Characterization of Enteroaggregative *Escherichia coli* in children with diarrhoea in Porto Velho, Rondônia, Western Brazilian Amazon

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Enteroaggregative *Escherichia coli* (EAEC) is considered a significant cause of acute and chronic diarrhoea in both children and adults. Several potential virulence factors have been described for EAEC. EAEC pathogenesis involves the processes of cell aggregation, biofilm production, mucosal toxicity, and inflammation. Resistance of EAEC to multiple antimicrobial products has been frequently reported in different regions of the world. In this study, 108 EAEC strains were isolated from 69 children with acute diarrhoea. Co-infections between EAEC and others enteropathogens were identified in 16.7% (18/69) of these samples. The *aggR* gene was detected in 50% (54/108) of isolates. A significant statistical correlation was observed between typical EAEC (presence of *aggR*) and *aatA* ($p < 0.0001$), *irp2* ($p = 0.0101$), and *shf* ($p = 0.0419$) gene. Typical EAEC was significantly associated with bloody diarrhoea. Of 108 EAEC strains analysed, 63% (68/108) were biofilm producers. Among biofilm producers, 63.2% (43/68) carried the *aggR* gene versus 27.5% (11/40) of the non-producers ($p = 0.0006$). We also identified an association between the *aatA* gene and biofilm production. This gene was identified in 54.4% (37/68) of producer strains versus 12.5% (5/40) of non-producer strains ($p < 0.0001$). Antibiotic sensitivity testing using antimicrobial agents revealed that the majority of the EAEC isolates were resistant to ampicillin 64.8% (70/108), sulfamethoxazole 54.6% (59/108), tetracycline 45.4% (49/108), and cefotaxime 19.4% (21/108). This is the first study in northern Brazil investigating EAEC virulence factors and demonstrating antimicrobial susceptibility of EAEC strains isolated from cases of childhood diarrhoea.

Keywords: Enteroaggregative *E. coli*, Diarrhoea, Children

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico – CNPq e Fundação Rondônia de Amparo ao Desenvolvimento das Ações Científicas e Tecnológicas – FAPERO