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Abstract (publication only)

Screening of antibiotic-resistant Gram-negative organisms in hospital settings from Bucharest, Romania

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The purpose of this study was to establish the main resistance phenotypes and their genetic determinants in Gram-negative bacilli (GNB) isolated from intensive care units (ICU). Material and methods: A number of 531 GNB strains (334 Enterobacteriaceae and 197 Pseudomonadaceae) were isolated from 1166 positive clinical samples collected from patients hospitalized during 2011, in the ICUs of two big hospital from Buhcarest, Romania. Their resistance phenotypes were established using: disk diffusion test, double-disk diffusion test (DDST) with amoxicillin-clavulanic acid (AMC), cefotaxime (CTX) and ceftazidime (CAZ), DDST with AMC plus EDTA, imipenem (IPM) and IMP plus EDTA, Modified Hodge Test (MHT) and E-test ESBL, MBL and AmpC. The genetic support of the antibiotic resistance was investigated by simple and multiplex PCR reactions for class A Ser- beta-lactamases (PSE, CARB, TEM genes families), class B – metallo-b-lactamases -MBL (IMP, VIM, SPM gene families), class C – AmpC and ESBL, as well as ciprofloxacin resistance genes (gyrA, parC) as well as the presence of mexB, mexD, mexF and mexY genes, encoding for multi-drug efflux pumps. In accordance with the recommended definitions of the degree of multidrug resistance, 32% of the GNB exhibited a multi-drug resistance (MDR) phenotype (Escherichia sp., Klebsiella sp., Serratia sp., Acinetobacter sp., Pseudomonas sp.), 13.2% were extended-drug resistant (XDR) (Klebsiella sp., Acinetobacter sp.) and 5.6% pan-drug resistant (PDR) (Enterobacter sp. and Klebsiella sp.). The gyrA gene, as well as the mexB, mexD, mexF si mexY genes, encoding for the efflux pumps mexAB-oprM, mexEF-oprN10 si mexCD-oprJ were detected in ciprofloxacin resistant strains and also correlated with the phenotypic resistance to aminoglycosides and carbapenems. The ESBL phenotype was correlated with the presence of blaSHV, blaTEM and blaPSE genes, while the MBL phenotype with the presence of blaVIM gene. Conclusion: The increasing resistance in GNR provides an important signal that we need to improve our understanding of the genetic and biochemical basis of resistance mechanisms in the bacterial strains circulating in our geographical area, by using phenotypic and resistance genotyping tools.