Prevalence of Shiga-toxigenic *Escherichia coli* in Mauritian dairy cattle

Prévalence de la toxine Shiga d'*Escherichia coli* chez les bovins laitiers mauriciens

Predominio de la toxina Shiga *Escherichia coli* en el ganado lechero de las Islas Mauricio

S.I.L. Thierry[1*] S.J. Santchurn[1] Y. Jaufeerally-Fakim[1] J.E. Gannon[2]

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Palabras clave: Mauricio – Ganado de leche – *Escherichia coli* – Microbiología – Contaminación.

Shiga-toxigenic *Escherichia coli* (STEC) are important human pathogens (1). They are characterized by their ability to produce Shiga toxins (*stx1* and *stx2*). Seven STEC have been shown to withstand food processing procedures that are expected to ensure food safety. Clinical symptoms associated with STEC infection can vary from abdominal cramps and acute bloody diarrhea to more severe aftereffects including hemorrhagic colitis, hemolytic uremic syndrome and thrombocytopenic purpura, which can lead to kidney failure and death.

Dairy cattle, which excrete STEC in their feces, are a major source of STEC infection (2). Humans become infected with STEC through direct contact with infected animals or by ingestion of contaminated water, raw and unpasteurized milk, meat products, and/or plant-derived products (4–6). The objectives of this study were to estimate both cow-level and farm-level point prevalence estimates of STEC fecal shedding in Mauritian dairy cattle and to characterize putative STEC isolates based on their virulence factors.

A cross-sectional study was conducted to investigate the prevalence of STEC in the dairy cattle population of Mauritius. Fecal samples were collected from 150 individual dairy cattle from 38 dairy farms located throughout the nine district regions of the island. Collected samples were enriched in modified Tryptic Soy broth followed by isolation on CHROMagar™ STEC (3). Suspected isolates were streaked onto EMB agar, further purified on nutrient agar and subsequently cryopreserved in glycerol until further investigation. Putative isolates were characterized using molecular techniques (7, 8) for the presence of chromosomal sequences encoding Shiga toxin genes (*stx1* and *stx2*), the intimin protein (*eaeA*) and the plasmid-encoded hemolysin (*hlyA*).

Out of the 38 farm samples, 29 farms (76%) were found to be positive for presumptive STEC isolates. From the 150 fecal samples collected, 111 (74%) were found to harbor presumptive STEC isolates (Table I). Polymerase-chain-reaction- (PCR-) based characterization has confirmed the presence of STEC in a number of fecal samples. Results obtained so far indicate that STEC are common members of the gut microbiome of dairy cattle in Mauritius.

Presumptive STEC isolates are currently being screened with PCR targeting *stx1*, *stx2*, *eaeA* and *hlyA* genes. This epidemiological study on STEC is the first of its kind in Mauritius and in the Indian Ocean region. It aims at providing new information concerning the presence of STEC in Mauritian dairy cattle. It involves the use of the latest chromogenic agar (CHROMagar™ STEC) available on the market. This culture medium has been designed for the detection of a wide range of STEC from different sources. The study highlights the importance of implementing proper sanitary

Table I

Cow-level prevalence of presumptive Shiga-toxigenic *Escherichia coli* in Mauritian dairy cattle sampled from 38 dairy farms (July-Nov. 2014)

Location	Prevalence (%)	95% CI
Pamplemousses	27/33 (82)	64–93
Rivière du Rempart	10/24 (42)	22–63
Flacq	13/16 (81)	54–96
Grand Port	8/12 (67)	35–90
Savanne	12/13 (92)	64–100
Plaines Wilhems	5/8 (62)	24–91
Moka	15/18 (83)	59–96
Black River / Port-Louis	21/26 (81)	61–93
Cow-level prevalence estimate	111/150 = 74%	66–81
Farm-level prevalence estimate	29/38 = 76%	60–89

CI: Confidence interval

1. University of Mauritius, Réduit, Mauritius.
2. University of Montana, 32 Campus Drive, Missoula, MT 59812, USA.

* Corresponding author
E-mail: sebastien.thierry1@umail.uom.ac.mu

measures at the dairy farm level to prevent cross contamination of milk and the surrounding environment.

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