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Occurrence of virulence genes associated with diarrheagenic *Escherichia coli* isolated from raw cow's milk from two commercial dairy farms in the Eastern Cape Province, South Africa

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Escherichia coli remains a public health concern worldwide as an organism that causes diarrhea and its reservoir in raw milk may play an important role in the survival and transport of pathogenic strains. Diarrheagenic *E. coli* strains are diverse food-borne pathogens and causes diarrhea with varying virulence in humans. We investigated the prevalence of pathogenic *E. coli* in raw milk from two commercial dairy farms. Four hundred raw milk samples, 200 from each dairy farm, were screened for the presence of *fliCH7*, *eagR*, *ial*, *eae*, *lt*, and *papC* genes. In dairy farm A, 100 *E. coli* were identified based on culture, oxidase and Gram staining, while 88 isolates from dairy farm B were identified in the same manner. Gene detection showed *fliCH7* 27 (54%) to be the highest gene detected from farm A and *lt* 2 (4%) to be the lowest. The highest gene detected in dairy farm B was *fliCH7* 16 (43.2%) and *papC* 1 (2.7%) was the least. The amplification of pathogenic genes associated with diarrheagenic *E. coli* from cows' raw milk demonstrates that potentially virulent *E. coli* strains are widely distributed in raw milk and may be a cause of concern for human health.

Biography

Lesley-Anne Caine has completed her MSc in Microbiology (cum laude) in 2014 from University of Fort Hare and is currently doing her PhD in Microbiology. She has published one paper.

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