TITLE: ANALYSIS OF CTX-M- ENZYMES DNA SEQUENCE OF UROPATHOGENIC *Escherichia coli* ISOLATED FROM PATIENTS WITH COMMUNITY-ACQUIRED URINARY TRACT INFECTION IN BRASÍLIA, BRAZIL.

AUTHORS: MOREIDA DA SILVA, R.C.R.[1]; GONÇALVES, L.F.[1]; MARTINS, V.P.[1]; ALMEIDA, A.P.C.[1]; CAETANO, A.R.[2]; IANELLA, P.[2]; CAMPOS, T.A.[1]

INSTITUTIONS: [1]CEL/UNB- DEPARTAMENTO DE BIOLOGIA CELULAR, INSTITUTO DE CIÊNCIAS BIOLÓGICAS, UNIVERSIDADE DE BRASÍLIA (ASA NORTE, BRASÍLIA, DF); [2]LGA/EMBRAPA – LABORATÓRIO DE GENÉTICA ANIMAL, EMBRAPA RECURSOS GENÉTICOS E BIOTECNOLOGIA, EMPRESA BRASILEIRA DE PESQUISA AGROPECUÁRIA – EMBRAPA (ASA NORTE, BRASÍLIA, DF).

Abstract:

Uropathogenic E*scherichia coli* strains (UPECs) are the major causes of urinary tract infections (UTIs), the most frequent human bacterial infection. For the majority of community-acquired UTIs, conventional antimicrobial therapy still provides effective treatment. however, the high occurrence multidrug resistance (MDR) dissemination clones in humans, animals and the environment has become the treatment ineffective by increasing the intensity of the symptoms, forcing the selection of other chemotherapeutics, prolonging therapy time, and in some cases, leading the patient to death. β-lactamase extended-spectrum enzymes (ESBLs) present high molecular diversity and are commonly associated with *E. coli* resistance. Currently CTX-M is the most widespread ESBLs in the world having more than 40 types described. The aim of this work was to analyze the diversity of CTX-M enzymes found in UPECs MDR strains isolated from patients at Hospital Universitário de Brasília (HUB/UnB). During July 2013 to April 2014, 323 UPEC strains were isolated at HUB/UnB and had their antibiotic resistance profile analysed. *E. coli* strains identification and its antibiogram were obtained by VITEK 2. The 74 MDR identified strains were used for CTX-M genetic diversity by PCR and DNA sequencing. Chi-square Fisher's exact test analysis showed that CTX-M were significantly associated with MDR the analysis of CTX-M amplicons by BLAST tool (https://blast.ncbi.nlm.nih.gov/blast.cgi) showed a total of 22 strains for CTX-M ESBLs producers. The multiple CTX-M-type ESBLs found were: 15 (54,5% or 12/22), 8 (31,8% or 7/22), 20 (9,1% or 2/22) and 71 (4,5% or 1/22). the analysis of UPGMA-dendogram generated by MEGA 7 software (http://www.megasoftware.net/) showed that CTX-M strains were grouped in 5 main clusters compounded mainly by two clonal group: one characterized by CTX-M-15 ESBLs producers and other compounded by CTX-M-8 ESBLs producers strains. Genetic divergence observed among CTX-M-15 ESBLs sequences and among CTX-M-8 ESBLs suggests the occurrence of structural changes in these enzymes, probably by the selective pressure exerted by antimicrobials. All together, the results suggest that the dissemination of the multiple CTX-M-type ESBLs can be the dissemination of MDR strains among community acquired UPEC strains during 2013/2014.

Keywords: Uropathogenic *Escherichia coli* (UPEC), urinary tract infections (UTIs), β-lactam resistance, β-lactamase extended spectrum enzymes (ESBL), multi-drug-resistance (MDR), CTX-M enzymes

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