
Antimicrobial resistance profiles of Enterotoxigenic *Escherichia coli* strains recovered from selected rivers of Osun State, Southwest Nigeria

Osuolale Y. Titilawo^{1,2*}, Larry C. Obi^{1,2} and Anthony I. Okoh^{1,2}

¹SAMRC Microbial Water Quality Monitoring Centre, University of Fort Hare, Alice 5700, South Africa

²Applied and Environmental Microbiology Research Group, Department of Biochemistry and Microbiology, University of Fort Hare, Alice 5700, South Africa

*Corresponding author email: olayinkatemi@yahoo.co.uk, telephone: +27 (0) 845731855

Despite advances in knowledge, understanding and management that have ensued in recent years, diarrhoeal disease remains the most prevalent and important public health hazard worldwide, as well as leading cause of morbidity and mortality in the paediatrics. Water samples from selected rivers in Osun State, Nigeria were collected and analyzed using standard procedures. Confirmed *Escherichia coli* isolates ($n=300$) were screened for *Stx* virulence gene using polymerase chain reaction technique. The antimicrobial susceptibility testing of the pathovars was determined by the disc-diffusion assay and the resistant pathovars were elucidated for their genotypic antimicrobial resistance determinants. The results indicated that *Stx* encoding ETEC pathotype was detected in (138) 46% isolates. Antimicrobial resistance profiling conducted *in-vivo* on the strains showed complete resistance to sulphamethoxazole (100%) and high levels of resistance against ampicillin (63%), amoxicillin (55%), gentamycin (41%), cefuroxime (39%), chloramphenicol (28%) and cefepime (26%). Of the 106 resistant strains, 14 (13%) possessed *bla*_{TEM}, whereas 40 (38%) had *bla*_{TEM}. Eight (10%) of the 82 ampicillin-resistant strains were *ampC* positive. The genes *bla*_{TEM} and *bla*_{TEM} were frequently detected in 13 (18%) and 20 (28%) of 71 amoxicillin-resistant strains respectively. Of the four tetracycline-resistance genes targeted, *tetD* was the predominant allele detected. Overall the detection of the tet alleles was *tetA* > *tetB* < *tetC* < *tetD* > *tetK*, being spotted in 6 (19%), 3 (9%), 6 (19%), 20 (63%) respectively. Surprisingly, each of *cmiA1*, *catI* and *catII* were detected in 5 (16%) of 27 chloramphenicol-resistant strains. Only 3 (7%) of 46 gentamycin-resistant strains were *aacC2* positive. Conclusively, this study signifies high prevalence of virulence gene and multidrug-resistant ETEC pathotype in the river water sources which consequently poses threat to public health.

Keywords

Surface water, antibiogram, genetic marker, ETEC, toxin, diarrhoeal disease, public health.