TITLE: Molecular characterization of *ESCHERICHIA COLI* isolated from patients presenting urinary tract infections.

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ABSTRACT:

Urinary tract infections (UTIs) due to beta-lactam-resistant uropathogenic *Escherichia coli* are an important public health problem, as those are the main recommended antimicrobials. Treatment failure may result in progression to severe conditions with renal failure, sepsis and death. In this study, *E. coli* strains resistant to third generation cephalosporins isolated from patients with UTI were investigated and compared with respect to the diversity of genes responsible for ESBL production, virulence genes and phylogenetic group. Also, they were submitted to molecular typing by pulsed field electrophoresis (PFGE) and multilocus sequencing (MLST). Sixty-four *E. coli* identified as ESBL producers were isolated from the urine of different patients admitted a to Hospital Base of São José do Rio Preto - SP, between December 2014 and May 2015. Of these, 45 presented variants of *bla*$_{\text{CTX-M}}$, with 33 carriers of *bla*$_{\text{CTX-M-15}}$, 7 of *bla*$_{\text{CTX-M-9}}$, 3 of *bla*$_{\text{CTX-M-2}}$, 1 of *bla*$_{\text{CTX-M-55}}$, 1 of *bla*$_{\text{CTX-M-3}}$ and 1 of *bla*$_{\text{CTX-M-8}}$. Twenty-nine *E. coli* were identified from group B2, 19 from group A, 10 from group D and 5 from group B1. Among the 21 virulence genes investigated, 13 were detected in different combinations and distributed in *E. coli* from all phylogroups. A wide genetic diversity was observed, and the percentage of similarity between the strains varied between 38.1% and 100%. Most of the strains were considered as non-derived from the same cluster, and between 2 and 8 strains were distributed within the 9 identified clusters, with similarity between 80.7% and 92.3%. MLST typing was performed for 55 of the 64 strains included in this study. Of these, 24 were identified as ST131, nine as ST90/23, two as ST10/10, six as ST405/405, two as ST224 and the others were identified as ST57/350, ST155/155, ST354/354, ST648/648, ST1177 and ST2851 with one representative on each clone. The results show that *E. coli* ST131 is the main major agent of UTI among patients included in this study. The production of ESBL type CTX-M-15 is the main mechanism of resistance to third-generation cephalosporins, but other variants are also associated with this resistance phenotype. The identification of different *E. coli* clones associated with UTI is consistent with the endogenous nature of UTIs, and the presence of multiple CTX-M variants and diverse virulence phenotypes shows the genetic plasticity of this pathogen and its ability to acquire different resistance genes.

KEYWORDS: *Escherichia coli;* Urinary tract infections; ESBL; PFGE, MLST.

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