FREQUENCY OF VIRULENCE GENES RELATED TO DIARRHEOGENIC *E. coli* IN CATTLE FROM CORDILLERA DEPARTMENT OF PARAGUAY IN 2016.

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Escherichia coli are a gram-negative bacillus present in the normal intestinal flora of people. However, certain strains can cause diarrheal disease, and are called diarrheogenic E. coli (DEC). DECs include enterotoxigenic (ETEC), enteropathogenic (EPEC), enteroinvasive (EIEC), enteroaggregative (EAEC), and Shiga toxin producing (STEC) strains of E. coli. The intestinal tract of cattle constitutes one of the main reservoirs of DECs, humans are infected through the ingestion of contaminated meat products. The present work was carried out with the objective of detecting the presence of stx1, stx2, ehxA, saa, eae, elt, est, aggR, ipaH genes in fecal samples of bovine cattle.

This observational study has a protocol approved by the Scientific and Ethics Committees of the Health Sciences Research Institute of Paraguay. Fifty fecal samples were taken from bovine cattle from a ranch of the Cordillera department of Paraguay in 2016. Sampling was performed by rectal swab to selected cattle for convenience; samples were grown on McConkey agar for the boiling of DNA from the confluent bacterial zone. The presence of the virulence factors associated with each pathotype was then analyzed by conventional PCR.

The frequency of animals bearing STEC-related genes was 82% (41/50) for stx1 and / or stx2, 74% (37/50) for ehxA, and 68% (34/50) for saa. In 2% (1/50) of the animals *eae* was detected, it can mean the presence of EPEC or STEC strains. The elt, est, aggR, and ipaH genes associated with the ETEC, EAEC, and EIEC pathotypes respectively were not detected.

The high frequency of STEC-related gene bovine carriers represents a problem for public health, because failures in good hygiene practices in the production chain can lead to contamination of the meat products that constitute the source of transmission to humans. These results demonstrate the need to establish control systems in the meat production chain, from animal breeding to final product that is why we consider that the molecular methods used in this study are excellent alternative for this purpose.

Keywords: cattle, conventional PCR, diarrheogenic E. coli (DEC), Paraguay, virulence genes.

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