

Phenotypic and Genotypic Antibiotic Resistant diarrheagenic *Escherichia coli* pathotypes isolated from Children with Diarrhea in Nairobi City, Kenya

Abstract.

Background: The marked genome plasticity of diarrheagenic *Escherichia coli* promotes emergence of pathotypes displaying unique phenotypic and genotypic resistance. This study examined phenotypic and genotypic antibiotic resistant diarrheagenic *Escherichia coli* pathotypes among children in Nairobi City, Kenya.

Methods: In a cross-sectional study, diarrheagenic *Escherichia coli* pathotypes were isolated from stool samples and their phenotypic and genotypic resistance against eight antimicrobial agents assayed.

Results: Diarrheagenic *Escherichia coli* was detected in 136(36.4%) children. Most of diarrheagenic *Escherichia coli* that were resistant to ampicillin, ceftriaxone, streptomycin, gentamycin, ciprofloxacin, chloramphenicol, erythromycin and tetracycline, harbored *citm*, *bla* CMY, *aadA1*, *aac(3)-IV*, *qnr*, *catA*, *ere(A)* and *tet(A)* corresponding resistant genes.

Conclusion: Antimicrobial-resistant genes are highly prevalent among phenotypic resistant ETEC pathotypes indicating a possibility of horizontal gene transfer in spreading antibiotic resistant genes among *E. coli* pathotypes.

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