Centers for Disease Control and Prevention
MMWR
Morbidity and Mortality Weekly Report
Weekly / Vol. 66 / No. 30
August 4, 2017

Solid Organ Transplant–Transmitted Tuberculosis Linked to a Community Outbreak — California, 2015

Alexander Kay, MD[1]; Pennan M. Barry, MD[1]; Pallavi Annambhotla, DrPH[2]; Carol Greene[1]; Martin Cilnis, MS, MPH[1]; Peter Chin-Hong, MD[3]; Nicholas Arger, MD[4]; Louise McNitt, MD[5]; Nikole Neidlinger, MD[6]; Neha Shah, MD[1,7]; Sridhar V. Basavaraju, MD[2]; Matthew Kuehnert, MD[2]; Tambi Shaw, MPH[1]

In the spring of 2015, a local health department (LHD) in county A notified the California Department of Public Health (CDPH) about three adults with close ties to one another and a congregate community site who had received diagnoses of tuberculosis (TB) disease within a 3-month period. Subsequent review revealed matching TB genotypes indicating that the cases were likely part of a chain of TB transmission. Only three TB cases in California in the preceding 2 years shared this same genotype. One of those three previous cases occurred in a lung-transplant recipient who had no identified epidemiologic links to the outbreak. CDPH, multiple LHDs, and CDC conducted an investigation and determined that the lung-transplant donor (patient 1) was epidemiologically linked to the three outbreak cases and had a tuberculin skin test (TST) conversion detected in 2012 upon reentry at a local jail. Three other solid organ recipients from this donor were identified; none had developed TB disease. This investigation suggests that review of organ donors' medical records from high-risk environments, such as jails, might reveal additional information about TB risk. The evaluation of TB in organ recipients could include genotyping analysis (*1*) and coordination among local, state, and national partners to evaluate the potential for donor-derived TB.

Investigation and Findings

Organ donor. The adult organ donor (patient 1), from county A, was admitted to the hospital following a motor vehicle crash in the fall of 2014 (Figure). A chest computed tomography (CT) scan on admission revealed diffuse nodular infiltrates consistent with pulmonary contusions, but also raised suspicion for TB. However, a TST and interferon gamma release assay (IGRA) were negative and indeterminate, respectively. Two sputum specimens were obtained, by endotracheal aspirate and one by bronchoalveolar lavage; all were negative for acid-fast bacilli (AFB) by smear and culture. Nucleic acid amplification testing (NAAT) was not performed. On the third hospital day, the patient deteriorated to neurologic death and next-of-kin consented to organ donation. As part of predonation screening, a questionnaire was administered to next-of-kin, and they did not recall TB symptoms, prior TB infection, or TB testing for the prospective donor. Follow-up CT scan performed 5 days after admission revealed resolution of the nodular infiltrates. On the seventh hospital day, six organs (heart, two lungs, liver, and two kidneys) were recovered and transplanted into four patients. The donor had immigrated to the United States approximately 8 years earlier and had been incarcerated several times with a negative TST result less than 2 years before having a positive TST result in early 2012 upon reentry to a local jail. The donor never received a diagnosis of TB disease.

INSIDE

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

U.S. Department of Health and Human Services
Centers for Disease Control and Prevention

Transplant recipient. The transplant recipient (patient 2), from county C, received the two donor lungs in the fall of 2014 (Figure). Three months after transplantation, and before identification of cases with a matching genotype based on spoligotyping (a polymerase chain reaction [PCR]–based method) and 24-locus variable-number tandem repeat of mycobacterial interspersed repetitive units (VNTR-MIRU) (a PCR method that analyzes specific regions of the genome), the recipient developed a persistent cough and fatigue. A CT scan revealed bilateral pleural effusions with a large pericardial effusion. The effusions were drained, and sputum was collected; cultures from pleural fluid, pericardium, and sputum yielded *Mycobacterium tuberculosis*. The recipient had minimal foreign travel and no epidemiologic links to other TB cases. Pretransplant TST and IGRA were negative. Initially, the recipient's TB was thought not to be donor-derived because of the organ donor's negative predonation TB evaluation. The recipient responded well to TB treatment.

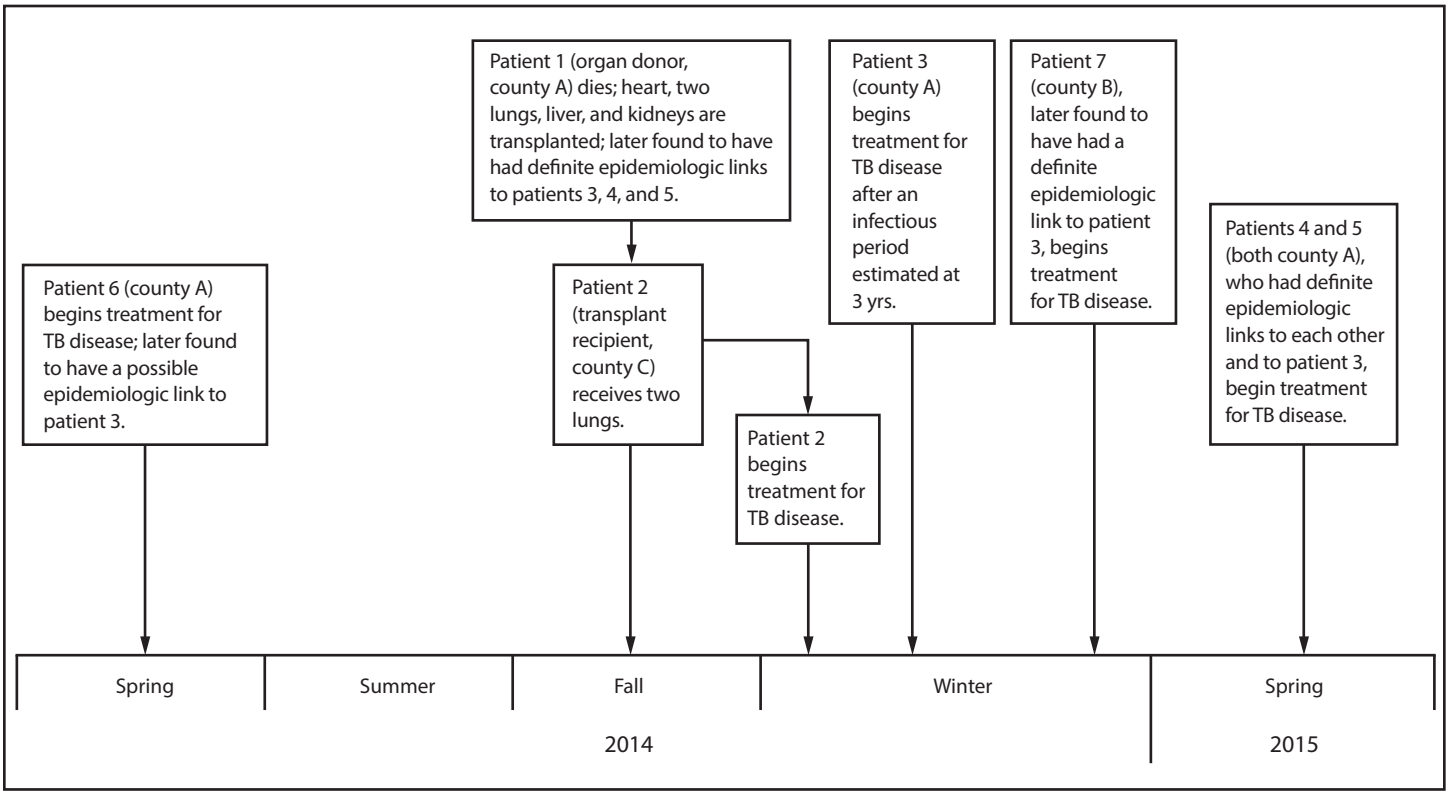
Outbreak. In the spring of 2015, 3 months after TB was diagnosed in the lung transplant recipient (patient 2), county A notified CDPH about three TB cases in adults (patients 3, 4, and 5) from the same country (Figure). These patients were linked by social and familial ties, as well as a congregate community setting, and received their TB diagnoses during a 3-month period. The isolates from patients 3, 4, and 5 were subsequently found to have the same genotype, which was rare in California and the United States, and which confirmed recent transmission. Only three other TB patients in California in the preceding 2 years had this genotype (patient 2 [the transplant recipient, county C], patient 6 [county A], and patient 7 [county B]). Outbreak-associated cases for this report were defined as TB diagnoses in patients during January 2012–May 2015 with a matching genotype and an epidemiologic link (*2*). TB cases with matching genotypes not initially linked to the outbreak (patients 2, 6, and 7) were subsequently linked after reinterviews of the three patients. Reinterviews determined patients 6 and 7 had possible or definite epidemiologic links to patient 3 during patient 3's estimated infectious period of 3 years. Subsequent whole-genome sequencing and phylogenetic analysis confirmed that the isolates from all six patients were closely related genetically.

