

**TITLE:** Antimicrobial susceptibility and molecular characterization of uropathogenic *Escherichia coli* strains isolated from outpatients in Botucatu, Brazil.

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**ABSTRACT:**

Uropathogenic *Escherichia coli* (UPEC) cause the majority of urinary tract infections (UTIs), including cystitis and pyelonephritis, in the human host. UPEC utilizes numerous virulence factors to entry, adhere, colonize, acquire essential nutrients, multiply and cause damage in the urinary tract environment. Recent studies have shown that some UPEC isolates carry virulence factors associated with diarrheagenic *E. coli* (DEC) pathotypes, such as EAEC (enteroaggregative *E. coli*) and EPEC (enteropathogenic *E. coli*). A major concern in UPEC infections is the constant increasing of antimicrobial resistance, thus leading to treatment failure in some UTIs caused by this pathogen. In this study a total of 120 UPEC isolates were obtained from outpatient urine samples, attended at University Hospital of Botucatu Medical School between March and May of 2018, and diagnosed with cystitis. Polymerase chain reaction (PCR) was used to detect 28 virulence factor-encoding genes, as well as diarrhoeagenic *E. coli* (DEC) markers (*escN*, *stx1/2*, *aatA* and *aggR*), and eleven genes encoding adhesins and toxins associated with the EAEC pathotype. The UPEC isolates were assigned in the distinct *E. coli* phylogroups, using a quadruplex PCR; and the determination of the antimicrobial resistance profile was performed using the disk-diffusion method. Among the isolates studied, 42.0% were assigned to phylogroup B2, while UPEC isolates from other phylogroups were detected as follows: B1 (14.0%), A (14.0%), D (13.0%), F (9.0%), E (3.0%), *E. clades* (3.0%) and C (2.0%). Among the virulence-encoding genes searched, *fimH* (98.0%), *ecpA* (78.0%), *traT* (82.0%) and *ompT* (63.0%) were the most frequent detected. Genes used for the identification of EAEC (*aatA* and *aggR*) and EPEC (*escN*) were identified in five (4.0%) and one (0.8%) of the UPEC isolates, respectively. The highest resistance rates were observed for the following antimicrobials drugs: Ampicillin (46.0%), Trimethoprim-Sulfamethoxazole (34.0%) and Nalidixic acid (32.0%). In conclusion, we observed that UPEC isolates assigned to the phylogroup B2 harbored a higher number of virulence-encoding genes that can assist in the colonization and survival in the genitourinary tract. Also, the increase of the number of UPEC isolates non-susceptibility to some of the antimicrobial drugs tested, may serve as an alert for the physicians in order to empirically select the treatment to be used in the UTIs.

**Keywords:** Uropathogenic *E. coli*, virulence factors, antimicrobial susceptibility, phylogroups, urinary tract infection.

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