suppl):583–7. <https://doi.org/10.3201/eid0707.017741>
- Gunnlaugsson G, Einarsdóttir J, Angulo FJ, Mentambanar SA, Passa A, Tauxe RV. Funerals during the 1994 cholera epidemic in Guinea-Bissau, West Africa: the need for disinfection of bodies of persons dying of cholera. *Epidemiol Infect* 1998;120:7–15. <https://doi.org/10.1017/S0950268897008170>
- Korthuis PT, Jones TR, Lesmana M, et al. An outbreak of El Tor cholera associated with a tribal funeral in Irian Jaya, Indonesia. *Southeast Asian J Trop Med Public Health* 1998;29:550–4.
- Ali M, Nelson AR, Lopez AL, Sack DA. Updated global burden of cholera in endemic countries. *PLoS Negl Trop Dis* 2015;9:e0003832. <https://doi.org/10.1371/journal.pntd.0003832>

Notes from the Field:

Investigation of an Outbreak of *Salmonella* Paratyphi B Variant L(+) tartrate + (Java) Associated with Ball Python Exposure — United States, 2017

Vikram Krishnasamy, MD^{1,2}; Lauren Stevenson, MHS^{2,3}; Lia Koski, MPH^{2,4}; Marilee Kellis, MPH⁵; Betsy Schroeder, DVM⁶; Madhura Sundararajan, MPH⁶; Stephen Ladd-Wilson, MS⁷; Ashley Sampsel⁷; Mike Mannell, MPH⁸; Andrew Classon²; Darlene Wagner, PhD^{2,9}; Kelley Hise, MPH²; Heather Carleton, PhD²; Eija Trees, DVM, PhD²; Linda Schlater, DVM¹⁰; Kristina Lantz, DVM¹⁰; Megin Nichols, DVM²

In July 2017, PulseNet, the national molecular subtyping network for foodborne disease surveillance, identified a cluster of five *Salmonella* Paratyphi B variant L(+) tartrate + (Java) clinical isolates that were indistinguishable by pulsed-field gel electrophoresis (PFGE). Initial questionnaires administered by state and local health department investigators indicated animal exposure as a possible source of infection, with all five patients reporting snake exposure. An outbreak investigation was initiated to identify the source of infection.

A case was defined as isolation of *Salmonella* Paratyphi B variant L(+) tartrate + (Java) from June 17, 2017, to July 23, 2017, with a PFGE enzyme pattern indistinguishable from the outbreak strain. A snake-specific questionnaire regarding snake type, snake purchase location, and reptile food, including feeder rodents, was developed and administered to patients by state and local health department investigators. In addition, animal and environmental sampling was conducted at patient residences. Traceback of patients' snakes was conducted by contacting snake purchase locations to identify common suppliers. Finally, whole genome sequencing (WGS) was performed on clinical, environmental, animal, and pet food isolates to further characterize their genetic relatedness, measured in single nucleotide polymorphism (SNP) differences (1).

Five cases were identified in four states: one each in Arizona, Oklahoma, and Oregon, and two in Indiana from different households with no epidemiologic link. Median patient age was 10 years (range = <1–40 years), and four were female. No patient was hospitalized, and no deaths occurred. Five patients or their proxies completed the snake-specific questionnaire, four of whom reported exposure to a ball python in the residence. Ball python sampling occurred in the Arizona, Oregon, and one of the Indiana patient residences by sampling the python cloaca, environment, water, and bedding. Feeder rodent sampling occurred in the Arizona and Indiana patient residences. No common suppliers of either ball pythons or feeder rodents were identified by traceback.

A ball python bedding sample from the Arizona residence and a ball python cloacal sample from the Indiana residence yielded *Salmonella* Paratyphi B variant L(+) tartrate + (Java). Sampling also identified *Salmonella* Mbandaka from a feeder rodent and a ball python at the Arizona residence. In addition, Oregon ball python environmental samples yielded *Salmonella* Oranienburg. Further investigation of the *Salmonella* Mbandaka and Oranienburg isolates did not identify human illnesses linked to snake exposure. Finally, the National Veterinary Services Laboratories (NVSL) identified three *Salmonella* Paratyphi B var L(+) tartrate + (Java) isolates from other pythons in 2017.

