Antibiotic Susceptibility Patterns and Detection of Genes Responsible for Resistance of *Klebsiella* species and *Escherichia coli* Isolated from Environmental Sources around Nairobi, Kenya

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ABSTRACT

The Enterobacteriaceae are a large family of Gram negative bacteria which inhabit the intestines of man and animals. Members of this family are not only found in the gastrointestinal tract but are also in soil and water and in the respiratory tracts of human and animals where they cause a variety of septic and urinary tract infections. Many of these organisms harbor antibiotic-resistance genes, usually inserted into genetic mobile platforms (plasmids, transposons, and integrons) able to spread among water and soil bacterial communities. The organisms have developed various mechanisms of drug resistance which include extended spectrum β-lactamases (ESBLs) production, Ambler Class C β-Lactamases *(AmpC)* β-lactamase production, efflux mechanisms and porin deficiency.

To determine susceptibility patterns and resistance mechanisms in environmental *Klebsiella* and *Escherichia coli* (*E. coli*), bacteria strains were isolated from streams/rivers, sewage dams and bore holes in Nairobi and its environs. Isolates were identified by biochemical typing. Susceptibility to aminoglycosides, nucleic acids inhibitors, fluoroquinolones and β-lactamases antibiotics was done using the disk diffusion method. Polymerase Chain Reaction (PCR) was used to screen for the presence of aminoglycoside modifying enzymes (*ame*) and integron 1 and 2 genes (*int1 and int2*). Presence of plasmid mediated resistance was also screened by isolation of plasmids from multi resistant isolates and the plasmids were characterized according to their sizes. Ability for bacteria to transfer resistance plasmid was determined by conjugation experiments with *E. coli* C600. Chi square or Fisher's Exact test was used as appropriate to determine any significant association of data that can be put into tables with mutually

exclusive and exhaustive cells. The prevalence of *E. coli* (40.1%) was significantly higher than *Klebsiella* spp. (29.1%) ($p<0.05$). Resistance to nucleic acid inhibitors was the highest (57%) compared to aminoglycosides (27%), beta lactams (17%) and lastly fluoroquinolones (10%) ($p<0.05$; chi-squared for independence). Presence of *Int1* was significantly lower in *E. coli* (47.4%; [18/38]) than in *Klebsiella* spp (73.0% [27/37]), ($p<0.05$; chi-squared for independence). Integron 2 was not detected in any of the isolates. Aminoglycoside modifying enzyme gene *aac(6')-lb-cr* was detected in 18.2% (2/11) of *E. coli* and 25% (5/20) of *Klebsiella* species. Two *E. coli* and three *Klebsiella* spp transferred ampicillin resistance to *E. coli* C600. In this study, *E. coli* and *Klebsiella* spp isolated from water samples obtained from boreholes, streams/rivers, sewage sources showed resistance to the four main groups of antibiotics tested namely; quinolones, aminoglycosides, nucleic acid inhibitors and beta-lactam antibiotics tested. Resistance was plasmid mediated in *E. coli* and *Klebsiella* spp from environmental sources and due to production of *int1* and *ame* genes enzymes.