

TITLE: EVALUATION OF THE VIRULENCE PROFILE OF SHIGA TOXIN-PRODUCING *ESCHERICHIA COLI* ISOLATED FROM RUMINANT ANIMALS

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ABSTRACT:

Shiga toxin-producing *Escherichia coli* (STEC) are important food-borne pathogens associated with human diseases including mild diarrhea, hemorrhagic colitis and hemolytic uremic syndrome. Cattle and other ruminants are natural reservoirs for STEC that can also be found in the environment. The O157:H7 serotype has been recognized as the most important agent of disease. However, several non-O157 STEC serotypes unable to cause attaching and effacing lesion (A/E) have also been responsible for causing serious human infections. The main aim of this study was to evaluate the pathogenic potential of 125 STEC strains devoid of A/E isolated from sheep, goat, buffalo and cattle. The distribution of gene sequences related to Stx1 and Stx2 subtypes, autotransporter proteins (EspP, EspI, EpeA, Sab), adhesins (Saa), toxins (EhxA), iron uptake protein (Irp2) and metalloprotease (StcE) were sought by PCR. The strain phylogroup was also determined. STEC isolates most frequently harbor *stx2* (52%) and *stx1stx2* (38%). Subtypes *stx1a* (57%), *stx1c* (47%), *stx2a* (67%), and *stx2d* (38%) were those most frequently identified, and the distribution of subtypes varied according to the reservoir. *stx1a* prevailed in cattle and buffalo isolates, *stx1c* predominate in sheep and goat, *stx2a* in cattle, and *stx2d* prevailed in goat and buffalo. The *saa*, *espP*, *ehxA*, *espI*, *epeA*, *sab*, *irp2* and *stcE* genes were identified in 89%, 58%, 55%, 43%, 30%, 13%, 11% and 9% of the STEC isolates, respectively, and differences were also observed depending on the reservoir. *espP* and *ehxA* molecular characterization showed that variants C (90%) and A (100%) prevailed, respectively. Phylogroup B1 was the one most frequently identified. In summary cattle STEC isolates most frequently carry the *stx2* subtypes related to human infections, and harbor virulence factors at higher frequencies compared to the other animals studied.

Keywords: non-O157, ruminants, STEC, virulence profile

Development Agency: FAPESP, CNPQ