

O0757 Genetic characterization of enterohaemorrhagic *Escherichia coli* O157:H7 isolates from clinical specimens and environmental samples in Gauteng region, South Africa

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Background: Enterohaemorrhagic *Escherichia coli* (EHEC) O157:H7 or Shiga toxin-producing *E. coli* is an important foodborne and waterborne pathogen causing bloody diarrhoea and severe diseases such as haemolytic uremic syndrome. The reservoirs for EHEC O157:H7 are healthy ruminant animals. Humans acquire EHEC O157:H7 by direct contact with animals or *via* the ingestion of contaminated food or water. In South Africa, limited information is available on the genetic diversity of EHEC O157:H7. The aim of this study was to characterise the EHEC O157:H7 isolates in the Gauteng region of South Africa.

Materials/methods: Water samples and stool specimens were collected from October 2016 to September 2017. Samples were cultured on selective chromogenic media and presumptive EHEC O157:H7 were confirmed by using latex agglutination test. Isolates were characterised using multiplex PCR assays to screen for the *uidA*, *rfbEO157* and *fliCH₇* genes that encode for β -glucuronidase, somatic-O and flagellar-H antigens respectively and for the virulence genes: Shiga-toxins 1 and 2 (*Stx-1*; *Stx-2*), enterohaemolysin (*hlyA*) and *E. coli* attaching and effacing lesion (*eae*). Genetic relatedness of isolates was determined using pulsed-field gel electrophoresis (PFGE).

Results: A total of 306 samples were analysed of which 7% (21/306) of isolates were identified as EHEC O157:H7 by M-PCR assay. Run-off water represented 90% (19/21) and stool specimens represented 10% (2/21) of isolates. The *uidA* gene was detected in 100% (21/21) of the isolates confirming *E. coli*. The *rfbEO157* and *fliCH₇* genes were detected in 29% (6/21) and 33% (7/21) respectively. The *Stx-1*, *Stx-2*, *hlyA* and *eae* genes were present in 10% (2/21), 19% (4/21), 5% (1/21) and 14% (3/21) of isolates respectively. In 48% (10/21) of the isolates no virulence genes were detected. The EHEC O157:H7 isolates are genetically diverse based on the PFGE results.

Conclusions: This study reports the presence of EHEC O157:H7 in stool specimens and environmental samples. The inclusion of molecular testing for EHEC O157:H7 can improve the detection of this important pathogen in clinical settings. Environmental surveillance plays an important role in reducing the potential health risk to close human contacts as well as to consumers of untreated water and undercooked meat.