Abstract

Introduction: Cholera, a disease caused by Vibrio cholerae O1 and O139 remains an important public health problem globally. In the last decade, Kenya has experienced a steady increase of cholera cases. In 2009 alone, 11,769 cases were reported to the Ministry of Public Health and Sanitation. This study sought to describe the phenotypic characteristics of the isolated V. cholerae isolates.

Methods: This was a laboratory based cross-sectional study that involved isolates from different cholera outbreaks. Seventy six Vibrio cholerae O1 strains from different geographical areas were used to represent 2007 to 2010 cholera epidemics in Kenya, and were characterized by serotyping, biotyping, polymerase chain r(PCR), pulsed-field gel electrophoresis (PFGE) and ribotyping along with antimicrobial susceptibility testing.

Results: Seventy six Vibrio cholerae O1 strains from different geographical areas were used to represent 2007 to 2010 cholera epidemics in Kenya. Serotype Inaba was dominant (88.2%) compared to Ogawa. The isolates showed varying levels of antibiotic resistance ranging from 100% susceptible to tetracycline, doxycycline, ofloxacin, azithromycin, norfloxacin and ceftriaxone to 100% resistant to furazolidone, trimethoprim-sulfamethoxazole, polymyxin-B and streptomycin. The isolates were positive for ctxA, tcpA (El Tor), rtxC genes and were biotype El Tor variant harboring classical ctxB gene. All the isolates were classified as cholera toxin (CT) genotype 1 as they had mutation in the ctxB at positions 39 and 68. All the isolates had genetically similar NotI PFGE and BglI ribotype patterns. The absence of any observed variation is consistent with a clonal origin for all of the isolates.

Conclusion: Kenya experienced cholera numerous outbreak from 2007-2010. The clinical Vibrio cholerae O1 isolates from the recent cholera epidemic were serotypes Inaba and Ogawa, Inaba being the predominant serotype. The Vibrio cholerae O1 strains were biotype El Tor variants that produce cholera toxin B (ctx B) of the classical type and were positive for ctxA, tcpA El Tor and rtxC genes.