ABSTRACT

One of the most important causes of morbidity and mortality among children in developing countries is diarrhea, often associated with bacterial pathogen *Escherichia coli*. This pathogen is sub classified into 6 categories according to differential presence of specific virulence genes from chromosome and/or bacterial plasmid, and in relation to its interaction patterns with tissue and cell cultures, once each category has different pathological and epidemiological characteristics from each other: Enteropathogenic (EPEC Typical and Atypical), enterotoxigenic (ETEC), enteroinvasive (EIEC), enteroaggregative (EAEC), enterohemorrhagic or producing shiga toxin (STEC / EHEC), and diffuse adherence (DAEC). In this research we aimed to classify by molecular techniques and cellular interaction patterns 60 *E. coli* isolates collected from children with 0-1 month old admitted in public hospitals with diarrhea at Manaus - Amazon. To perform PCR, the virulence genes were selected - *uidA* (*E.coli*), *eae* (EPEC and EHEC), *bfpB* (Typical EPEC), *escV* (EPEC, EHEC, and DAEC), *stx1* (EHEC), *invE* (EIEC), *Ent* (EHEC), *EAF* (EPEC) and *stx2* (EHEC) - and all standard procedures were submitted to an *E. coli* representative of each serotype. As results, all 60 samples amplified to *uidA* gene, genetic marker of *Escherichia* species, confirming the isolates identity. In relation to subtype, 15 were identified as EHEC, 45 as EPEC (41 Typical and 4 Atypical). These results were confirmed at cell interaction assays were all isolates shown adherence patterns in concordance to found at molecular assays. Studies aiming the characterization of Amazon *E.coli* subtypes are rare. We believe this study may contribute to elucidate the pattern of *E. coli* in Amazon, and the molecular methodology here standardized could future be applied at laboratorial routine.

**Keywords**: Childhood diarrhea, *Escherichia coli*, Virulence Genes.

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