The lung recipient (patient 2) was reinterviewed to confirm absence of an epidemiologic link to the other patients. CDPH determined that the organ donor (patient 1) for the lung recipient had been a social contact of the three patients with outbreak-associated TB (patients 3, 4, and 5). Medical records obtained from the jail where the donor had been briefly incarcerated several times revealed documentation of a negative TST in 2010 but a positive TST (18 mm) and normal chest radiograph during incarceration in 2012. Patient 3's lengthy estimated infectious period and the date of patient 1's documented TST conversion from negative to positive indicate patient 3 was the most likely source case of patient 1's TB infection. The donor did not receive therapy for latent TB. These results were not known to the organ procurement organization at the time of organ recovery.

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 2017;66:[inclusive page numbers].

FIGURE. Timeline of events and epidemiologic links for a tuberculosis (TB) outbreak (N = 7*) in which an organ donor was infected with TB by one outbreak case and then transmitted TB via lung transplant to an organ recipient† — California, 2014–2015



* Includes one organ donor with TB infection and six patients diagnosed with TB disease during January 2012–May 2015 with matching TB genotypes (and, if available, whole-genome sequencing results consistent with transmission), in addition to an epidemiologic link between patients. Definitions of the strength of epidemiologic links are adapted from National TB Controllers Association/CDC Advisory Group on Tuberculosis Genotyping. Guide to the application of genotyping to tuberculosis prevention and control. Atlanta, GA: US Department of Health and Human Services, CDC; 2004.

† The lung-transplant donor (patient 1) had a predonation tuberculin skin test (TST) and interferon gamma release assay that were negative and indeterminate, respectively. However, investigators learned that the donor had a positive TST result upon reentry to a local jail in early 2012 after having a documented negative TST <2 years earlier during a previous incarceration.

Public Health Response

County A and CDPH worked together to detect and prevent additional TB cases in the community. Prevention activities were intensified following identification of additional outbreak-associated cases after May 2015. CDPH also contacted the California LHDs of residence of all recipients of the donor's organs to notify them of the potential TB risk. CDC reviewed the medical records of all of the organ recipients and contacted their treating physicians. One recipient received treatment for presumptive latent TB infection, although no further evidence of new TB infection or disease was confirmed in that patient or any other organ recipient.

Discussion

This report describes likely donor-derived TB transmission, despite adherence to currently recommended guidelines for TB evaluation in organ donors. Investigation of the social, familial, and congregate community setting led to identification of the linkage between the organ donor and the recipient with TB, and the donor's social ties to patients with outbreak-associated TB. All organ donors in the United States are evaluated to mitigate the risk for infectious disease transmission by organ transplantation. The Organ Procurement and Transplantation Network has defined standards for screening of deceased donors (*3*), and donor evaluation includes a chest radiograph. For lung donors suspected of infection, bronchoscopy specimens for mycobacterial testing including AFB smear and culture are recommended, although addition of NAAT is preferred (*4*). Additional recommendations include ascertaining epidemiologic and medical history from next-of-kin for all deceased solid organ donors to determine TB risk. In this case, the organ donor risk assessment questionnaire administered to family members included questions about TB risk factors, but family members were not aware of or did not recall the donor's previous positive TST result.

Current guidelines acknowledge the challenges in using epidemiologic data to guide TB risk stratification from deceased donors (*4*). Chemoprophylaxis is recommended only in lung

Summary

What is already known about this topic?

Donor-derived tuberculosis (TB) is a rare but important complication of solid organ transplantation. When donor-derived TB disease is identified in an organ recipient, other patients who received organs from the same donor should be evaluated and, when indicated, treated for TB infection or disease.

What is added by this report?

This report describes a case of donor-derived TB disease and illustrates some limitations in determining the TB status of organ donors through medical evaluation or interviewing next-of-kin. This report also describes how the organ recipient's TB genotyping results helped link the recipient with patients within an ongoing TB outbreak.

What are the implications for public health practice?

Clinicians and local health departments (LHDs) should assess the likelihood of donor-derived transmission in organ recipients who develop TB disease. State TB programs can help LHDs obtain and analyze TB genotyping results of organ recipients with TB disease for evidence of possible donor-derived TB. Detection and investigation of suspected donor-derived TB are aided by communication among organ procurement organizations, clinicians, and public health programs at the local, state, and federal level. Retrieving the transplant donor's medical records from settings such as jails and prisons might augment the predonation TB risk assessment.

transplant recipients when there is laboratory documentation of untreated or inadequately treated latent TB or apical fibrosis in a donor with epidemiologic risk factors (*4*). It is difficult to evaluate for latent infection in deceased donors with unknown TB status. The 48–72 hour window required to interpret a TST is often incompatible with organ donation, and the test performance of both TST and IGRA might be diminished in persons with brain death (*5*). In this case, the donor's TST was negative, and the IGRA was indeterminate, at the time of organ donation evaluation. However, TST conversion was documented in records from a previous incarceration, which was unknown to the organ procurement organization at the time of organ recovery.

To prevent future transmissions, if there is clinical suspicion, organ procurement organizations or transplant centers might work with the TB control program in the donor's state or county of residence to seek further information regarding TB risk (*6*). Even delayed reporting to transplant centers could prevent TB-related morbidity and mortality among recipients through testing and empiric treatment for LTBI. Reporting systems for latent TB are available in some states, and might make this information more readily available (*7*). Organ procurement organizations and transplant centers could also obtain and review medical records from previous medical homes and from high-risk settings such as jails and prisons to ascertain TB risk. However, this might not be feasible for most organ donors.

Genotyping results were crucial to this investigation. The organ donor was epidemiologically linked after death to an ongoing TB outbreak occurring outside the jurisdiction in which the organ recipient resided. Organ recipients and donors are often not located within a single health jurisdiction, and state TB control programs can play a critical role in systematically reviewing and interpreting TB genotypes from organ recipients. This information is essential when determining whether disease was likely to be donor-derived, and this distinction can have significant implications for the recipient with TB and recipients of other organs from the same donor. In addition, analysis of a genotype in an organ recipient might provide additional information, as it did in this case, about the transmission dynamics of associated TB outbreaks. Coordination between organ procurement, transplant center, and public health partners is essential to ensure timely identification of donor-derived TB infection or disease and facilitate prompt clinical interventions to prevent recipient morbidity.

Acknowledgments

Benjamin Silk, Lauren Cowan, Division of TB Elimination, National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention, CDC; Leslie Henry, Tuberculosis Control Branch, California Department of Public Health.

Conflict of Interest

No conflicts of interest were reported.

[1]Tuberculosis Control Branch, California Department of Public Health; [2]Division of Healthcare Quality Promotion, National Center for Emerging and Zoonotic Infectious Diseases, CDC; [3]Division of Infectious Disease, University of California, San Francisco; [4]Division of Pulmonary, Critical Care, Allergy and Sleep Medicine, University of California, San Francisco; [5]Communicable Disease Programs, Contra Costa County Public Health, California; [6]Donor Network West, San Ramon, California; [7]Division of TB Elimination, National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention, CDC.

Corresponding author: Tambi Shaw, Tambi.Shaw@cdph.ca.gov, 510-620-3016.

