Characterization of Antimicrobial Resistance and Virulence Factors in Environmental and Clinical *Vibrio cholerae.*

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ABSTRACT

Since 1970, East Africa has been suffering an increased number of cholera epidemics. In 1997, it accounted for 56% of the annual clinical cases notified by the entire continent to WHO, remaining high (20%) in 1998–99. The upsurge of cholera outbreaks in the late 1990s was also characterized by a high number of multidrug-resistant *Vibrio cholerae* O1 strains. There has been an upsurge of cholera cases in Kenya with 3091 cases in 2008 and 11,769 cases (CFR=2.3%) reported to Ministry of Public Health and Sanitation in 2009. Thus there was need to carry out antimicrobial susceptibility tests on environmental strains and to determine if they carried resistance. Multidrug resistance is on the increase amongst the *V. cholerae* due to the acquisition of the SXT-like element. An increase in outbreak by this drug resistant strain will thus pose a major challenge in control and management of the disease worldwide. The main aim of study was to determine the environmental reservoirs of *V. cholerae* during the interepidemic periods and to characterize antimicrobial resistance and virulence factors in environmental *V. cholerae.* Environmental samples including sediment, algae, brackish water, sewerage water, zooplanktons, phytoplanktons and aquatic plants were collected from epidemic prone areas in Kenya which included the coastal region and the Lake Victoria Basin regions. Isolates from environmental samples were tested for susceptibility to cephalothin, furazolidone, chloramphenicol, tetracycline, ampicillin/sulbactam, streptomycin, kanamycin, tobramycin, cefuroxime, nalidixic acid, sulphamethoxazole and trimethoprim antibiotics, genotyped by PCR for 11 virulence factors and SXT element. Archived recent outbreak strains of *V. cholerae* were also characterized along for comparison. A hundred (50 clinical, 50 environmental) *V. cholerae* isolates were used in the study. Overall, sediments followed by algae collected from fishing and

landing bays were samples which mostly harboured *V. cholerae*. All clinical strains were susceptible to tetracycline while all environmental strains were susceptible to cefuroxime. All clinical strains were resistant to streptomycin, sulfamethoxazole, trimethoprim and furazolidone, while 92% were resistant to nalidixic acid. Environmental strains were 64%, 60%, 60% resistant to cephalothin, sulphamethoxazole and sulbactam/ampicillin respectively. All clinical strains harboured *ctxA, tcpA* (El Tor), *ompU, zot, ace, toxR, hylA* (El Tor), *hyl*A (classical) and *tcpI* genes. Environmental strains prevalence for virulence genes was *hyl*A El Tor (10%), *toxR* (24%), *zot* (22%), *ctxA*(12%), *tcpI*(8%), *hylA*(26%), *tcpA* (12%) and *ace* (2%). Clinical strains possessed SXT-element which was rare in environmental strains. Study sites including landing bays and beaches contained environmental *V. cholerae*. Presence of resistance to antibiotics and some virulence factors showed pathogenic potential of the environmental isolates and may be reservoirs for frequent epidemics. Improved hygiene and fish handling techniques will be important in prevention of persistence of reservoirs.