Genomic and phenotypic features of extended-spectrum β-lactamase-producing uropathogenic Escherichia coli isolates

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Escherichia coli is a Gram-negative bacillus commonly found in the microbiota of humans and other warm-blooded animals. It typically maintains a mutualistic relationship with the host; however, certain strains can cause a variety of infections in both the gastrointestinal tract and extraintestinal sites. Uropathogenic *E. coli* (UPEC) refers to strains responsible for urinary tract infections (UTIs) and represents the most common etiological agent of these infections worldwide. Its pathogenicity is associated with the production of several virulence factors, which give UPEC strains the ability to establish themselves in the host and cause disease. Extended-spectrum β-lactamases (ESBLs) are enzymes encoded by the *bla* genes that degrade β-lactam class antimicrobial drugs, including third-generation cephalosporins. The production of ESBLs is very prevalent in UPEC strains, and this pathogen ranks second on the bacterial pathogens priority list published by the World Health Organization in 2024. In light of the above, this study aimed to sequence 60 ESBL-producing UPEC strains to investigate their molecular characteristics, including their resistome, virulome, and antimicrobial resistance profiles. A total of 60 UPEC-ESBL^{+} strains were sequenced by Illumina short-reads, and the draft genomes were used to determine their molecular background, as well as to detect the presence of virulence factor- and resistance-encoding genes. The antimicrobial resistance profile was determined using the disk-diffusion assay for 19 different drugs. According to our genomic analysis, the isolates were assigned into several phylogroups, sequence types (STs) and serotypes. The two most predominant groups were B2/ST131/O25:H4 (35%) and C/ST90/O8:H9 (8.3%). The most prevalent ESBL-encoding genes were $bla_{CTX\text{-}M\text{-}8}$ (18.3%), $bla_{CTX\text{-}M\text{-}15}$ (40%) and $bla_{CTX\text{-}M\text{-}55}$ (23.3%), frequently detected in association with other resistance-encoding genes. The number of virulence factor-encoding genes ranged from 7 to 33 and the most frequent were *fimH* (98.3%), *sitA* (73.3%) and *ompT* (63.3%). The highest resistance rates were observed for ampicillin (100%), cefotaxime (100%), ceftriaxone (96.7%), ciprofloxacin (71.7%), norfloxacin (70%) and trimethoprim (46.7%). A total of 37 (61.7%) strains were classified as multidrug-resistant (MDR), with 59.0% of them assigned into the ST131. The high prevalence of ESBL-producing UPEC strains from the ST131 and/or MDR are an important alert to public health authorities regarding the constant evolution of the molecular mechanisms that mediate antimicrobial resistance among these pathogens.

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