References

1. Mortensen E, Hellinger W, Keller C, et al. Three cases of donor-derived pulmonary tuberculosis in lung transplant recipients and review of 12 previously reported cases: opportunities for early diagnosis and prevention. Transpl Infect Dis 2014;16:67–75. https://doi.org/10.1111/tid.12171
2. CDC. Guide to the application of genotyping to tuberculosis prevention and control. Atlanta, GA: US Department of Health and Human Services, CDC; 2004. https://www.cdc.gov/tb/programs/genotyping/chap4/4_combining_1_definitions.htm
3. Organ Procurement and Transplantation Network. Identification of transmissible diseases in organ recipients, 2015. Richmond, VA: US Department of Health and Human Services, Health Resources and Services Administration; 2017. https://optn.transplant.hrsa.gov/governance/policies/

4. Morris MI, Daly JS, Blumberg E, et al. Diagnosis and management of tuberculosis in transplant donors: a donor-derived infections consensus conference report. Am J Transplant 2012;12:2288–300. https://doi.org/10.1111/j.1600-6143.2012.04205.x
5. Schmidt T, Schub D, Wolf M, et al. Comparative analysis of assays for detection of cell-mediated immunity toward cytomegalovirus and *M. tuberculosis* in samples from deceased organ donors. Am J Transplant 2014;14:2159–67. https://doi.org/10.1111/ajt.12787
6. CDC. Transplantation-transmitted tuberculosis—Oklahoma and Texas, 2007. MMWR Morb Mortal Wkly Rep 2008;57:333–6.
7. Hochberg NS, Kubiak RW, Tibbs A, et al. Effectiveness of reporting on latent tuberculous infection in Massachusetts, 2006–2008. Public Health Action 2014;4:53–5. https://doi.org/10.5588/pha.13.0085

Meningitis Outbreak Caused by Vaccine-Preventable Bacterial Pathogens — Northern Ghana, 2016

Fortress Y. Aku, MPhil[1,2]; Fernanda C. Lessa, MD[3]; Franklin Asiedu-Bekoe, MD[2]; Phoebe Balagumyetime, MPH[4]; Winfred Ofosu, MD[5]; Jennifer Farrar, MPH[3]; Mahamoudou Ouattara, PhD[3]; Jeni T. Vuong, MS[3]; Kofi Issah, MD[6]; Joseph Opare, MPhil[6]; Sally-Ann Ohene, MBChB[7]; Charles Okot[7]; Ernest Kenu, PhD[1,2]; Donne K. Ameme, MBChB[1,2]; David Opare, MD[8]; Abass Abdul-Karim, MPhil[9]

Bacterial meningitis is a severe, acute infection of the fluid surrounding the brain and spinal cord that can rapidly lead to death. Even with recommended antibiotic treatment, up to 25% of infected persons in Africa might experience neurologic sequelae (*1*). Three regions in northern Ghana (Upper East, Northern, and Upper West), located in the sub-Saharan "meningitis belt" that extends from Senegal to Ethiopia, experienced periodic outbreaks of meningitis before introduction of serogroup A meningococcal conjugate vaccine (MenAfriVac) in 2012 (*2*,*3*). During December 9, 2015–February 16, 2016, a total of 432 suspected meningitis cases were reported to health authorities in these three regions. The Ghana Ministry of Health, with assistance from CDC and other partners, tested cerebrospinal fluid (CSF) specimens from 286 patients. In the first 4 weeks of the outbreak, a high percentage of cases were caused by *Streptococcus pneumoniae*; followed by an increase in cases caused by *Neisseria meningitidis*, predominantly serogroup W. These data facilitated Ghana's request to the International Coordinating Group* for meningococcal polysaccharide ACW vaccine, which was delivered to persons in the most affected districts. Rapid identification of the etiologic agent causing meningitis outbreaks is critical to inform targeted public health and clinical interventions, including vaccination, clinical management, and contact precautions.

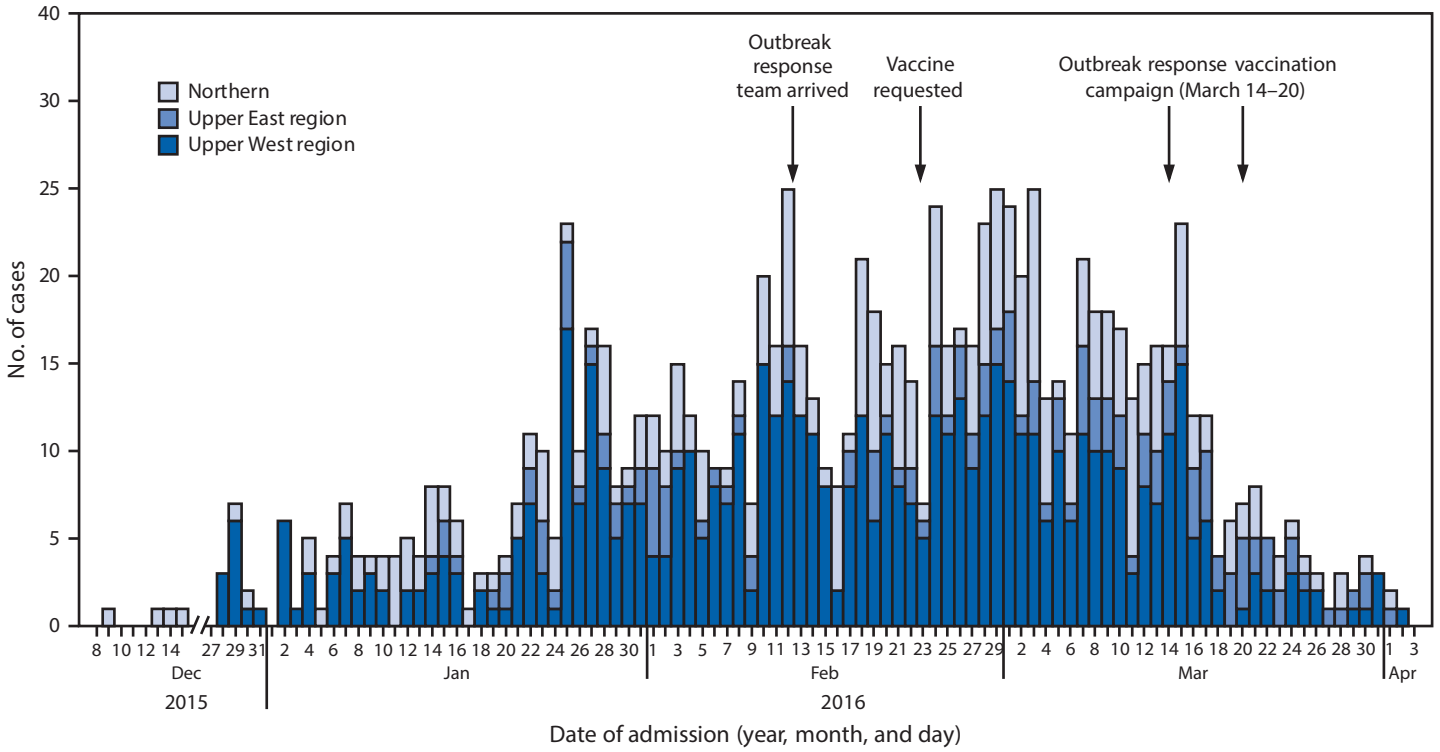
On December 9, 2015, a patient was evaluated at a hospital in the Savelugu-Nantom district of the Northern Region for fever, headache, vomiting, and neck stiffness. By December 31, 2015, five more patients in the Northern Region and 11 in the Upper West Region were hospitalized with similar symptoms. After ruling out malaria, hospital personnel suspected meningitis and alerted district and regional health authorities. The Ministry of Health was also notified, and meningitis surveillance was intensified across the Upper West, Northern, and Upper East regions. Health officials implemented control measures, including case management, contact tracing, community education on early identification of symptoms, and antimicrobial chemoprophylaxis for close contacts. As local measures led to increased awareness about meningitis, the number of reported cases increased. Health officials used community-based volunteers to identify possible meningitis cases and deaths. On February 12, at the request of the Ghanaian Ministry of Health, a team from the Ministry of Health and CDC joined local public health officials in the investigation.

A suspected meningitis case was defined as the occurrence of fever, neck stiffness, or other meningeal signs (e.g., headache, altered mental status, or bulging fontanelle in an infant) in a resident of northern Ghana. Patients with suspected meningitis who were evaluated at hospitals had a lumbar puncture performed for laboratory testing by Gram stain and culture or latex agglutination, where these were available. Probable cases were defined as the presence of at least one of the following in a patient with suspected meningitis: 1) turbid or cloudy CSF; 2) CSF white blood cell count >100/mm^3; 3) CSF white blood cell count of 10–100/mm^3 with either protein >100 mg/dl or glucose <40 mg/dl; or 4) an organism seen on Gram stain. Confirmed cases were defined as identification of a pathogen by real-time polymerase chain reaction (qPCR) in a patient with suspected or probable meningitis (CSF culture results were not included in the confirmed case definition because of lack of media and laboratory reagents required for pathogen growth and identification at health care facilities). Officials conducted active case finding, reviewed admission logbooks, and interviewed physicians treating patients. CSF specimens were also sent to the Tamale Public Health Laboratory, the reference laboratory for the three northern regions, for qPCR testing and serogrouping or serotyping of qPCR-positive specimens (*4*,*5*).

