

## Abstract

**Background:** *Escherichia coli* are well known to be part of the normal intestinal flora. However, some may be pathogenic hence capable of causing diarrhoea commonly in children under five. To understand the pathogenic *E. Coli*, virulence genes had to be investigated. Antimicrobial resistance was also studied this being a global concern.

**Objective:** To determine the molecular pathotypes of *E.coli* isolated from diarrheal children and their antibiotic resistance trends to the commonly used antibiotics.

**Methodology:** A descriptive experimental study was conducted using 196 stool samples collected from diarrheal children under five between 1st January to 30th June 2019. *E. coli* was isolated and Polymerase chain reaction was used to characterize the pathogenic subtypes. Antibiotic resistance was evaluated using the Kirby-Bauer technique.

**Results:** From the 196 samples collected, 79(40%) cases of enteric pathogens were isolated out of which Enteroaggregative *E.coli* were 27(34.2%), Enterohaemorrhagic *E.coli* 14(17.7%), Enterotoxigenic *E.coli* 12(15.2%) while Enteropathogenic *E.coli* was 6(10%). Virulence genes detected include: Intimin (*eae*), Shigatoxin (*stx*), *est*, *elt*, *AggR*, *Cvd432*, *Aspu*. All *E.coli* pathotypes isolated were over 75% resistant to Tetracycline, Augmentin and Cotrimoxazole except EHEC being 100% resistant to Ampicillin.

**Conclusion:** Diarrheagenic *E. coli* is a key contributor to children below five years. Drug resistance to the isolated bacteria was found to be a challenge.