

October 11-12, 2018
Edinburgh, Scotland

Collins Njie Ateba et al., J Infect Dis Treat 2018, Volume 4
DOI: 10.21767/2472-1093-C2-005

Molecular characterization of virulent *Escherichia coli* O157: H7 isolated from cattle using pulsed-field gel electrophoresis

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E. coli O157:H7 is an important causative agent of a variety of food-borne infections including hemorrhagic colitis (HC) and hemolytic uremic syndrome (HUS) in humans. The main source of infection is contaminated food of animal origin and a number of animal species, especially cattle have been associated with this pathogen. Contamination usually occurs when faeces of animals get into contact with carcass during slaughtering. The aim of the present study was to determine the virulence profiles and genetic relationships of *E. coli* O157:H7 strains isolated from cattle of some commercial farms in the North West Province, South Africa. A motivation is that results may enhance our knowledge of on-farm ecology of *E. coli* O157:H7 strains as well as their potential to cause diseases in humans. A total of 260 faecal samples were collected from eight farms over a six-month period and assessed for the presence of *E. coli* O157:H7 through PCR analysis. STEC virulence genes *stx1*, *stx2*, *eaeA* and *the hlyA* were detected using PCR. The genetic relatedness of the isolates was determined using random amplified polymorphic DNA (RAPD) and pulsed-field gel electrophoresis (PFGE) bacteria 16S rRNA gene fragments were amplified as an internal control, while the *rfbO157* and *flicH7* gene PCR were used to confirm identities of isolates. A total of 69 (26.5%) *E. coli* O157:H7 isolates were detected in samples obtained from all the eight farms. The large proportions of the *E. coli* isolates possessed the *stx1* (66.7%) and *stx2* (97.1%) genes, respectively. In addition, other accessory virulence genes such as *eaeA* and *hlyA* were detected in 30 (43.5%) and 43 (62.3%) of the *E. coli* isolates, respectively. Pulsed-field gel electrophoresis (PFGE) analysis grouped these isolates into

six clusters of closely related types, and the predominant cluster comprising of 17 isolates originating from different farms under study. These results provide valid evidence that cattle harbor virulent and genetically similar *E. coli* strains particularly those belonging to the serotype O157 and therefore these animals may serve as possible source for zoonotic transfer of these pathogens to humans. The implication is that these isolates may have severe public health consequences on consumers.

Biography

Collins Njie Ateba has completed his PhD from the North-West University, South Africa. He also received professional training in the Centre of Medical Genetics and Primary Health Care, Yerevan State University, Yerevan, Armenia in 2006; Department of Microbiology, Tartu University, Tartu, Estonia in 2007 and the Lethbridge Research Centre, Lethbridge Alberta, Canada in 2014. He is currently an Associate Professor in the Department of Microbiology, Faculty of Natural and Agricultural Sciences, North-West University, Mafikeng Campus and is the Head of the Department of Microbiology as well as the Water, Food Safety and Phage Therapy/Biocontrol Research Laboratory. He is actively involved in research training and lecturing at both undergraduate and postgraduate levels. He has been serving as a Host Mentor for the DST/NRF internship program from 2011 till date. He has published more than 30 papers in reputed journals and has been serving as an Editorial Board Member of repute. He has presented research papers in a number of conferences locally and internationally. He is currently classified as an Established Researcher in the "C3" category by the National Research Foundation of South Africa.

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