During December 8, 2015–April 3, 2016, a total of 1,006 suspected meningitis cases were reported, including 574 (57%) from the Upper West, 290 (29%) from the Northern, and 142 (14%) from the Upper East regions (Figure 1). During the first 10 weeks of the outbreak investigation (December 9, 2015–February 16, 2016), 432 suspected cases were identified among persons ranging in age from 1 month to 90 years; 44 (10%) met the probable case definition. Tamale laboratory received 286 CSF specimens for testing during December 9, 2015–February 16, 2016; among these, 133 (46.5%) were laboratory-confirmed (Figure 2). *N. meningitidis* was the most commonly detected pathogen among confirmed cases (n = 83, 62.4%), followed by *S. pneumoniae*

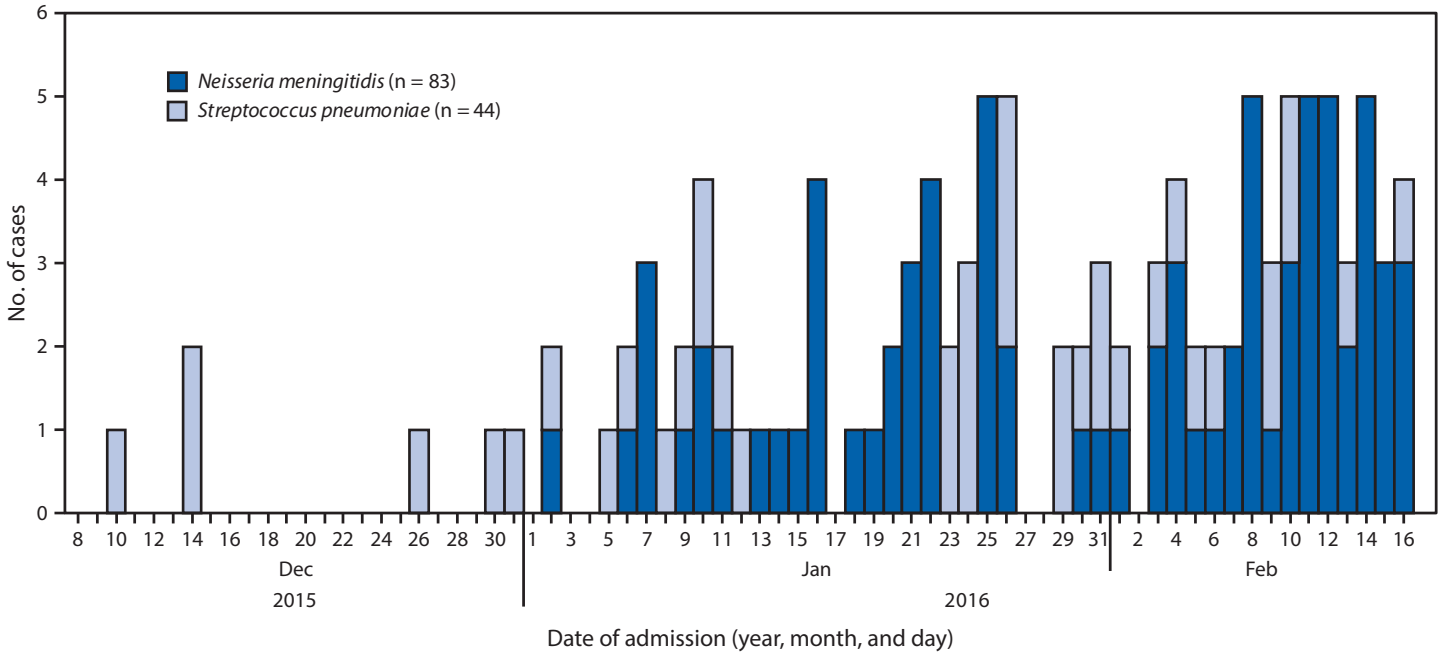
* The International Coordinating Group was established in 1997 following major outbreaks in Africa. It has four member agencies: the World Health Organization, Médecins sans Frontières, UNICEF, and the International Federation of Red Cross and Red Crescent Societies.

FIGURE 1. Suspected meningitis cases (N = 1,006), by date of admission and region and dates of vaccination campaigns with meningococcal polysaccharide ACW* vaccine — northern Ghana, December 2015–April 2016



* *Neisseria meningitidis* serogroups A, C, and W.

FIGURE 2. Laboratory-confirmed meningitis cases (N = 127),*,† by date of admission and pathogen — northern Ghana, December 9, 2015–February 16, 2016



* Among 432 suspected cases, 286 of which were laboratory tested and 133 of which were confirmed.
† Two confirmed *Haemophilus influenzae* cases and four cases with multiple pathogens excluded from figure.

(44, 33.1%) and *Haemophilus influenzae* (2, 1.5%). In four cases, more than one pathogen was detected: three had both *N. meningitidis* and *S. pneumoniae* and one had *S. pneumoniae* and *H. influenzae*. Among 103 confirmed cases with available outcome information, 8 (7.8%) were fatal. The case-fatality rate was higher among patients with pneumococcal meningitis (18.2%) than among those with meningococcal meningitis (3.1%) (p = 0.01).

Pneumococcal meningitis patients were significantly older (median age = 25 years, range = 3–72 years) than were meningococcal meningitis patients (median age = 15 years, range = 2–87 years); no significant differences were found by sex or geographic region (Table). Cases of pneumococcal meningitis were more prevalent early in the outbreak, whereas meningococcal meningitis cases predominated later in the outbreak (Figure 2). Among 83 meningococcal meningitis cases on which serogroups were examined, 82 (98.8%) were serogroup W; only one serogroup C case was detected. Among 37 serotyped pneumococcal meningitis cases, 20 (54%) were serotype 1, followed by serotype 23F (two cases, 5%), serotype 6A/6B (two, 5%), serogroup 18 (two, 5%); serotypes 3, 4, 5, 14, 19A, 19F and serogroup 12 accounted for one case each. CSF specimens from four patients with pneumococcal meningitis tested negative for all 21 serotypes/serogroups included in the qPCR assay and were probably caused by a different serotype. In the Upper West Region, the most affected region, meningococcal meningitis accounted for 42 (72.4%) of 58 confirmed cases (Table); in this region, three of 11 districts experienced rates above the epidemic threshold (10 suspected meningitis cases/100,000 population) during the week of February 7–13, 2016.

On February 12, a team of four CDC epidemiologists and laboratorians joined local health authorities in Ghana to assist with the investigation. On February 23, based on the large number of confirmed meningitis cases caused by meningococcal serogroup W, Ghana Health Service, an autonomous executive agency responsible for implementation of national policies under the Ministry of Health, requested meningococcal serogroup W containing–vaccine from the International Coordinating Group for the most affected districts. On February 27, in conjunction with the Ghana Health Service, the International Coordinating Group released 160,000 doses of meningococcal polysaccharide ACW vaccine to the most affected districts in the Upper West Region. A mass outbreak response vaccination campaign was conducted during March 14–20, 2016, in collaboration with district officials, the national government, and the World Health Organization. By March 20, with assistance from the World Health Organization Ghana office, 135,679 persons aged 2–29 years had been vaccinated in three districts with coverage exceeding 98%.

TABLE. Characteristics of confirmed meningitis cases (N = 127)* caused by *Streptococcus pneumoniae* and *Neisseria meningitidis*, by pathogen — northern Ghana, December 2015–February 2016

Characteristic	*Streptococcus pneumoniae* (n = 44)	*Neisseria meningitidis* (n = 83)	p-value
Age (yrs), median (IQR)	25 (15–42)	15 (8–28)	0.01
Female, no. (%)	21 (48.8)†	43 (52.4)†	0.70
Region			0.29
Northern region, no. (%)	21 (47.7)	32 (38.5)	
Upper West region, no. (%)	16 (36.4)	42 (50.6)	
Upper East region, no. (%)	7 (15.9)	9 (10.8)	
Died, no. (%)	6 (18.2)§	2 (3.1)§	0.01

Abbreviation: IQR = interquartile range.
* Four cases with >1 pathogen isolated and two cases with *Haemophilus influenzae* isolated were excluded.
† Among patients whose sex was known: 43 with *S. pneumoniae* and 82 with *N. meningitidis*.
§ Among patients with outcome data available: 33 with *S. pneumoniae* and 65 with *N. meningitidis*.

