Combining the official cholera line list data and outbreak investigation reports from the ministries of health in Uganda and South Sudan with molecular analysis of *Vibrio cholerae* strains revealed the interrelatedness of the epidemics in both countries in 2014. These results highlight the need for collaboration to control cross-border outbreaks.

**The Study**

We used the official cholera dataset and outbreak investigation reports from the ministries of health in Uganda and South Sudan. Both countries use the Integrated Disease Surveillance and Response System (https://www.cdc.gov/globalhealth/healthprotection/idsr/about.html) and have adopted similar case definitions from the World Health Organization for areas with confirmed transmission. A suspected cholera case was defined as acute watery diarrhea in a person >2 years of age. A confirmed case was defined as a suspected case in which a stool sample had a culture-positive result for *Vibrio cholerae* O1 or O139.

Cholera case reporting began on April 25, 2014, in Moyo District in northern Uganda, bordering with Kajo-Keji County in South Sudan (Figure 1, panel A). This region reported 88 cases and 3 deaths in the subsequent weeks (Figure 2). The epidemic was contained after rapid implementation of control measures.

Cholera case reporting began on April 29, 2014, in Juba, South Sudan (300 km from Moyo town, Uganda), with a case investigation finding no evidence of travel outside of Juba. Within days, the first reported cholera outbreak in South Sudan since 2009 began, resulting in 6,269 suspected cases, including 105 deaths in health facilities and 51 community deaths (case-fatality ratio 2.4%) by the end of October 2014 (7). Transmission continued in Juba throughout the epidemic, and outbreaks occurred throughout the country, including large outbreaks in the north.

In early July 2014, months after the last confirmed case in Uganda but during a period of intense transmission in South Sudan, a new outbreak was reported in Moyo district, in subcounties (Metu and Dufile) that were not

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**Author affiliations:** World Health Organization, Cairo, Egypt (A. Abubakar); Uganda Ministry of Health, Kampala, Uganda (G. Bwire, A. Kagirita); Médecins Sans Frontières, Geneva, Switzerland (A.S. Azman); Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, USA (A.S. Azman, F.J. Luquero); Epicentre, Paris, France (M. Bouhenia, L. Grout, F.J. Luquero); Republic of South Sudan Ministry of Health, Juba, South Sudan (L.L. Deng, J. Rumunu); World Health Organization, Juba (J.F. Wamala); Institut Pasteur, Paris, France (J. Rauzier, M.-L. Quilici); World Health Organization, Geneva (S. Martin); Makerere University School of Public Health, Kampala (C.G. Orach)

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affected during the first outbreak (Itirikwa, Aliba, and Gimara); cases were eventually reported in the neighboring Arua district. An investigation revealed that the presumed index case-patient of this second outbreak had traveled to South Sudan. In total, 86 cases and 4 deaths were reported in Moyo and Arua Districts by October 22.

Although not all suspected cases were confirmed during the outbreaks, both countries routinely sent samples to their respective national reference laboratory for microbiological confirmation. We characterized 56 strains at Institut Pasteur (Paris, France) by determining the antimicrobial drug resistance patterns using the disk diffusion method following CA-SFM (Comité de l’Antibiogramme de la Société Française de Microbiologie) 2013 standards for Enterobacteriaceae (http://www.sfm-microbiologie.org/); subtyping with pulse-field gel electrophoresis (8) with SfiI and NolI restriction enzymes (Roche Molecular Biochemicals, Indianapolis, IN, USA); and multilocus variable number tandem repeat (MLVA) analysis targeting 6 loci in the V. cholerae genome (9), and by genotyping tests (10).

We used BioNumerics version 6.6 (Applied Maths, Inc., Austin, TX, USA) for clustering analysis. All 56 isolates were V. cholerae O1 serotype Inaba, atypical El Tor biotype, based on rstRET, tcpAET, and ctxBClass gene sequences (classical ctxBl allele) (10). The isolates shared similar antimicrobial drug resistance patterns and were resistant to trimethoprim/sulfamethoxazole, sulfonamides, streptomycin, and nalidixic acid (confirmed by MIC determination [MICs 16–256 mg/L] with Etest; AB bioMérieux, Solna, Sweden). Sequencing of the genes encoding DNA gyrase (gyrA and gyrB) and topoisomerase IV (parC and parE) detected 1 mutation in gyrA (substitution of serine by isoleucine at position 83), which has been associated with quinolone resistance in clinical V. cholerae.
isolates (11). PFGE analyses revealed a single SfiI profile and 2 NotI profiles, 1 represented by a single strain. We identified 8 highly related MLVA profiles (Figure 1, panel B) and found variability only in 2 loci on the small chromosome (VCA0171 and VCA0283). All MLVA profiles formed a single clonal complex, in which all isolates can be connected through mutations at a single locus. These results demonstrate genetic uniformity of isolates and provide strong evidence that these epidemics in 2 countries resulted from the spread of a single clone with probable epidemiologic links.

