



DETECTION OF VEROCYTOTOXIN-PRODUCING *ESCHERICHIA COLI* AND CHARACTERIZATION OF SUB-VARIANT OF *stx* GENES ISOLATED FROM THE ZANGO ABATTOIR AND SURROUNDING

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ABSTRACT

Escherichia coli O157:H7 and other non-O157 verotoxin-producing *E. coli* serotypes also known as Shiga-like producing *E. coli* (STEC) have been associated with human diseases as foodborne pathogens responsible for outbreaks and sporadic cases of diarrhoea, haemolytic uraemic syndrome (HUS) and haemorrhagic colitis. It is essential to generate further information on the occurrence of different serotypes of STEC, subvariants of *stx*₁ and *stx*₂ genes circulating in the abattoir environment. Cattle faeces, abattoir effluent, water samples from stream receiving the abattoir effluent and vegetables samples irrigated with water from the stream were taken from the abattoir environment. *E. coli* was phenotypically isolated from these samples using EMB agar and biochemically characterised. Biochemically characterised *E. coli* were subjected to conventional PCR and microtitre agglutination test to identify *stx* genes, subtypes of *stx* genes variants and also to serotype the isolated STEC isolates. The results of the characterisation showed the presence of both *stx*₁ and *stx*₂ genes in the three isolates of STEC. However O-serogroups O91 and O8 were identified from STEC isolates. In conclusion this study demonstrates the isolation of three STECs from cattle faeces and cabbage samples harbouring *stx*_{1a} and *stx*₂ (*stx*_{2a}, *stx*_{2b}, *stx*_{2d}) genes which are predisposing factors towards development of HUS in human infection.

Keywords: Verocytotoxin, *E. coli*, abattoir, environment, *stx* genes, public health

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