

Geographical dissemination of cholera from Kenya to Yemen

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Introduction

Between 2013 and 2016, Kenya reported 19,192 cholera cases and 156 cholera deaths to the World Health Organization. The majority of these cases and deaths were reported in 2015, when a countrywide outbreak spread to 22 out of 47 counties. In 2016, a massive cholera outbreak started in Yemen affecting almost all districts in the country. Here we explore the epidemiological relatedness of these events.

Methods

We investigated the phylogeny of *Vibrio cholerae* isolates from Yemen and recent isolates from neighboring regions. Overall the analysis was conducted from 116 genomic sequences (42 from Yemen), which were placed within the phylogenetic context of the seventh *V. cholerae* pandemic. The sequencing and analysis were carried out in collaboration with Institute Pasteur and Sanger Institute. We also described the epidemiology of cholera in Yemen and the neighboring countries.

Results

The isolates from Yemen were collected during the two waves of the epidemic—the first between 28 September 2016 and 23 April 2017 with

25,839 suspected cases and the second beginning on 24 April 2017 with more than 1 million suspected cases—are *V. cholerae* serotype Ogawa isolates from a single sub-lineage of the seventh pandemic *V. cholerae* O1 El Tor lineage. This sub-lineage originated from South Asia and caused outbreaks in East Africa between 2013 and 2016 before appearing in Yemen.

Conclusion

The outbreaks in Kenya and Yemen are part of a larger regional outbreak, which has affected several hundreds of thousand people and caused thousands of related deaths. These findings highlight the importance of considering both the regional nature of cholera epidemics and the need to nationally control spread to protect local and neighboring populations. They also show that the systematic integration of genomic analysis in the surveillance of cholera could help to identify new lineages at the beginning of outbreaks and should help to trigger intensified control measures.

This combined epidemiological and genomic analysis shows that the ongoing cholera epidemic in Yemen is part of a larger regional outbreak that started in East Africa in 2013-2014, and reinforces the importance of detecting the emergence of new lineages earlier.