

FREQUENCY OF GENES ENCODING SERINE PROTEASE AUTOTRANSPORTER PROTEINS OF ENTEROBACTERIACEAE (SPATEs) IN ENTEROAGGREGATIVE *Escherichia coli* (EAEC)

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The type V secretion system is the most widespread secretion pathway for the transport of molecules across the outer membrane of Gram-negative bacteria. Members of this family have been identified in *Escherichia coli* and other Gram-negative bacteria, and are often associated with virulence functions, such as adhesion, aggregation, invasion, biofilm formation and toxicity. The aim of this study was to evaluate in enteroaggregative *E. coli* (EAEC) strains the presence of genes encoding serine protease autotransporter proteins of Enterobacteriaceae (SPATEs) produced by *E. coli* pathotypes. A total of 193 EAEC strains (108 typical, or *aggR* positive and 85 atypical, or *aggR* negative) of several serotypes were isolated during two epidemiological studies on the etiology of acute diarrhea. The strains were analyzed by PCR for the presence of 11 genes encoding SPATEs proteins: *eatA*, *epeA*, *espC*, *espl*, *espP*, *pet*, *pic*, *sat*, *sigA*, *tsh* and *vat*. With the exception of *espC*, the other genes investigated were detected among the EAEC strains. There was a higher frequency of *pic* (47%) and *pet* (19%) originally described in EAEC, *sat* (24%) of the diffusely adhering *E. coli* (DAEC), and *espl* (21%) of the enterohemorrhagic *E. coli* (EHEC). These genes were found in both typical (tEAEC) and atypical (aEAEC) EAEC strains, but mainly in the typical strains. The other investigated genes were detected at low frequencies: *eatA* of the Shiga toxin producing *E. coli* (STEC), and *sepA* of *Shigella* spp. were detected in both EAEC groups; *tsh* and *vat* of the avian pathogenic *E. coli* (APEC) were detected only in the aEAEC; and *sigA* of *Shigella* spp., and *espP* of the EHEC were detected only in the tEAEC group. We concluded that most of the SPATEs - encoding genes, formerly thought to occur only in specific *E. coli* pathotypes, are detected among tEAEC and aEAEC strains in frequencies varying between 0.5% and 47%. Thus, the presence of such genes may to increase the virulence potential of these strains, contributing to the severity of disease.

Keywords: PCR, SPATEs, Enteroaggregative *Escherichia coli*.

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