PREVALENCE OF *tccP* AND *tccP2* GENES IN CLINICAL ATYPICAL ENTEROPATHOGENIC *Escherichia coli* ISOLATES

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Atypical enteropathogenic *Escherichia coli* (aEPEC) is an important etiological agent of infantile diarrhea worldwide. Pathogenic aEPEC strains employ LEE-encoded proteins to subvert normal host cell functions, culminating in intestinal pathologic alterations termed attaching and effacing (A/E) lesions. In addition, some aEPEC strains harbor non-LEE effectors that may contribute to pathogenesis, such as Tir-cytoskeleton Coupling Protein (TccP/TccP2 - also named EspFu), which is involved in the formation of A/E lesions and intestinal colonization. However, there are few studies regarding the frequency of *tccP*/*tccP2* genes in clinical aEPEC isolates. Here we examined a total of 72 aEPEC strains isolated during an epidemiological study of the etiology of acute diarrhea in Salvador, Brazil. The presence of *tccP* and *tccP2* genes was investigated by polymerase chain reaction (PCR). The positive isolates were further screened using the new Clermont phylotyping method, in order to assess the impact of the phylogeny on presence of these genes in aEPEC. The *tccP* and/or *tccP2* genes were detected in 31 (43%) isolates, which belonged to 21 O:H serotypes and harbored eight intimin subtypes. A significant association was observed between the presence of *tccP*/*tccP2* genes and the presence of epsilon-intimin ($p<0.005$) or the ONT:H19 serotype ($p<0.05$). Seven isolates carried *tccP*, 23 harbored *tccP2*, and one was positive for both genes. All O55:H7 and O111:H38 isolates tested were positive for *tccP* and *tccP2* genes, respectively. The *tccP*-carrying isolates were assigned to E (five), A (one) and B2 (one) phylogroups, while the *tccP2*-positive ones fall into B1 (17) and A (four). Two *tccP2*-postive isolates could not be classified according to the phylotyping method used. Interestingly, an O55:H7 isolate harboring both *tccP* and *tccP2* genes was assigned to A phylogroup, while those *tccP*-positive belonged to E, indicating distinct phylogenetic lineages within O55:H7 serotype. In conclusion, *tccP*/*tccP2* genes are widely distributed in clinical aEPEC isolates, with predominance of the *tccP2* allele. Moreover, *tccP* seems to be related to strains belonging to E group, particularly O55:H7, whereas *tccP2* is more associated with B1 strains from several serotypes, suggesting a phylogenetic distribution of these genes among pathogenic aEPEC.

Keywords: Enteropathogenic *Escherichia coli*; atypical EPEC; *tccP*; *tccP2*; phylogeny.

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