WGS analysis indicated that among human isolates, only the two Indiana patient isolates were closely related genetically (0–2 SNP differences) (Figure). The Arizona, Oklahoma, and Oregon patient isolates were not closely related genetically to each other or to the Indiana patient isolates. In addition, the Arizona ball python bedding sample was indistinguishable from the Arizona patient isolate (0 SNP differences), and the Indiana ball python and environmental samples were closely related to both Indiana patient isolates (0–2 SNP differences). Finally, the three python isolates identified at NVSL were not closely related to any human, animal, or environmental isolate.

Python regius, also known as ball or royal pythons, are a python species native to sub-Saharan Africa. Their tame nature and small size relative to other pythons make them popular pets in the United States (2,3). However, like other reptiles, ball pythons are known carriers of multiple *Salmonella* serovars (4). As a result, CDC recommends that children aged <5 years avoid contact with reptiles (5). The median age of patients in this investigation was 10 years, indicating that children aged >5 years are also at risk for illness. Identifying and investigating zoonotic clusters of salmonellosis require a One Health (6) approach using multidisciplinary collaboration with departments of agriculture and health.

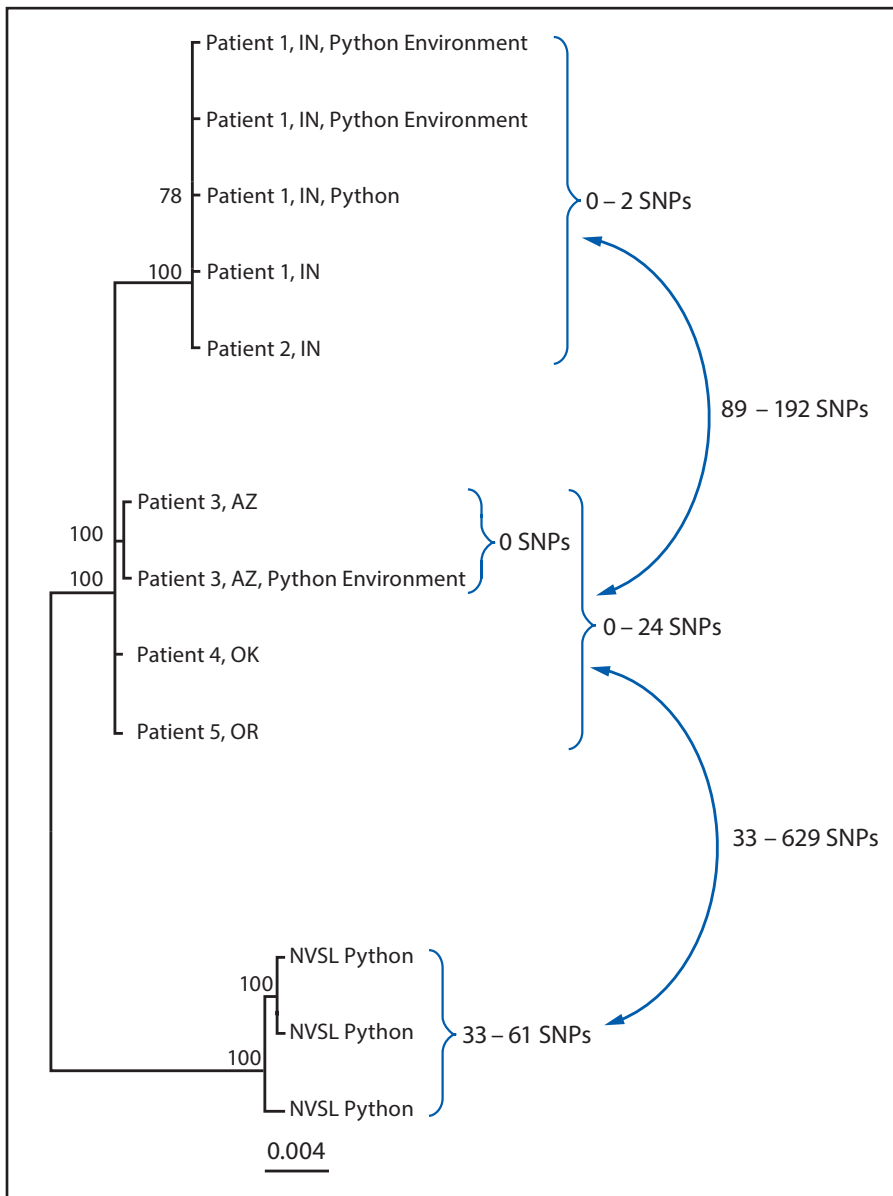
Acknowledgments

Hayley Yaglom, Joli Weiss, Kaitlyn Snyder, Ginny De La Cruz, Roumen Penev, Joe Huynh, Nannette Washington, Logan Fink, Joel Sevinsky.

