

P0871 Molecular epidemiology of enterohaemorrhagic *Escherichia coli* O157:H7 isolates from Gauteng, South Africa

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Background: Enterohaemorrhagic *Escherichia coli* (EHEC) O15:H7 has emerged as an important enteric pathogen causing human gastrointestinal disease, outbreak and haemolytic uremic syndrome (HUS) associated with the production of Shiga toxins specifically Stx2. The intestinal tract of ruminants, particularly cattle, have been regarded as the primary reservoir of EHEC O15:H7. 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 genotype distribution of EHEC O157:H7, therefore the aim of this study was to determine the molecular epidemiology of EHEC O157:H7 isolates using pulsed-field gel electrophoresis (PFGE) and multilocus sequence typing (MLST) of selected isolates collected in Gauteng province, South Africa.

Materials/methods: Clinical stool specimens and run-off water samples collected from August 2016 to December 2017 were cultured on selective agar followed by phenotypic susceptibility testing and identification of EHEC O157:H7 using multiplex PCR assay. The genes screened included the *uidA*, *rfbEO157* and *fliC_{H7}* genes encoding for β -glucuronidase, somatic-O and flagellar-H antigens respectively and colistin resistance gene. Genetic relatedness of isolates was determined using PFGE and MLST on selected isolates.

Results: In total 520 samples were analysed and 132 presumptive EHEC O157:H7 were identified of which 36% (48/132) of the isolates were identified as EHEC O157:H7. Run-off water and stool specimens showed a prevalence of EHEC O157:H7 of 85% (41/48) and 15% (7/48) respectively. Ampicillin, imipenem, meropenem and ertapenem resistance were detected in 50% (24/48), 13% (6/48), 10% (5/48) and 4.2% (2/48) respectively. No *mcr-1* or *mcr-2* genes were detected. The dendrogram constructed after PFGE showed six minor pulsotypes, which indicated that the EHEC O157:H7 strains were diverse. The MLST analysis identified three sequence types (STs) (ST10, ST11 and ST1204) that have been previously associated with outbreaks.

Conclusions: This study revealed that EHEC O157:H7 isolates obtained from run-off water samples and clinical specimens were diverse. However one clinical isolate clustered with a run-off water from an abattoir. The STs identified in this study pose a potential public health risk to consumers of untreated water and closed human contact since they have been implicated in outbreak.

