

Title: MDR (MULTIDRUG RESISTANCE) AND CTX-M-15 BETA-LACTAMASES DISSEMINATION BY UPECS (UROPATHOGENIC *Escherichia coli*) WAS CLONALLY INDEPENDENT IN ACQUIRED-COMMUNITY UTI (URINARY TRACT INFECTION) IN BRASÍLIA-DF DURING 2013-2014.

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Uropathogenic *Escherichia coli* strains (UPEC) are the most frequent etiological agent of Urinary Tract Infection (UTI), the most prevalent bacterial infection in humans. For the majority of community-acquired UTI, conventional antimicrobial therapy still provides effective treatment. However, the recent emergence and increasing prevalence of antibiotic resistant UPECs clones has complicated the management of UTI. Extended Spectrum Beta-lactamases (ESBL)-producing UPEC clones are commonly related with multidrug-resistant (MDR) extraintestinal pathogens, thus limiting further the treatment options currently therapy for UTI. These clones are frequently associated with the production of CTX-M15 enzyme, currently the most widespread ESBL. The aimed of this work was to characterize the ESBL UPECs isolated in Hospital Universitário de Brasília (HUB/UnB) from July 2013 to April 2014. During this period, 324 *E. coli* strains from urine culture were identified and have its antimicrobial susceptible profile determined by VITEK 2. All strains identified as ESLB were used for plasmid profile characterization and submitted to genomic DNA extraction for *E. coli* typing of Clermont Phylogenetic Group, ERIC-PCR, and to CTX-M-15-alleles detection. Among the strains analyzed, 23 UPECs strains were CTX-M-15 ESBL-producing and MDR. The plasmid profile analysis showed that all strains harbored several plasmids including that ones with high weigh (over 30 MDa). G1 were the most frequent CTX-M-15 allele detected (9/23), followed by G9 (3/23), G2 (3/23) and G8 (1/23). Among the 5 main branches observed in dendrogram obtained by ERIC-PCR analysis, two presented outstanding features: one were compounded by 3 strains D derived phylogroup sharing 52% of genetic similarity and isolated from July to December 2013; and other compounded by strains isolated from July 2013 to February 2014 sharing 66.9% of genetic similarity and belong to B2 phylogroup. Genetic similarity results showed by ERIC-PCR suggest the existence of a successful clonal line of ESBL-MDR dissemination in community-acquired UTI characterized by B2 phylogroup strains. The G1 CTX-M-15 distribution in the majority of the ERIC clusters suggests that this allele was the main ESBL source among UPEC strains analyzed, independently of clonal origin. The MDR profile exhibited by all strains showed that MDR was disseminated together with ESBL profile, and that this dissemination was clonally independent.

Key words: Extended-spectrum Beta-lactamases, Multidrug resistance; Uropathogenic *Escherichia coli*, Urinary Tract Infection

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