Discussion

The 2015–2016 meningitis outbreak in northern Ghana was caused by two main pathogens: *S. pneumoniae* predominated during the early weeks of the outbreak and *N. meningitidis* predominated during the latter. *S. pneumoniae* has been previously documented as the predominant pathogen at the beginning of meningitis outbreaks in Ghana, and it is not uncommon to identify cases of pneumococcal meningitis during meningococcal meningitis outbreaks (*6*). In this outbreak, persons with pneumococcal meningitis were older than those with meningococcal meningitis and were also older than persons with pneumococcal meningitis in outbreaks that occurred in Ghana before introduction of the 13-valent pneumococcal conjugate vaccine (PCV13) (*6*). PCV13 was introduced into Ghana's national infant immunization program in 2012 as a 3-dose schedule at ages 6, 10, and 14 weeks†; children aged >4 years during this outbreak were not age-eligible to receive PCV13 when it was introduced. High coverage with PCV13 after 2012 likely resulted in the low pneumococcal infection rates observed in younger age groups. Among meningococcal meningitis cases, the age distribution was consistent with previous publications, indicating that persons aged 5–29 years are the primary carriers of *N. meningitidis* and are most affected during epidemics (*7*).

Almost all meningococcal meningitis cases in this outbreak were caused by serogroup W. Pneumococcal meningitis cases were caused by a number of different serotypes, predominantly serotype 1, which is one of the serotypes included in PCV13. This serotype, which is known to cause invasive pneumococcal infection (*8*), was associated with meningitis outbreaks in Africa before PCV introduction (*9*). This increase in serotype 1

† International Vaccine Access Center (IVAC). http://view-hub.org/viz/#.

Summary

What is already known about this topic?

The introduction of serogroup A meningococcal conjugate vaccine (MenAfriVac) in Ghana in 2012 had a substantial impact on the periodic outbreaks of meningitis in the Northern Ghana. However, seasonal increases in bacterial meningitis continue to occur; the most prevalent etiologies are *Neisseria meningitidis*, *Streptococcus pneumoniae,* and *Haemophilus influenzae.*

What is added by this report?

During December 9, 2015–February 16, 2016, a total of 432 suspected meningitis cases were reported from three regions in northern Ghana. Among 286 cerebrospinal fluid specimens tested, 133 (46.5%) were positive, including 83 (62.4%) for *N. meningitidis* and 44 (33.1%) for *S. pneumoniae*. The predominant *N. meningitidis* serogroup was serogroup W (99%). Based on laboratory and epidemiologic data, 135,679 doses of meningococcal polysaccharide ACW vaccine were administered to the age groups most affected, resulting in substantial reduction in the number of meningitis cases.

What are the implications for public health practice?

Rapid identification of the etiologic agent in meningitis outbreaks is important for informing targeted public health interventions. Building and sustaining laboratory capacity in countries where meningitis outbreaks are common will be critical in ensuring rapid and effective response to these outbreaks.

pneumococcal meningitis in a country in which PCV13 has been introduced was surprising and might be related to several factors, including lack of a robust herd immunity (i.e., decrease in vaccine-type pneumococcus transmission because of childhood vaccination), reported low coverage the first year after introduction (43% in 2012),[§] and potential waning of immunity to serotype 1 after the first year of life in the absence of a PCV13 booster dose.

The findings of this report are subject to at least four limitations. First, lack of laboratory reagents and supplies required for bacterial culture might have led to underdiagnosis or misidentification of the etiologic agent. Second, only 286 of 432 (66%) suspected meningitis cases had CSF specimens sent to the reference laboratory for qPCR testing. Third, outcome data were only available for a subset of patients with confirmed meningitis, and among those patients, it is possible that some might have died after case notification. Finally, some persons with severe bacterial meningitis might have died before seeking health care.

Rapid and coordinated response and collaboration among national and international partners led to prompt identification of the outbreak cause and implementation of control measures. The International Coordinating Group's approval and provision of *N. meningitidis* serogroup W vaccine facilitated the mass reactive vaccination campaign, in which approximately 135,000 persons or 98% of the population aged 2–29 years in the most affected districts were vaccinated in less than 1 week. The International Coordinating Group does not maintain a stockpile of pneumococcal vaccine for outbreak response, because meningitis outbreaks in sub-Saharan Africa have been predominantly caused by *N. meningitidis*. Although pneumococcal mass vaccination could be used during pneumococcal meningitis outbreaks, the effectiveness of this approach in outbreak control needs to be better explored. It is still unclear if the same threshold used for meningococcal meningitis mass vaccination response can be used for pneumococcal outbreaks and what the optimal timeframe between outbreak onset and mass vaccination response should be for a pneumococcal vaccination campaign to have an impact in preventing further cases (*10*).

Outbreaks of bacterial meningitis are not uncommon in countries located in Africa's meningitis belt. Rapid detection of the etiology of these outbreaks can lead to targeted public health interventions. Building and sustaining laboratory capacity in countries where meningitis outbreaks are common will be critical to ensure rapid and effective response to these outbreaks.

[§] http://apps.who.int/immunization_monitoring/globalsummary/estimates?c=GHA.

Acknowledgments

The Health Directorates of the Upper East, Northern, and Upper West regions of Ghana; Division of Public Health and Disease Surveillance Department of the Ghana Health Service; Celia Woodfill, CDC, Ghana; Richard Seme-Wodah, Frank Emmanuel Abu, Donatus Dery, Benjamin Amiyure, Michael Ghansah, Abraham Amanor, Emmanuel Ormuoh, Jirapa district health directorate; John Moran, CDC.

Conflict of Interest

No conflicts of interest were reported.

[1]Ghana Field Epidemiology and Laboratory Training Programme, School of Public Health, University of Ghana, Accra, Ghana; [2]Ghana Health Service, Accra, Ghana; [3]Division of Bacterial Diseases, National Center for Immunization and Respiratory Diseases, CDC; [4]Jirapa Health District, Jirapa, Ghana; [5]Upper West Regional Directorate, Wa, Ghana; [6]Upper East Regional Directorate, Bolgatanga, Ghana; [7]World Health Organization Country Office Ghana, Accra, Ghana; [8]National Public Health Reference Laboratory, Ghana Health Service, Accra, Ghana; [9]Zonal Public Health Laboratory, Tamale, Ghana.

Corresponding author: Fernanda C. Lessa, flessa@cdc.gov, 404-345-2939.

References

1. Ramakrishnan M, Ulland AJ, Steinhardt LC, Moïsi JC, Were F, Levine OS. Sequelae due to bacterial meningitis among African children: a systematic literature review. BMC Med 2009;7:47. https://doi.org/10.1186/1741-7015-7-47
2. Leimkugel J, Hodgson A, Forgor AA, et al. Clonal waves of *Neisseria* colonisation and disease in the African meningitis belt: eight-year longitudinal study in northern Ghana. PLoS Med 2007;4:e101. https://doi.org/10.1371/journal.pmed.0040101

3. World Health Organization. Meningitis vaccine provides hope to people in Ghana. Geneva, Switzerland: World Health Organization; 2012.
4. Vuong J, Collard J-M, Whaley MJ, et al. Development of real-time PCR methods for the detection of bacterial meningitis pathogens without DNA extraction. PLoS One 2016;11:e0147765. https://doi.org/10.1371/journal.pone.0147765
5. Pimenta FC, Roundtree A, Soysal A, et al. Sequential triplex real-time PCR assay for detecting 21 pneumococcal capsular serotypes that account for a high global disease burden. J Clin Microbiol 2013;51:647–52. https://doi.org/10.1128/JCM.02927-12
6. Leimkugel J, Adams Forgor A, Gagneux S, et al. An outbreak of serotype 1 *Streptococcus pneumoniae* meningitis in northern Ghana with features that are characteristic of *Neisseria meningitidis* meningitis epidemics. J Infect Dis 2005;192:192–9. https://doi.org/10.1086/431151
7. Mueller JE, Borrow R, Gessner BD. Meningococcal serogroup W135 in the African meningitis belt: epidemiology, immunity and vaccines. Expert Rev Vaccines 2006;5:319–36. https://doi.org/10.1586/14760584.5.3.319
8. Ritchie ND, Mitchell TJ, Evans TJ. What is different about serotype 1 pneumococci? Future Microbiol 2012;7:33–46. https://doi.org/10.2217/fmb.11.146
9. Traore Y, Tameklo TA, Njanpop-Lafourcade BM, et al. Incidence, seasonality, age distribution, and mortality of pneumococcal meningitis in Burkina Faso and Togo. Clin Infect Dis 2009;48(Suppl 2):S181–9. https://doi.org/10.1086/596498
10. World Health Organization. Pneumococcal meningitis outbreaks in sub-Saharan Africa. Wkly Epidemiol Rec 2016;91:298–302.

