EXPRESSION PROFILES OF HEAT LABILE AND HEAT STABLE TOXINS IN ENTEROTOXIGENIC *Escherichia coli*

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Enterotoxigenic *Escherichia coli* (ETEC) is one of the most important diarrheagenic *E. coli* pathotype responsible for diarrhea outbreaks in low-income countries and involved in cases of traveller's diarrhea. The main virulence factors are the heat labile toxin (LT) and heat stable toxin (ST) secreted after bacterial colonization. The genes encoding LT (*eltA*) and ST (*sta1* and *sta2*) are located in plasmids. Up to now, there are no reports in the literature indicating the differential expression capacity of these toxins in ETEC clinical isolates. This consists in significant information to understand the different pathogenic potential of these toxins. In this study, we analyze the transcription of the genes involved in LT and ST proteins synthesis in clinical isolates. The ETEC prototype strain (H10407) was cultivated in Luria Bertani broth at 37^{o}C under constant shaking (250 rpm). At different growth period (1, 4, 8 and 18 h), RNA was extracted and used to obtain cDNA for amplification by quantitative real-time polymerase chain reaction (qPCR) of *eltA*, *sta1* and *sta2* genes. As control, the *rrs* housekeeping gene was used. The reactions of qPCR were performed and standardized using Power SYBR Green PCR Master Mix. The obtained melting curves were specific for each analyzed gene, since only one fluorescent emission peak was detected. Herein, *eltA*, *sta1* and *sta2* genes were more expressed in 4 h growth. It is worth to mention that *eltA* gene expression was higher than *sta1* and *sta2* genes. For *eltA,* the highest expression level occurs at this time. For the *sta1* and *sta2* genes, different expression levels were observed depending on growth period, with a low expression at 1 and 8 h, and a maximum expression at 4 and 16 h. These results indicate that LT and ST are differentially expressed in ETEC.

Keywords: ETEC*,eltA, sta1*,*sta2*, expression

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