TITLE: INVESTIGATION OF VIRULENCE FATORS AT DIARRHEOGENIC E.COLI FROM

MANAUS AMAZON

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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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