Notes from the Field

Epidemic Keratoconjunctivitis Outbreak Associated with Human Adenovirus Type 8 — U.S. Virgin Islands, June–November 2016

Marie E. Killerby,[1,2]; Matthew J. Stuckey, PhD[2,3]; Irene Guendel, PhD[4]; Senthilkumar Sakthivel, PhD[1]; Xiaoyan Lu, MS[1]; Dean D. Erdman, PhD[1]; Eileen Schneider, MD[1]; Ryan Fagan, MD[3]; Michelle S. Davis, PhD[4]; John T. Watson, MD[1]; Susan I. Gerber, MD[1]; Holly M. Biggs, MD[1]; Esther M. Ellis, PhD[4]

On October 11, 2016, the U.S. Virgin Islands Department of Health (USVI DOH) was notified by a local ophthalmologist of an unexpected increase in the number of patients with suspected epidemic keratoconjunctivitis (EKC) during the preceding month. EKC is a severe form of acute conjunctivitis caused by human adenoviruses (HAdVs). Clinical illness typically lasts 1 to 3 weeks and is usually self-limited; treatment is supportive (*1*). HAdVs can survive for weeks in the environment and are resistant to common disinfectants (*2,3*). USVI DOH and CDC investigated during October 11–November 29, 2016 to determine the scope of the outbreak, and provide infection control recommendations.

A case of EKC was defined as 1) a diagnosis by an ophthalmologist or optometrist of EKC, adenoviral conjunctivitis, or viral conjunctivitis (excluding conjunctivitis diagnosed in association with presumed Zika virus infection); or 2) laboratory confirmation of HAdV type 8 (HAdV-8) from a specimen collected by conjunctival swab in a person on the affected island during June 1–November 29, 2016. A health care–associated case, was defined as a case in a person who had visited an eye care practice ≤14 days before onset of symptoms.

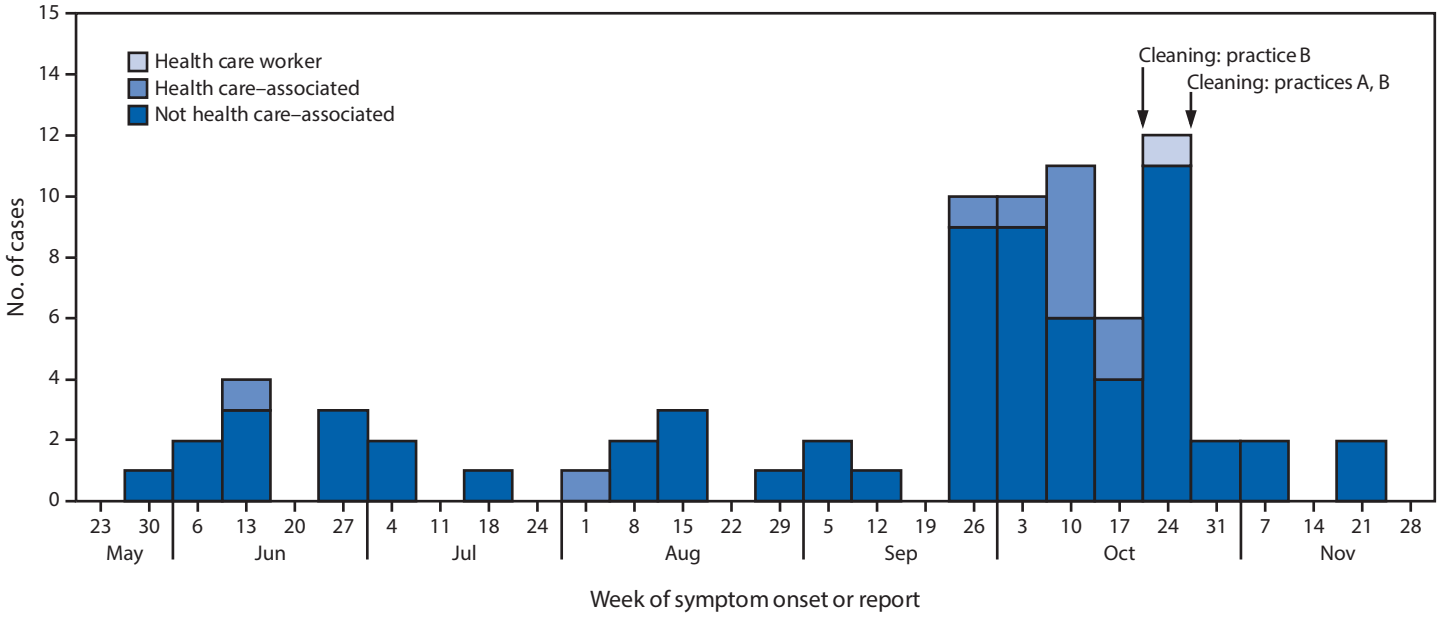
Available medical records were reviewed for patients with diagnoses of acute conjunctivitis during June 1–November 4, 2016 from all six eye care practices on the affected island. Additional cases were identified prospectively through collection of conjunctival swabs from patients evaluated for acute conjunctivitis at eye care practices, a hospital emergency department, and two family practice clinics during October 14–November 29, 2016.

Environmental testing was conducted, and routine infection control practices were assessed at the two eye care practices where health care–associated transmission was suspected to have occurred: the initial reporting practice (practice A) and a second eye care practice (practice B). Environmental samples were collected from eye care equipment and high-touch surfaces in waiting areas and patient examination rooms. Conjunctival and environmental swabs were tested at CDC using HAdV real-time polymerase chain reaction (qPCR). Positive specimens were molecularly typed, based on sequencing of hexon hypervariable regions 1–6 and inoculated into A549 cells for virus isolation. Whole genome sequencing was performed on five selected cell culture isolates, obtained from patients who were infected at the beginning, middle, and end of the outbreak.

Seventy-eight cases were identified in patients from four eye care practices, two family practices, and the hospital emergency department. The median patient age was 45 years (range = 9 months–90 years), and 33 (42%) were men. Ocular signs and symptoms included redness (68%), watery discharge (50%), and pain (29%). Severe signs included corneal infiltrates (17%) and pseudomembranes (6%). At least 12 cases (15%) were health care–associated (Figure). One health care–associated case occurred in a health care worker. Seventeen patients whose infections were not health care–associated reported a symptomatic household or community contact. Among 45 conjunctival swabs available for testing, 19 (42%) were positive for HAdV-8. Genome sequences obtained from five HAdV-8 isolates were 100% identical with one another and showed 97.7% (accession number AB861610.1) to 99.9% (accession number KT340070.1) nucleotide sequence similarity to other HAdV-8 genome sequences available in GenBank, the National Institutes of Health genetic sequence database. Among 39 environmental samples collected from practice A, eight (21%) were positive for HAdV from the following surfaces or devices: a doorknob, an eye occluder, phoropter (refractor), an examination light, two hand sanitizer dispensers, a bathroom faucet, and the surface of a multiuse eye drop bottle. Among 10 environmental samples collected from practice B, two (from a phoropter and a waiting room chair) were positive for HAdV. Environmental samples were unable to be typed because of the low viral load present. Nine HAdV positive environmental swabs were inoculated into A549 cells, and no cytopathic effect was observed after one blind passage, therefore the presence of live virus could not be confirmed. Observed gaps in infection control at the practices A and B included use of disinfectants without a proven efficacy against HAdV.

Infection prevention and control guidance was provided to six eye care practices and the emergency department. Recommendations included 1) maintaining proper hand hygiene, 2) cohorting patients with suspected EKC in the health care setting, 3) refraining from using contents from eye drop bottles for more than one patient, 4) using an Environmental Protection Agency–registered disinfectant with proven activity against HAdVs to decontaminate surfaces and equipment,

FIGURE. Cases of epidemic keratoconjunctivitis* (N = 78), by date of symptom onset or report — U.S. Virgin Islands, June 1–November 29, 2016



* Diagnosis by an ophthalmologist or optometrist of epidemic keratoconjunctivitis, adenoviral conjuctivitis, or viral conjunctivitis (excluding conjunctivitis diagnosed in association with presumed Zika virus infection); or laboratory confirmation of human adenovirus type 8 from a specimen collected by conjunctival swab during June 1–November 29, 2016. A health care–associated case was defined as a case in a person who had visited an eye care practice ≤14 days preceding symptom onset.

and 5) furloughing symptomatic employees (*1,2*). Thorough cleaning according to recommendations was performed at both practice A and practice B, after which reports of EKC declined markedly (Figure). Patient education resources were provided to six eye care practices and the hospital emergency department to support prevention of community spread. No further reports of EKC were received after December 31, 2016.

