

TITLE: BETA-LACTAMASES AND EXTENDED SPECTRUM BETA-LACTAMASES AMONG MULTIDRUG RESISTANT UROPATOGENIC *ESCHERICHIA COLI* ISOLATED FROM OUTPATIENTS AT HOSPITAL UNIVERSITÁRIO DE BRASÍLIA, UNB, DF.

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ABSTRACT

Uropathogenic *Escherichia coli* (UPECs) strains are considered the most frequent cause of Urinary Tract Infection (UTI), the most prevalence infection among humans. UTIs are frequently resolved by empirical antibiotic administration; however the high increase of multi-drug resistant (MDR) prevalence among UPEC has been make difficult the treatment. Beta-lactamases (BLs) and extended spectrum Beta-lactamases (ESBL) are frequently associated with multi-drug resistance among uropathogenic. Among them, CTX-M, TEM, SHV and OXA are ESBL enzymes frequently found in MDR UPECs. Thus, the aim of this work was to identify the occurrence of these enzymes among MDR UPCs strains by PCR. For this purpose, 323 UPECs strains isolated from outpatients at Hospital Universitário de Brasília (HUB/UnB) had their antibiogram analyzed. Then, the 74 MDR strains identified were submitted to DNA extraction for BL and ESBL enzymes gene detection by PCR. Among 74 MDR strains, 24 (32%) presented CTX-M gene, 13 (17.5%) OXA, 51 (69%) TEM and 1 (1.35%) presented SHV gene. TEM and TEM/SHV was the most frequently genotype observed (29% and 24.3% respectively). Seven strains did not present any gene analyzed and 10 strains presented three or more gene studied. Together these data showed that TEM was the most prevalent BL enzyme identified among MDRs UPECs isolates. The occurrence of strains harboring more than two enzymes is a very concern scenario for the community-acquired UTI treatment.

Key words: Uropathogenic *Escherichia coli* (UPEC), Multidrug resistance (MDR), Extended Spectrum Beta-Lactamases (ESBL)

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