Conflict of Interest

No conflicts of interest were reported.

FIGURE. Whole-genome sequencing analysis* of isolate genomes of *Salmonella* Paratyphi B variant L(+) tartrate + (Java) from human, from *Python regius*, and from environmental sources associated with the outbreak investigation† — United States, 2017



Abbreviations: AZ = Arizona; hqSNP = high-quality single nucleotide polymorphism; IN = Indiana; NVSL = National Veterinary Services Laboratories; OK = Oklahoma; SNPs = single nucleotide polymorphisms.

* Analysis performed using Lyve-SET version 1.1.4f (<https://github.com/lkatz/lyve-SET>), and hqSNPs were called at >20x coverage, >95% read support, and allowed flanking set to five base pairs. Reference used was draft assembly of Arizona case (78 contigs) without phage masking.

† Three isolates from different pythons submitted to NVSL for testing.

¹Epidemic Intelligence Service, CDC; ²Division of Foodborne, Waterborne, and Environmental Diseases, National Center for Emerging and Zoonotic Infectious Diseases, CDC; ³CAITTA, Inc., Herndon, Virginia; ⁴Oak Ridge Institute for Science and Education, Oak Ridge Tennessee; ⁵Arizona Department of Health Services; ⁶Indiana State Department of Health; ⁷Oregon Health Authority, Public Health Division; ⁸Oklahoma State Department of Health; ⁹IHRC, Inc., Atlanta, Georgia; ¹⁰National Veterinary Services Laboratories, Science, Technology and Analysis Services, Veterinary Services, Animal and Plant Health Inspection Service, U.S. Department of Agriculture, Washington, DC.

Corresponding author: Vikram Krishnasamy, krishnasamy@cdc.gov, 404-718-5504.

References

1. CDC. Whole genome sequencing (WGS). Atlanta, GA: US Department of Health and Human Services, CDC; 2017. <https://www.cdc.gov/nceid/dfwed/keyprograms/tracking-foodborne-illness-wgs.html>
2. Reed RN. An ecological risk assessment of nonnative boas and pythons as potentially invasive species in the United States. *Risk Anal* 2005;25:753-66. <https://doi.org/10.1111/j.1539-6924.2005.00621.x>
3. De Vosjoli PD, Barker T, Klingenberg R. The ball python manual. Los Angeles, CA: i5 Publishing; 2012.
4. Ebani VV, Cerri D, Fratini F, Meille N, Valentini P, Andreani E. *Salmonella enterica* isolates from faeces of domestic reptiles and a study of their antimicrobial in vitro sensitivity. *Res Vet Sci* 2005;78:117-21. <https://doi.org/10.1016/j.rvsc.2004.08.002>
5. CDC. Healthy pets, healthy people—infants and young children. Atlanta, GA: US Department of Health and Human Services, CDC; 2017. <https://www.cdc.gov/healthypets/specific-groups/children.html>
6. CDC. One health. Atlanta, GA: US Department of Health and Human Services, CDC; 2018. <https://www.cdc.gov/onehealth/index.html>

Erratum:

