

Microbiological spotlights

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Virulence potential and antibiotic resistance of Shiga toxigenic *Escherichia coli* (STEC) isolates from raw cow milk in Ghana**Akabanda F.¹, Owusu-Kwarteng J.¹, Wuni A.², Tano-Debrah K.³**¹University for Development Studies, Department of Applied Biology, Navrongo, Ghana, ²University for Development Studies, Department of Biotechnology, Nyankpala, Ghana, ³University of Ghana, Department of Nutrition and Food Science, Accra, Ghana

Shiga toxigenic *Escherichia coli* (STEC) is an important food-borne pathogen of public health concern in both developed and developing countries. STEC can cause haemorrhagic colitis and haemolytic-uremic syndrome, which can lead to kidney failure and death, particularly in young children. Currently, there is little or no information on the virulence potential and antibiotic resistance profile of STEC isolates in raw milk collected from agro-pastoral farms in Ghana. This study therefore sought to investigate the prevalence, virulence potential and phenotypic antibiotic resistance of STEC isolates in raw cow milk collected from agro-pastoral farms in Ghana. A total of 210 raw cow milk samples were collected from 42 agro-pastoral units made up of 15 small scale (1-20 cattle), 23 medium scale (21-100 cattle) and 4 large scale (> 100 cattle) farms in Ghana. *Escherichia coli* was isolated from raw milk and identified using the Vitek II Compact system. PCR analyses were performed using specific primers targeting the major STEC virulence genes that encode Shiga toxin (*stx1* and 2), intimin (*eaeA*), and STEC autoagglutination adhesin (*saa*). The O-serotypes of STEC isolates were determined by using *E. coli* antisera. Antibiotic susceptibility profiles of STEC isolates was examined by the determination of the minimal inhibitory concentrations (MIC). In total 58.1% (122/210) of raw milk samples collected from agro-pastoral farms were positive for *E. coli*. *Escherichia coli* was frequently detected in milk from large-scale farms (42/60; 70%), medium-scale farms (47/90; 52.2%) and small-scale farms (33/70; 47.1%). Ten of 423 (2.4%) *E. coli* isolates harbored the *stx* genes. The *stx* genes were detected in *E. coli* isolates originating from large-scale (6/130 isolates; 4.6%) and medium-scale (4/185 isolates; 2.2%) farms, while no *stx* gene was detected in *E. coli* isolates originating from small-scale farms. All 10 STEC isolates belonged to different serogroups, with no O157 serotype detected. Again, all STEC isolates harbored *eae* gene but not *saa* gene. In addition, 40% (4/10) harbored only *stx1* gene, 10% (1/10) harbored only *stx2* gene and 50% (5/10) possessed both *stx1* and *stx2* genes. STEC isolates showed phenotypic antibiotic resistance to ampicillin (10/10; 100%), streptomycin (10/10; 100%) and tetracycline (8/10; 80%). All STEC isolates showed resistance to at least two different antibiotics.

Keywords: STEC, virulence potential, raw milk, antibiotic resistance, serogroups