Health care–associated transmission of EKC in this outbreak highlights the importance of infection control in eye care practices, including the use of disinfectants with proven efficacy against adenoviruses. The occurrence of household transmission also underscores the importance of patient education regarding measures to prevent the spread of EKC.

Conflict of Interest

No conflicts of interest were reported.

[1]Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, CDC; [2]Epidemic Intelligence Service, CDC, [3]Division of Healthcare Quality Promotion, National Center for Emerging and Zoonotic Infectious Diseases, CDC; and [4]U.S. Virgin Islands, Department Of Health.

Corresponding author: Marie Killerby, lxo9@cdc.gov, 470-316-5645.

References

1. CDC. Adenovirus-associated epidemic keratoconjunctivitis outbreaks—four states, 2008–2010. MMWR Morb Mortal Wkly Rep 2013;62:637–41.
2. Rutala WA, Weber DJ; Healthcare Infection Control Practices Advisory Committee. Guideline for disinfection and sterilization in healthcare facilities, 2008. Atlanta, GA: US Department of Health and Human Services, CDC; 2017. https://www.cdc.gov/infectioncontrol/pdf/guidelines/disinfection-guidelines.pdf
3. Rutala WA, Peacock JE, Gergen MF, Sobsey MD, Weber DJ. Efficacy of hospital germicides against adenovirus 8, a common cause of epidemic keratoconjunctivitis in health care facilities. Antimicrob Agents Chemother 2006;50:1419–24. https://doi.org/10.1128/AAC.50.4.1419-1424.2006

Notes from the Field

Preliminary Results After Implementation of a Universal Treatment Program (Test and Start) for Persons Living with HIV Infection — Lesotho, October 2015–February 2017

Amee M. Schwitters, PhD[1]

Lesotho, a small, mountainous country completely surrounded by the Republic of South Africa, has a population of approximately 2 million persons with an estimated gross national income of $1,280 per capita; 73% of the population resides in rural areas (*1*). Lesotho has a generalized human immunodeficiency virus (HIV) epidemic (*2*). In 2014, the prevalence of HIV infection among persons aged 15–49 years was 24.6%, with an incidence of 1.9 new infections per 100 person-years of exposure (*3*). As the leading cause of premature death, HIV/AIDS (acquired immunodeficiency syndrome) has contributed to Lesotho's reporting the shortest life expectancy at birth among 195 countries and territories (*4*). In 2015, antiretroviral therapy (ART) coverage among HIV-positive persons in Lesotho was estimated to be 42% (*5*). In April 2016, Lesotho became the first country in sub-Saharan Africa to adopt the World Health Organization (WHO) recommendations for universal initiation of antiretroviral therapy for all HIV-positive persons, regardless of CD4 count (known as the "Test and Start" program or approach), with nationwide implementation occurring in June 2016 (*6,7*). Before implementation of Test and Start, many persons living with HIV infection in Lesotho were not eligible to initiate treatment until their CD4 count was <500 cells/mm^3.

The President's Emergency Plan for AIDS Relief (PEPFAR) supports treatment activities in 120 sites (114 public and six private) in five of Lesotho's 10 districts. The five districts supported by PEPFAR are home to approximately 75% of all HIV-positive persons in the country. Sites that have a minimum of 200 persons undergoing treatment for HIV infection are eligible for inclusion in the program.

In the 8 months preceding implementation of Test and Start (October 2015–May 2016), 14,948 HIV-positive persons were initiated on ART at the 120 PEPFAR-supported sites. In the 9 months since implementation of Test and Start (June 2016–February 2017), 30,146 persons were initiated on ART at the same sites, representing a 79% increase in the average monthly number of HIV-positive persons who were initiated on treatment (Figure). During the same time, treatment coverage increased 80% among males and 79% among females. The average monthly increases in coverage among persons aged <15 years, 15–24 years, and ≥25 years were 72%, 84%, and 79%, respectively. The average monthly increase in coverage varied by PEPFAR-supported district, ranging from 62% in Mohale's Hoek to 109% in Leribe. In fiscal year 2018 an additional 32 sites that have ≥200 HIV-infected persons undergoing treatment will be supported by PEPFAR in the five districts. Information is not currently available on the percentage of HIV-positive persons newly initiated on treatment who were previously known to be infected, but who did not meet the eligibility criteria for treatment initiation, and the percentage of persons in whom HIV infection was newly diagnosed.

Aligned with the Joint United Nations Programme on HIV and AIDS strategy,* PEPFAR's goal in Lesotho is 80% ART coverage among HIV-positive persons in five districts to achieve epidemic control (i.e., the point at which newly diagnosed HIV infections have decreased and fall below the number of AIDS-related deaths) (*8*). The partnership between the Lesotho Ministry of Health, PEPFAR, and implementing partners has resulted in promising preliminary results after implementation of Test and Start; sustained progress will represent a critical step toward achieving epidemic control. Successful implementation of Test and Start in all sites and districts across Lesotho, coupled with additional measures to retain HIV-positive persons newly initiated on treatment, could help maximize the success of Test and Start and the benefit of treatment to prevent new HIV cases.

*The Joint United Nations Programme on HIV and AIDS strategy is the following: 90% of all persons living with HIV will know their HIV status, 90% of all persons with diagnosed HIV infection will receive sustained antiretroviral therapy, and 90% of all persons receiving antiretroviral therapy will achieve viral suppression.

Acknowledgements

Lesotho Ministry of Health; Elizabeth Glaser Pediatric AIDS Foundation; and President's Emergency Plan for AIDS Relief Lesotho Team.

Conflict of Interest

No conflicts of interest were reported.

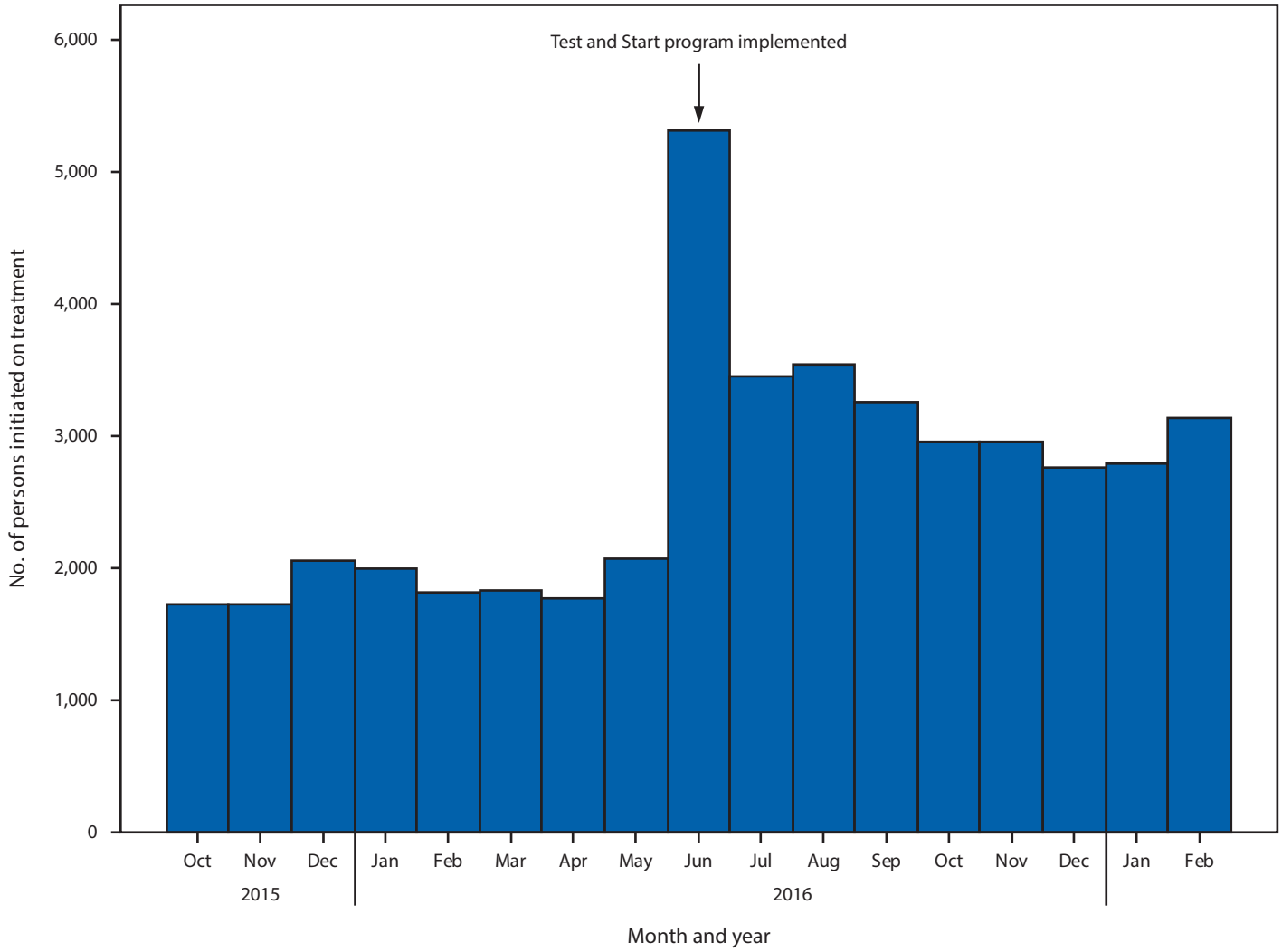
[1]Division of Global HIV and TB, Center for Global Health, CDC.