Vol. 67, No. SS-6

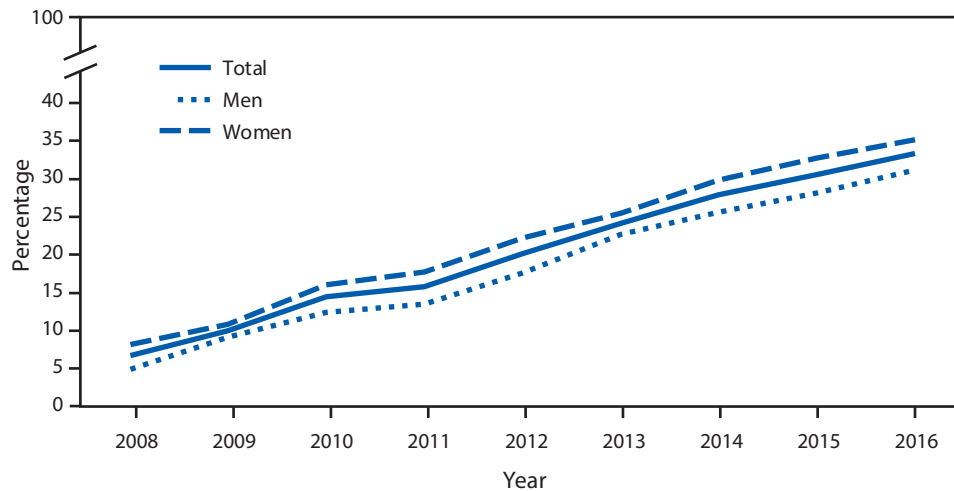
In the report “Prevalence of Autism Spectrum Disorder Among Children Aged 8 Years — Autism and Developmental Disabilities Monitoring Network, 11 Sites, United States, 2014,” on page 12, the first sentence of the second paragraph of the Discussion section should have read “Among the six ADDM sites completing both the 2012 and 2014 studies for the same geographic area, all six showed higher ASD prevalence estimates for **2014 compared to 2012**, with a nearly 10% higher prevalence in Georgia ($p = 0.06$) and Maryland ($p = 0.35$), 19% in New Jersey ($p < 0.01$), 22% in Missouri ($p = 0.01$), 29% in Colorado ($p < 0.01$), and 31% in Wisconsin ($p < 0.01$).”

On page 13, the second sentence under the heading “Variation in Prevalence Among ADDM Sites” should have read “Although five of the 11 ADDM sites conducting the 2014 surveillance year reported prevalence estimates within a very close range (from 13.1 to 14.1 per 1,000 children), New Jersey’s prevalence estimate of **29.3** per 1,000 children was significantly greater than that from any other site, and four sites (Georgia, Maryland, Minnesota, and North Carolina) reported prevalence estimates that were significantly greater than those from any of the five sites in the 13.1–14.1 per 1,000 range.”

QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Percentage of Adults Aged ≥ 60 Years Who Ever Had the Shingles Vaccine,* by Sex — National Health Interview Survey, 2008–2016[†]



* Based on responses to the question "Have you ever had the zoster (ZOSS-ter) or shingles vaccine, also called Zostavax?"

[†] Estimates are based on household interviews of a sample of the noninstitutionalized U.S. civilian population and are derived from the National Health Interview Survey Sample Adult component.

The percentage of adults aged ≥ 60 years who ever had the shingles vaccine increased from 6.7% in 2008 to 33.4% in 2016. The percentage of men who had the vaccine increased from 4.9% to 31.2%, and the percentage of women who had the vaccine increased from 8.2% to 35.2%. For each year during 2008–2016, women were more likely than men to have had the shingles vaccine.

Source: National Center for Health Statistics. National Health Interview Survey, 2008–2016. <https://www.cdc.gov/nchs/nhis.htm>.

Reported by: Mary Ann Bush, MS, mbush@cdc.gov, 301-458-4130; Anita L. Powell.

Morbidity and Mortality Weekly Report

The *Morbidity and Mortality Weekly Report (MMWR)* Series is prepared by the Centers for Disease Control and Prevention (CDC) and is available free of charge in electronic format. To receive an electronic copy each week, visit *MMWR* at <https://www.cdc.gov/mmwr/index.html>.

Readers who have difficulty accessing this PDF file may access the HTML file at <https://www.cdc.gov/mmwr/index2018.html>. Address all inquiries about the *MMWR* Series, including material to be considered for publication, to Executive Editor, *MMWR* Series, Mailstop E-90, CDC, 1600 Clifton Rd., N.E., Atlanta, GA 30329-4027 or to mmwrq@cdc.gov.

All material in the *MMWR* Series is in the public domain and may be used and reprinted without permission; citation as to source, however, is appreciated.

Use of trade names and commercial sources is for identification only and does not imply endorsement by the U.S. Department of Health and Human Services.

References to non-CDC sites on the Internet are provided as a service to *MMWR* readers and do not constitute or imply endorsement of these organizations or their programs by CDC or the U.S. Department of Health and Human Services. CDC is not responsible for the content of these sites. URL addresses listed in *MMWR* were current as of the date of publication.

ISSN: 0149-2195 (Print)