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Antimicrobials: Epidemiology of MRSA, VRE and other Gram-positives

Genetic profiles of MRSA strains isolated during 5-year period in vascular surgery ward

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Objectives

The aim of the study was to determine the genetic profile and virulence factors of methicillin-resistant *Staphylococcus aureus* isolated from Vascular surgery ward in 5- year period. We also aimed to investigate the relatedness of strains and determine the proportion of community-associated MRSA among MRSA isolates.

Methods:

All clinical samples included in the study, were taken as a part of an diagnostic algorithm for detection of pathogens except for screening samples, which were taken according to local hospital guidelines. Along with swabs, data on gender, age, previous hospitalization, previous antibiotic use, were recorded, as well as the patient's diagnosis, previous MRSA status, presence of devices and treatment procedure.

Samples were analysed according to standardized laboratory procedure and susceptibility testing was performed according to Eucast standards, version 2.0. SCCmec testing and mecA detection was performed according to Deurenberg et al. , spa typing was performed as previously described by SeqNet protocol, and PFGE analysis was performed as previously described.

Results:

A total of 107 MRSA isolates was detected in 77 patients and only one isolate per patient was submitted to further analysis.

51/77 (74%) of patients were older than 60 years, 24/77 (31,2%) belonged to an age group 41-60 years, and one patient in each group 21-40 years and under 20 years old. 20 patients were receiving antimicrobials, 54 not, and for 2 it was not possible to record that data.

58 (75% )of patients with MRSA isolates were male, and 19 (25%) were female.

MRSA distribution- isolate site (77)
throat swab 4
nasal swab 2
perineal swab 2
wound swab 67
blood culture 1
central venous catheter-(cvc) 1

Percentage of patients from nursing homes was 8 out of 77.

Results:

All *S. aureus* isolates which were detected as methicillin-resistant by phenotypic testing, were confirmed by mecA gene detection (100%). SCCmec typing results are shown in table 2.

SCCmec TIP I	SCCmec TIP II	SCCmec TIP III	SCCmec TIP IV	SCCmec TIP V	NT*
43 (55,8%)	28 (36,4%)	3 (3,9%)	0	0	3(3,9%)

Spa typing revealed 10 different spa types.

By PFGE analysis, we detected 6 genetically related, clonal groups. A-F. 35 (46,8%) isolates belonged to group A, and second largest group was group D, consisting of 25 (33, 8%) of isolates. Majority of spa types in large groups, A and D is t041, typical hospital-acquired MRSA, a variant of Southern German clone

Conclusion:

Molecular analysis of MRSA strains in Vascular surgery ward showed genetic relatedness among two large groups of isolates indicating endemicity of isolates and possible transmission during patients stay on the ward. By SCCmec and spa typing, our isolates mostly belong to a group of typical „hospital-acquired' (HA) MRSA.