Titulo : **PREVALENCE AND DISTRIBUTION OF THE SERINE PROTEASE AUTOTRANSPORTER EspP IN SHIGA TOXIN-PRODUCING *Escherichia coli* FROM THE ANIMAL RESERVOIR**

Autores: Freire, C. F.[1] , Dos Santos, L. F.[2] , Matheus-Guimarães, C.[1] , Guth, B. E. C.[1]

Instituições: [1]EPM-UNIFESP - Escola Paulista de Medicina, Universidade Federal de São Paulo (Rua Botucatu 862, 3 andar, 04023-062), [2] IAL- Centro de Bacteriologia , Instituto Adolfo Lutz (Av Dr. Arnaldo 355, 9 andar- São Paulo, SP)

Resumo :

Shiga toxin-producing *E. coli* (STEC) are food-borne pathogens responsible for causing hemorrhagic colitis and hemolytic uremic syndrome. Cattle and other ruminants are natural reservoirs for STEC that can also be found in the environment in many different conditions. EspP belongs to the family of serine protease autotransporters of *Enterobacteriaceae* and considered as one of STEC additional virulence factor. Different subtypes of EspP have been described, and among them EspPα have been associated with isolates from patients with severe disease. The aim of this study was to evaluate the presence of *esp*P genes and the distribution of *esp*P subtypes in a collection of 128 STEC LEE-negative strains isolated from several animal species and belonging to different serotypes. Strains were screened for the presence of *espP* using PCR with specific primers that amplify a 1,830-bp internal fragment of the gene. For subtyping two methods were employed. The amplicon from *esp*P-positive strains was digested with AluI resctrition enzyme and RFLP analysis was performed by agarose gel electrophoresis. In addition, detection of *esp*Pα, *esp*Pβ and *esp*Pγ alleles was carried out by specific PCR. *esp*P was found in 74 (57.8%) STEC strains, being more frequent among isolates from cattle (72%) and buffalos (78%) compared to isolates from goats (19%). None of the STEC strains isolated from sheep carried *esp*P. *esp*P-positive isolates belonged to a diversity of serotypes. Subtypes C and *esp*Pβ prevailed among the STEC strains studied being identified in 92% and 59% of the isolates, respectively. *esp*Pγ was detected in 39% of the isolates, and all of which was also positive for *esp*Pβ. The subtype of one *esp*P-positive STEC strain could not be identified by the methods employed. In summary, although *esp*P is largely distributed among STEC isolates from the animal reservoir, the high frequency of *esp*Pβ allele identified suggests that these animals are not reservoirs of STEC encoding the biologically active EspP subtypes.