

**Title: Genotyping and phylogenetic analysis of enteroaggregative *Escherichia coli* (EAEC) strains isolated from extraintestinal infections**

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**Abstract**

*Escherichia coli* strains have evolved acquiring virulence genes that have contributed to the adaptation of pathogenic strains to different infection sites in humans. The diversity of behaviors showed by *E. coli* strains is supported by a high genetic plasticity that allows the transfer and maintenance of a diversity of virulence genes among *E. coli* strains. Enteroaggregative *E. coli* (EAEC) is a heterogeneous category of pathogenic strains classically associated with acute and persistent diarrhea. Here, three EAEC strains (pCVD<sup>+</sup>, *aggR*<sup>+</sup>) isolated from extraintestinal infections (two strain recovered from urinary tract infection and one from bacteremia) were genotyping and submitted to phylogeny analysis along with contemporaneous *E. coli* strains isolated from UTI in the same hospital. Twenty one *E. coli* strains, including the EAEC strains, were tested for the presence of 6 virulence markers of UPEC (*focA*, *pap*, *vat*, *fyuA*, *chuA* and *yfcV*), 2 of MNEC (*cnf* and *sfa*) besides *csgA* (curli fimbriae) and *ag43*. Amplification and sequencing of the genes *dinB* (DNA polymerase) and *icdA* (isocitrate dehydrogenase) were employing in the phylogenetic analysis. *dinB-icdA* concatenated sequences (966 base-long sequences) were used in bootstrap analysis (with 1000 replications) in order to infer phylogenetic relationship among strains that was illustrated as a maximum likelihood tree. The EAEC strains (pCVD<sup>+</sup> and *aggR*<sup>+</sup>) were tested positive for the presence of UPEC virulence markers: *fyuA*<sup>+</sup>*chuA*<sup>+</sup>*pap*<sup>+</sup>*csgA*<sup>+</sup>*ag43*<sup>+</sup>pCVD<sup>+</sup>*aggR*<sup>+</sup> in EAEC strain 1.1; *fyuA*<sup>+</sup>*vat*<sup>+</sup>*focA*<sup>+</sup>*pap*<sup>+</sup>*csgA*<sup>+</sup>*ag43*<sup>+</sup>pCVD<sup>+</sup>*aggR*<sup>+</sup> in EAEC strain 1.2; and *fyuA*<sup>+</sup>*chuA*<sup>+</sup>*pap*<sup>+</sup>*csgA*<sup>+</sup>pCVD<sup>+</sup>*aggR*<sup>+</sup> in EAEC strain 1.3. Among the other 18 strains isolated from urine, all were tested positive for virulence markers of uropathogenic *E. coli* (UPEC). These strains showed typical genetic array predictive for UPEC strain (6 strains typed as *fyuA*<sup>+</sup>*chuA*<sup>+</sup>*csgA*<sup>+</sup>; 4 typed as *fyuA*<sup>+</sup>*chuA*<sup>+</sup>*pap*<sup>+</sup>*csgA*<sup>+</sup>; 3 typed as *fyuA*<sup>+</sup>*yfcV*<sup>+</sup>*chuA*<sup>+</sup>*pap*<sup>+</sup>*csgA*<sup>+</sup>; 3 typed as *fyuA*<sup>+</sup>*yfcV*<sup>+</sup>*chuA*<sup>+</sup>*csgA*<sup>+</sup>; 1 typed as *yfcV*<sup>+</sup>*chuA*<sup>+</sup>*pap*<sup>+</sup>*csgA*<sup>+</sup>; and 1 typed as *fyuA*<sup>+</sup>*yfcV*<sup>+</sup>*chuA*<sup>+</sup>*vat*<sup>+</sup>*focA*<sup>+</sup>*pap*<sup>+</sup>*sfa*<sup>+</sup>*cnf*<sup>+</sup>*csgA*<sup>+</sup>). In phylogenetic tree, heteroathogenic EAEC strains 1.1 and 1.3 compose a large cluster along with 7 UPEC strains. Branching of this cluster was supported by a bootstrap value of 98. In this cluster, 6 of out 7 strains displayed the combination *fyuA*<sup>+</sup>*chuA*<sup>+</sup>*pap*<sup>+</sup>*csgA*<sup>+</sup> as shared gene set. Our data showed that heteropathogenic strains displaying hybrid genotype (EAEC/UPEC) can cause extraintestinal infections.

**Palavras-chaves:** heteropathogenic strain, genotyping, phylogenetic, UPEC

**Agência Fomento:** FAP-DF – custeio 193.000.019/2012.