

## ABSTRACT

Incidence of *Salmonella* resistance to various antibiotic agents, especially to the commonly available antibiotics in Kenya, is rising. Genetic elements such as Class 1 integrons have an important role in development and spread of resistance. In western Kenya, integron-mediated antibiotic resistance was reported in clinical *Salmonella* enteric serovars. However, no similar studies have been done to elucidate the role of class 1 integrons in fish isolates for multidrug resistant *Salmonella* spp. The aims of this study is to determine the levels of microbial contamination of fish, investigate antibiotic resistance mechanisms in *salmonella* spp isolated from *Rastrineobola argentea* obtained from markets (Kibuye, Luanda, Yala and Busia) and selected Winam Gulf beaches (Usenge, Dunga, Port Victoria and Uhanya). A cross sectional study design based on random sampling was used. 96 fish were sampled to determine antimicrobial susceptibility of the isolates, the incidence of resistant as well as screen *Salmonella* spp for the presence of class 1 integrons and characterize resistance genes. *Escherichia coli*, *Citrobactor* spp and *Salmonella* spp were isolated on MacConkey and XLD agar plates respectively. Biochemical tests (IMViC) confirmed *E. coli* while TSI, LIA, and urease confirmed the presence of *Salmonella* spp. API 20E further confirmed all the isolates. Susceptibilities of seven antimicrobials were determined by agar disk diffusion method on Mueller Hinton agar. PCR was used to; characterize *Salmonella* spp by *Malic acid dehydrogenase* genes, screen for the presence of resistance genes and class 1 integron. ANOVA was used to determine statistical significance. Mean Aerobic Plate Count of sun-dried *R. argentea* in markets was statistically higher ( $p=0.003$ ) while that of beaches varied with sampling time (wet,  $p=0.023$ ); (semi-dry,  $p=0.03$ ) (dry,  $p=0.02$ ). By using *chi-square* analysis, classes 1 integrons were not significantly associated with the antibiotics; tetracycline, ampicillin, streptomycin, chloramphenicol, and sulfamethoxazole ( $p>0.05$ ). *E. coli* was the most frequently isolated 36.66% followed by *Salmonella* spp 8.33% *Citobactor* spp, 5.83% *Klebsiella* spp and *protieus* spp 1.58% each. Relatively high antibiotics resistance frequencies were found especially for chloramphenicol (50%), ampiciline (33.33%). Tetracycline and sulphamethoxazol 20.63% each while nalidixic acid streptomycin and ciprofloxacin were 7.93%, 3.17% and 1.85% respectively. For *Salmonella* spp, resistance rates were; 30%, 20% and 10% to chloramphenicol, (tetracycline sulphamethoxazol and ampicilin each) and streptomycin respectively. All isolates tested were susceptible to nalidixic acid and ciprofloxacin. Three isolates (one from market and two from beach) were multidrug resistance with at least three antimicrobials. Tetracycline resistance genes (*tet A*) 20%, ampiciline resistance genes *bla*TEM 20%, and streptomycin resistance genes (*aadA*) 10% were detected. Integron gene was found in two isolates (20%). One was from market and the other from the beach. Fish landing sites and fish markets may be a reservoir of many and different antibiotic resistant genes. Integrons may not be associated with multidrug resistance ( $p>0.05$ ) isolates from fish. Thus presence of alternative resistance mechanisms.