

# Characterization and antimicrobial resistance profiles of *e. coli* pathotypes isolated from children under five years at two sentinel sites in Pretoria South Africa

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## Background and Objectives

In developing countries including South Africa, diarrhoeal disease is the second leading cause of deaths in children under 5 years of age. Enterotoxigenic *E. coli* (ETEC), shiga toxin-producing *E. coli* (STEC), attaching and effacing *E. coli* (AEEC) are important bacterial causes of diarrhoeal disease. Antimicrobial resistance (AMR) among enteric bacteria has become a public health threat by complicating effective treatment of diarrhoeal infections. Current studies on bacterial causes of childhood diarrhoea and associated antimicrobial resistance are limited in South Africa. This study was conducted to assess the presence of virulence potential of ETEC, STEC and AEEC isolates that were recovered from children under five presenting with diarrhoea at Dr George Mukhari Academic Hospital (DGMH) and Oukasi Primary Healthcare Centre (OPHC).

## Methods

A bacterial collection comprising of 129 ETEC, 29 STEC and 18 AEEC isolates was screened for the presence of genes that are considered virulence factors or markers including heat labile (LT), heat stable (STh, STp), shiga toxins (*stx1*, *stx2*), intimin (*eaeA*) and enterohemolysin (*hlyA*) genes respectively using two step multiplex PCR protocols. Furthermore, the recovered isolates were characterized for antimicrobial resistance patterns using Kirby-Bauer disk diffusion technique.

## Results

Among the ETEC recovered isolates, STp gene was found in 40% (32/80), STh 38.7% (31/80) and LT 37.5% (30/80). The following results were recorded for STEC and AEEC isolates: *stx1* 83.3% (15/18), *stx2* 50% (9/18), *eaeA* 100% (18/18) respectively. One of the isolates was found to possess strain combination *stx2* + *eaeA* + *hlyA* 5.6% (1/18). Highly resistance isolates to ampicillin and trimethoprim-sulfamethoxazole [ETEC 70% (56/80); 53.8% (43/80), STEC 55.6% (10/18); 50% (9/18), AEEC 77.8% (14/18); 61.1% (11/18)] were observed. Multidrug resistance (MDR) isolates rate were ETEC 43.8% (35/80), STEC 27.8% (5/18) and AEEC 61.1% (11/18).

## Conclusion

This study confirms that the most predominant gene found in ETEC was STp. While *stx2* and *eaeA* genes were commonly detected in STEC and AEEC isolates, respectively. The above-mentioned *E. coli* strains were resistant to commonly used antibiotics (ampicillin and trimethoprim-sulfamethoxazole). Furthermore, MDR isolates were detected from children under five presenting with diarrhoea. This is mostly associated with excessive use of broad-spectrum antimicrobials in treating human infections. Therefore, there is need for surveillance studies and control of antimicrobial usage in an appropriate manner.