Understanding the Prevalence and Expression of Virulence Factors Harbored by Enterotoxigenic Escherichia Coli

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Abstract : Enterotoxigenic Escherichia coli is one of the leading causes of diarrhea in infants and travelers in developing countries. Colonization factors play an important role in pathogenesis and are one of the main targets for Enterotoxigenic Escherichia coli (ETEC) vaccine development. However, ETEC vaccines had poorly performed in the past, as the prevalence of colonization factors is region-dependent. There are more than 25 classical colonization factors presently known to be expressed by ETEC, although all are not expressed together. Further, there are other multiple non-classical virulence factors that are also identified. Here the presence and expression of common classical and non-classical virulence factors were studied. Further studies were done on the expression of prevalent colonization factors in different strains. For the prevalence determination, multiplex polymerase chain reaction (PCR) was employed, which was confirmed by simplex PCR. Quantitative RT-PCR was done to study the RNA expression of these virulence factors. Strains negative for colonization factors expression were confirmed by SDS-PAGE. Among the clinical isolates, the most prevalent toxin was est+elt, followed by est and elt, while the pattern was reversed in the control strains. There were 29% and 40% strains negative for any classical colonization factors (CF) or non-classical virulence factors (NCVF) among the clinical and control strains, respectively. Among CF positive ETEC strains, CS6 and CS21 were the prevalent ones in the clinical strains, whereas in control strains, CS6 was the predominant one. For NCVF genes, eatA was the most prevalent among the clinical isolates and etpA for control. CS6 was the most expressed CF, and eatA was the predominantly expressed NCVF for both clinical and controlled ETEC isolates. CS6 expression was more in strains having CS6 alone. Different strains express CS6 at different levels. Not all strains expressed their respective virulence factors. Understanding the prevalent colonization factor, CS6, and its nature of expression will contribute to designing an effective vaccine against ETEC in this region of the globe. The expression pattern of CS6 also will help in examining the relatedness between the ETEC subtypes.

Keywords : classical virulence factors, CS6, diarrhea, enterotoxigenic escherichia coli, expression, non-classical virulence factors

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