

Title: ERIC-PCR ANALYSIS OF CIPROFLOXACIN-RESISTANT UPEC STRAINS (UROPATHOGENIC *Escherichia coli*) SHOWED THE MULTIDRUG RESISTANCE (MDR) DISSEMINATION IN COMMUNITY-ACQUIRED URINARY TRACT INFECTION (UTI) IN BRASÍLIA-DF DURING 2013 -2014.

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Uropathogenic *Escherichia coli* strains (UPEC) are the major cause of Urinary Tract Infection (UTI), the most frequent human bacterial infection. For the majority of community-acquired UTI, conventional antimicrobial therapy still provides effective treatment. However, the recent emergence and increasing prevalence of antibiotic resistant uropathogens has complicated the management of UTI. The fluoroquinolone Ciprofloxacin is the first-line drug used in UTI infection when Trimethoprim/Sulfamethoxazole (the first-line UTI therapy) resistance is notoriously prevalent. However, many UPEC strains are recognized to belong to drug-resistance worldwide dissemination clones, including Ciprofloxacin. Thus, as the most common pathogen associated with the most frequent human bacterial strains, the knowledge of antibiotic resistance dissemination by UPEC may be used as a tool for the drug-resistance eradication. The aimed of this work was to analyze the genetic similarity of Ciprofloxacin-resistant UPEC strains isolated in HUB/UnB. During July 2013 to April 2014, 324 UPEC strains were collected from Hospital Universitário de Brasília (HUB/UnB) for antibiotic resistance profile analysis. *Escherichia coli* strains identification and its antibiogram were obtained by VITEK 2. The 61 Ciprofloxacin-resistant strains were submitted to DNA extraction for *E. coli* typing of Clermont Phylogenetic Group and ERIC-PCR (Enterobacterial Repetitive Intergenic Consensus Sequences). The analysis of dendrogram obtained by ERIC –PCR showed that strains were grouped in 6 main clusters compounded mainly by MDR (Multidrug Resistant) strains. One cluster presented two clonal groups (sharing 100% of genetic similarity): one characterized by B2 MDR strains and other compounded by B2 R strains. All strains allocated in these two clonal groups were isolated from different patients during August and September 2013. All together, the results showed that the dissemination of Ciprofloxacin resistance also mediated the dissemination of MDR strains among community acquired UPEC strains during 2013/2014. The presence of MDR B2 clonal groups suggest that MDR characteristic were also disseminated by clonal pathogenic *Escherichia coli*.

Key words: Ciprofloxacin resistance, Multidrug resistance; Uropathogenic *Escherichia coli*, Urinary Tract Infection

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