Corresponding author: Amee M. Schwitters, aschwitters@cdc.gov, +266 5888 4048.

References

1. World Bank. Data: Lesotho. New York, NY: Work Bank; 2017. http://data.worldbank.org/country/lesotho
2. Coburn BJ, Okano JT, Blower S. Current drivers and geographic patterns of HIV in Lesotho: implications for treatment and prevention in Sub-Saharan Africa. BMC Med 2013;11:224. https://doi.org/10.1186/1741-7015-11-224

FIGURE. Number of persons infected with human immunodeficiency virus (HIV) initiated on antiretroviral treatment before and after implementation of the universal HIV treatment program Test and Start, by month — five PEPFAR-supported districts, Lesotho, October 2015–February 2017



Abbreviation: PEPFAR = President's Emergency Plan for AIDS Relief.

3. Ministry of Health and ICF International. Lesotho demographic and health survey, 2014. Maseru, Lesotho: Ministry of Health and ICF International; 2016. https://dhsprogram.com/pubs/pdf/FR309/FR309.pdf
4. Wang H, Naghavi M, Allen C, et al.; GBD 2015 Mortality and Causes of Death Collaborators. Global, regional, and national life expectancy, all-cause mortality, and cause-specific mortality for 249 causes of death, 1980–2015: a systematic analysis for the Global Burden of Disease Study 2015. Lancet 2016;388:1459–544. https://doi.org/10.1016/S0140-6736(16)31012-1
5. Joint United Nations Programme on HIV and AIDS. AIDSinfo. Geneva, Switzerland: Joint United Nations Programme on HIV and AIDS; 2016. http://aidsinfo.unaids.org/
6. World Health Organization. Consolidated guidelines on the use of antiretroviral drugs for treating and preventing HIV infection: recommendations for a public health approach. Geneva, Switzerland: World Health Organization; 2016. http://apps.who.int/iris/bitstream/10665/208825/1/9789241549684_eng.pdf?ua=1
7. Elizabeth Glaser Pediatric AIDS Foundation. Lesotho government launches Test and Treat, bringing HIV treatment to all. Maseru, Lesotho: Elizabeth Glaser Pediatric AIDS Foundation; 2016. http://www.pedaids.org/blog/entry/lesotho-government-launches-test-and-treat-bringing-hiv-treatment-to-all
8. Joint United Nations Programme on HIV and AIDS. 90–90–90: an ambitious treatment target to help end the AIDS epidemic. Geneva, Switzerland: Joint United Nations Programme on HIV and AIDS; 2014. http://www.unaids.org/sites/default/files/media_asset/90-90-90_en.pdf

Erratum

Vol. 66, No. 27

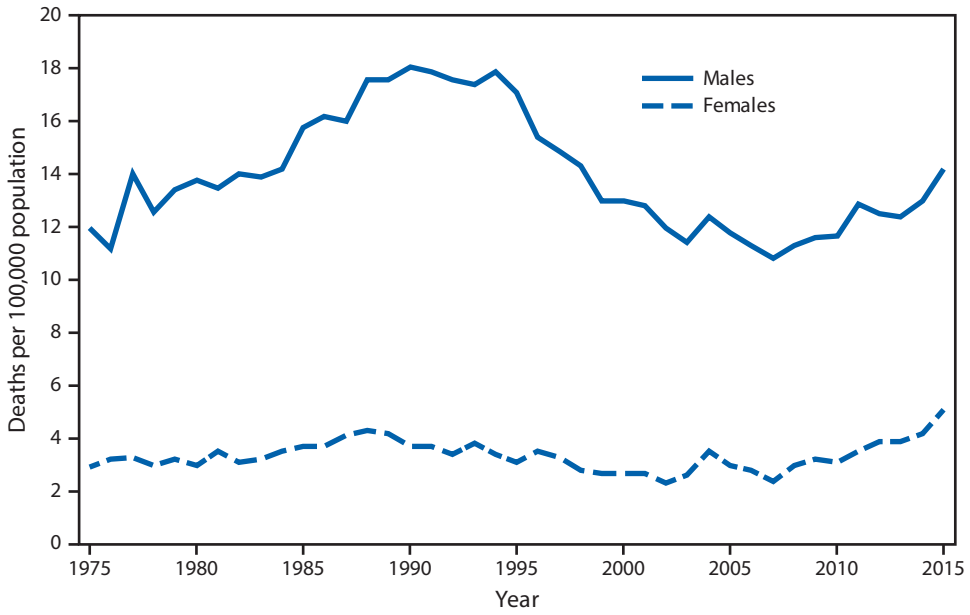
In "Racial and Geographic Differences in Breastfeeding—United States, 2011–2015," on page 723, in the first paragraph, the fifth sentence should have read, "Among the 34 states (including the District of Columbia [DC]) with sufficient sample size (≥50 per group), initiation rates were significantly ($p<0.05$) lower among black infants than white infants in **22** states; in 14 of these states (primarily in the South and Midwest), the difference was at least 15 percentage points."

On page 727, under "What is added by this report?" the second sentence should read, "Breastfeeding initiation rates were significantly lower among black infants in **22** states; in 14 of these states, the difference was at least 15 percentage points."

QuickStats

FROM THE NATIONAL CENTER FOR HEALTH STATISTICS

Suicide Rates*,† for Teens Aged 15–19 Years, by Sex — United States, 1975–2015



* Rates are per 100,000 population.
† Suicides are identified with *International Classification of Diseases* (ICD) *8th Revision* codes E950–E959 for 1975–1978; ICD 9th revision codes E950–E959 for 1979–1998; and ICD 10th revision codes U03, X60–X84 and Y87.0 for 1999–2015. In 1975, in the United States, there were 1,289 suicides among males and 305 suicides among females aged 15–19 years. In 2015, there were 1,537 suicides among males and 524 among females aged 15–19 years.

The suicide rate for males aged 15–19 years increased from 12.0 to 18.1 per 100,000 population from 1975 to 1990, declined to 10.8 by 2007, and then increased 31% to 14.2 by 2015. The rate in 2015 for males was still lower than the peak rates in the mid-1980s to mid-1990s. Rates for females aged 15–19 were lower than for males aged 15–19 but followed a similar pattern during 1975–2007 (increasing from 2.9 to 3.7 from 1975 to 1990, followed by a decline from 1990 to 2007). The rates for females then doubled from 2007 to 2015 (from 2.4 to 5.1). The rate in 2015 was the highest for females for the 1975–2015 period.

Source: CDC. National Vital Statistics System, mortality data. https://www.cdc.gov/nchs/nvss/deaths.htm.

Reported by: Sally C. Curtin, MA, sac2@cdc.gov, 301-458-4142; Holly Hedegaard, MD; Arialdi Minino, MPH; Margaret Warner, PhD; Thomas Simon, PhD.

For more information on this topic, CDC recommends the following link: https://www.cdc.gov/violenceprevention/suicide/index.html

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*'s free subscription page at *https://www.cdc.gov/mmwr/mmwrsubscribe.html*. Paper copy subscriptions are available through the Superintendent of Documents, U.S. Government Printing Office, Washington, DC 20402; telephone 202-512-1800.

Readers who have difficulty accessing this PDF file may access the HTML file at *https://www.cdc.gov/mmwr/index2017.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.

ISSN: 0149-2195 (Print)