Virulence and resistance genes in methicillin resistant Staphylococcus aureus and vancomycin resistant Enterococcus sp. clinical strains isolated from patients with cardiovascular surgery

Irina Gheorghe*1, Ilda Czobor2, Marcela Popa3, Otilia Banu4, Veronica Lazar2, Mariana Carmen Chifiriuc5

1University of Bucharest, Faculty of Biologyş Research Institute of the University of Bucharest, Microbiology, Bucharest, Romania

2University of Bucharest, Faculty of Biology, Microbiology, Bucharest, Romania

3Faculty of Biology, Research Institute of the University of Bucharest, Bucharest, Romania

4Institute for Cardiovascular Diseases "c.C. Iliescu", Bucharest, Romania

5University of Bucharest, Research Institute of Bucharest University, Microbiology Immunology, Bucharest, Romania, Bucharest, Romania

Background: The purpose of the present study was aimed to identify the SCCmec elements and types, the macrolides and vancomycin resistance, as well as virulence genes, among clinical S. aureus and Enterococcus sp. strains.

Material/methods: This study was conducted on a total of 81 isolates, 52 of S. aureus, 21 of E. faecalis and 8 of E. faecium, clinical strains isolated in 2015, out of which 56 from wound secretions, 12 from blood cultures, 12 from urine and 1 from catheters taken from patients hospitalized for cardiovascular surgery harboring infections with different localizations. Simplex and multiplex PCR was performed on genomic DNA from MSSA and MRSA isolates in order to identify the SCCmec central elements - ccr and mec complex and to establish the SCCmec type (type I, II, III, IVa-d, V); virulence genes in S. aureus - bone bound sialoprotein (bbp), elastin-binding protein (ebpS), fibronectin-binding proteins (fnbA, fnbB), clumping factors A and B (clfA and clfB), collagen-binding protein (cna), coagulase (coag), Panton-Valentine leucocidin (luk-PV), hemolysin (hlg), toxic shock toxin (tst); and vancomycin resistance genes (Van A, B, C) in Enterococcus sp. isolates.

Results: The incidence of MRSA was significantly high among the S. aureus isolates (86.53% of the analyzed strains). The following elements of the SCCmec were identified in the MRSA strains: mecI (30.76%), CIf2 and ccrC (15.38%), SCCmecVJ1 (11.53%). The inducible macrolide resistance phenotype (MLSBi) was correlated in 11.53% of the isolates with the presence of ermA gene. Only mecIVa and III SCCmec types were encountered among the MRSA strains. Regarding the virulence genes in S. aureus the most frequent was the tst gene (34.61%), followed by ebpS (28.84%), hlg and bbp (21.15%), coag gene (19.23%) and luk-PV gene (13.46%). In the case of Enterococcus sp. isolates the most frequent vancomycin resistance gene was VanB followed by the far less frequent VanA gene (44.82% versus 3.44% of the isolates).
Conclusions: These results confirm the high prevalence of SCCmec IVa, usually community-acquired, among the MRSA strains isolated from patients hospitalized for cardiovascular surgery and the high prevalence of VanB gene among the *E. faecalis* clinical isolates.