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EVALUATION OF TRANSFERABILITY OF KANAMYCIN RESISTANT GENES FROM RESISTANT TO SUSCEPTIBLE STRAINS OF *Escherichia coli*

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ABSTRACT

Resistance to multiple antimicrobial agents in bacterial pathogens is an emerging global problem With a serious impact on the treatment of infectious diseases .This resistance poses a major public health concern due to few therapeutic options available, and due to treatment failure arising from use of antibiotics that were no longer potent. There are undoubtedly many factors associated with the emergence of resistance to antibiotics and an understanding of these factors is crucial if we are to limit the spread of resistance. The dissemination of antimicrobial resistance is largely attributed to conjugative DNA exchange when a genetic marker encoding resistant to an antibiotic is transferred from a resistant to a susceptible strain. One antibiotic frequently used for treatment of E. coli infections especially in ICU settings is Kanamycin. Until recently, this aminoglycoside is isolated form streptomyces and has been in use for a long period of time to treat these infections with a good amount of success.

This study was conducted to investigate the transferability of kanamycin resistant markers from Kanamycin resistance *E.coli* strains to a susceptible recipient strain, *E. coli* J 53 that is resistant to Sodium Azide resistant. The objective of the study was to analyze the frequency of transfer of genetic markers encoding this gene and to examine its transferability with other unrelated antibiotics. This work was a part of an ongoing project at CMR-KEMRI by Kiiru J *et al* and the strains used in this project were obtained between 2007 and 2009 from various health institutions. In order to protect the confidentiality of the hospital and patients from which the isolates were obtained, no clinical data or the patient information was obtained from the project and these strains were only used for the 'proof of principle" of the experiments described herein. The strains had been isolated from urine, blood and pus samples using standard microbiological procedures. Upon confirmation of the identity on Mackonkey plates followed by API 20 E tests, susceptibility testing was done on the transconjugants and donors. The plasmid profiles were then determined. PCRs for the detection of the *aac (6')-lb-cr* gene encoding resistance to both aminoglycosides and ciprofloxacin were also done. All isolates were resistant to kanamycin and resistance to this antibiotic was also co-transferred with that of other classes of antibiotics. A 3.7 Kb plasmid was detected in all isolates and their transconjugants indicating that this conjugative plasmid may be implicated in the transfer of all the associated antibiotic resistance determinants.