This analysis has several limitations. The identified index cases in each country may not truly have been the initial case-patients, given that the surveillance systems in both locations are not highly sensitive. We selected the cases for culture by convenience sampling. Whereas random sampling is ideal, it is difficult to implement during epidemics because of competing priorities. Furthermore, although studies have shown that 6-locus MLVA can be highly discriminative for identifying a closely related pandemic strain isolated in a small timeframe and geographic area (12,13), our lack of knowledge of MLVA limitations makes it more difficult to draw inferences about strain relatedness and phylogenetic history, especially compared with whole-genome sequencing (14).

Conclusions
Through epidemiologic and molecular data, we illustrated that the 2 outbreaks in South Sudan and Uganda in 2014 clustered into a single epidemic. The spread of cholera from border communities in Uganda to South Sudan and from South Sudan back to Uganda is a critical issue that needs further clarification to improve control strategies. Isolating the neighboring communities from one another is not possible; however, we recommend coordinated interventions by the 2 countries to identify the sources of infection, as was done during Ebola outbreaks in West Africa during 2014–2016.

Figure 2. Epidemic curve of suspected cholera cases in South Sudan (A) and Uganda (B) in 2014, by hospital admission date and region.
The 2014 cholera epidemics probably evolved from a local outbreak in northern Uganda to a national outbreak in South Sudan; population movement, living conditions, and events in the capital, Juba, most likely played a key role in the spread of the disease to other areas in South Sudan and beyond. Refining our understanding of cholera beyond administrative boundaries, perhaps adopting regional approaches in addition to national cholera control efforts, and including key hubs of transmission, such as cities, may be key to minimizing the spatial extent and magnitude of future epidemics.

Joint implementation of disease control interventions and rapid information sharing platforms can strengthen collaboration between states to control the outbreaks. Further studies to describe the relatedness and routes of transmission of *V. cholerae* organisms and track the progression of the outbreaks, combining traditional and molecular epidemiologic tools, can aid public health decision making in Africa and beyond (15). International agencies should facilitate funding and support for joint country activities to expedite control of cross-border cholera epidemics.

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About the Author

Dr. Abubakar is a team lead for High-Threat Pathogens at the Infectious Hazard Management Unit in the Health Emergency Department of the World Health Organization Regional Office for the Eastern Mediterranean in Cairo, Egypt. His research interests are emerging and reemerging infectious diseases. Dr. Bwire is the head of Control of Diarrheal Diseases unit of Uganda Ministry of Health, Community Health Department. His research interests include molecular characterization, tropical infectious disease epidemiology, and global health.

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**Table.** Characterization of *Vibrio cholerae* O1 isolates from South Sudan and Uganda, 2014**

<table>
<thead>
<tr>
<th>Location</th>
<th>No. isolates*</th>
<th>Sample collection period</th>
<th>MLVA profile no.</th>
<th>VC 0147</th>
<th>VC 0437</th>
<th>VC 1457</th>
<th>VC 1650</th>
<th>VCA 0171</th>
<th>VCA 0283</th>
<th>PFGE profile†</th>
</tr>
</thead>
<tbody>
<tr>
<td>Uganda and South Sudan</td>
<td>9</td>
<td>2014 April–June</td>
<td>1</td>
<td>10</td>
<td>7</td>
<td>3</td>
<td>7</td>
<td>10</td>
<td>18</td>
<td>1/1 (8), 2/1 (1)</td>
</tr>
<tr>
<td>South Sudan</td>
<td>13</td>
<td>2014 May–July</td>
<td>3</td>
<td>10</td>
<td>7</td>
<td>3</td>
<td>7</td>
<td>9</td>
<td>18</td>
<td>1/1</td>
</tr>
<tr>
<td>South Sudan</td>
<td>11</td>
<td>2014 June</td>
<td>7</td>
<td>10</td>
<td>7</td>
<td>3</td>
<td>7</td>
<td>11</td>
<td>18</td>
<td>1/1</td>
</tr>
<tr>
<td>South Sudan</td>
<td>1</td>
<td>2014 June</td>
<td>7</td>
<td>10</td>
<td>7</td>
<td>3</td>
<td>7</td>
<td>9</td>
<td>16</td>
<td>1/1</td>
</tr>
</tbody>
</table>

*MLVA, multilocus variable-number tandem-repeat analysis; PFGE, pulsed-field gel electrophoresis; VNTR, variable-number tandem-repeat.
†PFGE profile number obtained after restriction with NotI and SfiI respectively (NotI/SfiI). The number in parentheses refers to the number of isolates sharing the same profile.


Address for correspondence: Marie-Laure Quilici, French National Reference Center for Vibrios and Cholera, Enteric Bacterial Pathogens Unit, Institut Pasteur, 28 rue du Dr Roux, 75724 Paris CEDEX 15, France; email: quilici@pasteur.fr

May 2015: Vectorborne Infections

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