

Abstract

Cholera remains a significant public health challenge in many sub-Saharan countries including Kenya. We have performed a combination of phylogenetic and phenotypic analysis based on whole genome DNA sequences derived from 40 environmental and 57 clinical *V. cholerae* from different regions of Kenya isolated between 2005 and 2010. Some environmental and all clinical isolates mapped back onto wave three of the monophyletic seventh pandemic *V. cholerae* El Tor phylogeny but other environmental isolates were phylogenetically very distinct. Thus, the genomes of the Kenyan *V. cholerae* O1 El Tor isolates are clonally related to other El Tor *V. cholerae* isolated elsewhere in the world and similarly harbour antibiotic resistance-associated STX elements. Further, the Kenyan O1 El Tor isolates fall into two distinct clades that may have entered Kenya independently.