EV0372
ePoster Viewing
Resistance surveillance & epidemiology: Gram-negatives

Presence of plasmid-mediated quinolone resistance gene qnrS is associated with extended spectrum beta-lactamase production in clinical enterobacterial isolates from an intensive care unit from Bucharest

Ilda Czobor*[1], Irina Gheorghe[2], Otilia Banu[3], Marcela Popa[4], Veronica Lazar[1], Mariana Carmen Chifiriuc[5]

[1]*University of Bucharest, Faculty of Biology, Microbiology, Bucharest, Romania*

[2]*University of Bucharest, Faculty of Biologyș Research Institute of the University of Bucharest, Microbiology, Bucharest, Romania*

[3]*Institute for Cardiovascular Diseases "c.C. Iliescu", Bucharest, Romania*

[4]*Faculty of Biology, Research Institute of the University of Bucharest, Bucharest, Romania*

[5]*University of Bucharest, Research Institute of Bucharest University, Microbiology Immunology, Bucharest, Romania, Bucharest, Romania*

Background: The aim of this study was to investigate the plasmid-mediated quinolone resistance (PMQR) in clinical *Enterobacteriaceae* isolates, as there is virtually no data concerning genetic support of quinolone resistance in Romania.

Material/methods: A total of 84 *Enterobacteriaceae* (45 *Klebsiella pneumoniae*, 26 *Escherichia coli*, 4 *Enterobacter cloacae*, 3 *Serratia marcescens*, 3 *Proteus vulgaris*, 2 *E. aerogenes* and 1 *Citrobacter freundii*) with decreased quinolone susceptibility were selected during July-August 2015. Bacterial identification and antibiotic susceptibility testing were performed by Vitek II method. Screening of PMQR genes (*qnrA*, *qnrB* and *qnrS*), extended-spectrum β-lactamases (ESBL) genes (bla_{TEM} and bla_{CTX-M}) and carbapenemases genes (bla_{NDM} and bla_{OXA-48}) were performed by PCR.

Results: 84% of the *K. pneumoniae* isolates were multi-drug resistant (MDR) and 91% exhibited the ESBL phenotype, being resistant to nalidixic acid (100%), ciprofloxacin (91%), to β-lactams: cefotaxime (91%) ceftriaxone (84%), cefoxitin (53%) and imipenem (11%), to aminoglycosides: kanamycin (82%), gentamicin (55%), tetracycline (82%) and trimethoprim-sulphametoxazole (9%). Genetic support of β-lactam resistance was determined by $bla_{CTX-M-like}$ genes in 56% and by $bla_{TEM-like}$ in 29% of the strains. Carbapenem resistance was mediated by $bla_{OXA-48-like}$ genes in 6% and by $bla_{NDM-like}$ genes in 2% of the strains. PMQR gene *qnrS* was identified in 22% of the strains, who also carried $bla_{CTX-M-like}$ genes and exhibited phenotypic resistance to ciprofloxacin.

67% of the *E. coli* and the other enterobacterial species (39 strains) were MDR and 69% of the strains exhibited the ESBL phenotype, being resistant to nalidixic acid (100%) and ciprofloxacin (72%), to β-lactams (cefotaxime 90%, ceftriaxone 87%, cefoxitin 74%), aminoglycosides (kanamycin 38%, gentamicin 28%), tetracycline (10%) and trimethoprim-sulfametoxazole (51%). The $bla_{TEM-like}$ gene was identified in 59% of the isolates, while $bla_{TEM-like}$ was encountered in 5%. The *qnrS* gene was identified

in 18% of the isolates (6 *E. coli* and 1 *S. marcescens*), always associated with the $bla_{\text{CTX-M-like}}$ gene and the ESBL phenotype.

Conclusions: Our study highlights the association of PMQR *qnrS* gene with the $bla_{\text{CTX-M-like}}$ genes in MDR enterobacteria, isolated from patients from an ICU in Bucharest, suggesting the existence of a common platform of dissemination.