ABSTRACT

Cholera is a substantial health burden in the developing world and is endemic in Africa, Asia, South and Central America. The exact scale of the problem is uncertain because of limitations in existing surveillance systems, differences in reporting procedures, and failure to report the disease to the World Health Organization. Lake Victoria basin bares the greatest burden of cholera outbreaks in Kenya due to sporadic cases and seasonal epidemic associated with poverty and low hygienic standards. The polluted water in the region enhances prolonged survival of V. cholerae through phage formation and therefore transmission is hypothesized to radiate from these sources. Therefore, establishing the relationship between physicochemical factors, colony forming unit and occurrence of Vibrio strains in this region is essential in order to discern confounding factors that enhance the epidemiology of the respective strain in the regions as well as annotate sequences that would be useful in molecular diagnostic kits and possibly add to the existing vaccine candidate sequences with the goal of controlling the occurrence and spread of cholera. The objective of this study therefore was to determine the relationship between physicochemical factors, colony forming unit and occurrence of Vibrio strains in the environment of the Lake Victoria Basin. This was a cross-sectional study where environmental (water) and clinical samples (stools) were collected from Migori, Nyando, Sondu, Bondo and Yala regions in Western Kenya and transported to the Molecular Microbiology Laboratory at the department of Zoology, Maseno University for isolation and identification of Vibrio species using conventional microbiological methods. A total of 811 samples (596 water and 215 stool samples) were collected during the study periods of May to December 2013 and August to September 2014. The human stool samples were collected from Migori District Hospital (120), Nyando District Hospital (82) and Bondo District hospital (13) using study permit issued by the Maseno University Ethics Review Committee and the hospital authorities. Water samples were collected from rivers, viz: Migori (147), Sondu-Miriu (99) Nyando (109), Yala (151) and Bondo swamps (90). The average colony forming unit and physicochemical factors variability was calculated as the geometric mean and standard deviation respectively. Quantitative Polymerase Chain Reaction (PCR) technique was used for molecular identification of Vibrio strains. Species-specific primers for Vibrio strains (V. cholera, V. parahaemolyticus and V. vulnificus) were used where DNA extracts did not amplify with the intended primer sequences. Species-confirmed isolates were screened for virulence-associated genes. Vibrio vulnificus and V. cholerae were isolated in the study region. However, V. parahaemolyticus was not found in any of the isolates during the study period. The waters where V. cholerae was isolated had a pH range of between 7.7 - 8.2 (P ≤ 0.01), temperature of 22-28°C (P ≤ 0.01), water salinity of 17-161.2 μS•cm~1 (0.2 to 2.3% (P ≤ 0.01). Serologically, the type of V. cholerae identified in these regions was inaba and ogawa. The PCR results for 16SrRNA, Vib 1, Vib 2 showed that there was polymorphism in the genes, an indication that there was high frequency recombination (Hfr) of genes from more than one strain in one isolate. The analysis showed the presence of species specific ctxA genes (564bp) responsible for cholera toxin. The study showed the presence V. cholerae (Ogawa and inaba) and Type B V. vulnificus in water and human stool in the study area. These results are crucial in controlling and managing unpredictable cholera outbreaks in this region. This can be done through ensuring that physicochemical parameters which enhance the growth of Vibrio strains in the region are monitored and constant surveillance undertaken to mitigate circulating strains of Vibrio cholerae and V. vulnificus in the region.