TITLE: GENETIC DIVERSITY ANALYSIS OF OXA ENZYME OF UROPATHOGENIC *Escherichia coli* STRAINS ISOLATED FROM PATIENTS WITH COMMUNITY-ACQUIRED URINARY INFECTION IN BRASÍLIA, BRAZIL.

AUTHORS: MOREIRA DA SILVA, R.C.R.[1]; NASCIMENTO, L.G.S.; 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 *Escherichia 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 has become the treatment ineffective by increasing the intensity of the symptoms and prolonging therapy time, and in some cases, leading the patient to death. extended spectrum β-lactamases (ESBLs) are frequently described among *E. coli* isolates. β-lactamase extended-spectrum enzymes (ESBLs) present high molecular diversity and are commonly associated with *E. coli* resistance. OXA-type ESBLs are enzymes were originally relatively rare and always plasmid mediated. The aim of this work was to analyze the diversity of OXA enzymes found in UPECs MDR strains isolated from patients at Hospital Universitário de Brasília (HUB/UnB). From June 2013 to April 2014, 323 strains of UPEC were isolated at HUB/UnB to antibiotics resistance profile analysed. *E. coli* strains identification and its antibiogram were obtained by VITEK 2. The 74 MDR identified strains were used for OXA genetic diversity by PCR and DNA sequencing. Chi-square Fisher's exact test analysis showed that OXA were significantly associated with MDR. The analysis of OXA amplicons by BLAST tool (https://blast.ncbi.nlm.nih.gov/blast.cgi) showed a total of 13 strains of OXA ESBLs producers. The multiple OXA-type ESBLs found were: 1 (2/13 OR 15,4%), 30 (8/13 OR 61,5%), 232 (3/13 OR 23,1%). All together, the results suggest that the dissemination of the multiple OXA-type ESBLs can be the dissemination of MDR strains among community-acquired UPEC strains during 2013/2014.

Keywords: Uropathogenic *Escherichia coli* (UPEC), Multidrug Resistance (MDR), ESBLs (Extended-Spectrum β-Lactamases), OXA enzymes, Community-Acquired Urinary Tract Infection (UTI).

Development Agency: CNPq e FAP-DF.