

Title: Genetic heterogeneity among uropathogenic *Escherichia coli* (UPEC) strains isolated in Brasília, Distrito Federal

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Escherichia coli strains can cause recurrent urinary infection episodes, pyelonephritis and even more severe infectious diseases, such as neonatal meningitis and urinary sepsis. Uropathogenic *E. coli* (UPEC) is the main pathogen associated with urinary tract infection (UTI). UTI pathogenesis and the correlated clinical settings can be assessed by the genotyping of UPEC virulence factors. The aim of this study was to characterize *E. coli* strains isolated from UTI patients who were admitted to the emergency room or were hospitalized in the *Hospital Regional de Ceilândia* (HRC), Brasília, Distrito Federal. The presence of 16 virulence genes of three *E. coli* pathotypes (UPEC, EAEC - enteroaggregative *E. coli* -, and MNEC - meningitis-associated *E. coli*) were tested in 78 strains using polymerase chain reaction (PCR). The most frequently detected genes were *chuA* (78% - 62/78), *csgA* (76% - 61/78) and *fyuA* (69% - 54/78). EAEC genes (*pCVD432* and *aggR*) were detected in 5% (4/78) of UPEC strains. The genetic characterization showed the presence of 40 different genotypes among tested strains. Hybrid genotypes (EAEC/UPEC) were identified in 3 strains. *E. coli* strains associated with urinary tract infections are also sorted by the number of detected virulence genes. UPEC strains isolated from children were found to be more virulent (6 virulence genes in average/strain) than strains isolated from adults (3 virulence genes/strain) ($p \leq 0.01$). Taken together, the results show a high genetic heterogeneity among UPEC strains with highly virulent strains being frequently isolated from children. Additionally, the data raise the possibility that genes typical of EAEC strains can be transferred to and stably maintained by UPEC strains, what can lead to the emergency of heteropathogenic categories.

Palavras-chaves: heteropathogenic strain, genotype, EAEC

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