

TITLE: HIGH CLONAL AND GENES PROFILE DIVERSITY OF ENTEROAGGREGATIVE *E. COLI* ISOLATES FROM "QUILOMBOLA" CHILDREN

AUTHORS: GUERRIERI, C.G.; MONFARDINI, M.V.; SCHUENCK, R.P.; SPANO, L.C.

INSTITUTION: UNIVERSIDADE FEDERAL DO ESPÍRITO SANTO (AV. MARECHAL CAMPOS 1468, CEP 29043-900 VITÓRIA - ES, BRAZIL)

ABSTRACT:

Enteroaggregative *Escherichia coli* (EAEC) is an emerging pathotype responsible for acute and persistent diarrhea in all ages individuals from different regions of the world. It is characterized by great heterogeneity regarding potential virulence factors. We aimed to investigate the genetic profile and geographic distribution of EAEC strains isolated from children of 22 quilombola communities from two counties in the north of Espírito Santo. Were analyzed EAEC isolates identified by pattern of aggregative adherence in HEp-2 cell culture, from faeces of 73 children with and without diarrhea, up to 11 years of age, from communities characteristically rural and semi-isolated. The genetic profile of the strains was verified by the chromosomal DNA fragmentation technique with *XbaI* restriction enzyme, followed by pulsed field gel electrophoresis (PFGE). The similarity between the strains was analyzed from a dendrogram generated by the software "GelJ" and correlated with 21 genes involved in the pathogenicity of EAEC, detected by PCR, as for AggR transcriptional regulator, adhesins (*aafA*, *aggA*, *agg3A*, *hdaA*, *PapC*), dispersin (*aap*), toxins (*pet*, *astA*, *sat*, *set1A*, *hlyA*) and siderophores (*irp2*, *iucA*, *chuA*). We observed: (i) 58 different PFGE patterns (pulsotype – PFT) (similarity $\geq 80\%$), 75.9% (44/58) of PFT belonged only one strain, 22.4% (13/58), two strains and only 1.7% (1/58), three strains; (ii) 37 isolates (50.7%) were distributed in 13 virulence profiles, the remaining 36 (49.3%) presented single profiles; (iii) all strains had no relation among the virulence and PFT profile or with the community of origin, except for two strains. The lack of relation of the geographical distribution between the PFGE patterns and the virulence gene profiles observed reflects the high heterogeneity of the EAEC strains.

Keywords: EAEC, clonal relation, virulence genes.

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