L0062 Methicillin-resistant Staphylococcus aureus spa-types t003, t586 and t014 common cause of MRSA infection in Czech Republic

Jan Tkadlec1, Oto Melter1, Pavel Drevinek1, Tamara Bergerova2, Sylvia Polivkova3, Magda Balejova4, Marketa Hanslianova5, Lenka Havlinova6, Daniela Fackova6, Katerina Habalova7, Renata Tejkalova8, Iva Vagnerova9, Natasa Bartonikova10, Marcela Krutova1

1 Department of Medical Microbiology, 2nd Faculty of Medicine, Charles University and Motol University Hospital, Prague, Czech Republic, 2 Department of Microbiology, Faculty of Medicine and University Hospital Plzen, Charles University in Prague, Plzen, Plzeň, Czech Republic, 3 Department of Infectious Diseases, 3rd Faculty of Medicine, Bulovka Teaching Hospital, Prague, Czech Republic, 4 Department of Medical Microbiology, Hospital Ceske Budejovice, Ceske Budéjovice, Czech Republic, 5 Department of Medical Microbiology, University Hospital Brno, Brno, Czech Republic, 6 Department of Medical Microbiology and Immunology, Hospital Liberec, Liberec, Czech Republic, 7 Department of Clinical Microbiology, University Hospital Hradec Kralove, Hradec Králové, Czech Republic, 8 Department of Medical Microbiology, Faculty of Medicine, Masaryk University and St. Anne’s University Hospital, Brno, Brno, Czech Republic, 9 Department of Microbiology, Faculty of Medicine and Dentistry, Palacky University Olomouc, University Hospital Olomouc, Olomouc, Czech Republic, 10 Department of Medical Microbiology, Tomas Bata’s Hospital Zlin, Zlín, Czech Republic

Background: Methicillin-resistant Staphylococcus aureus (MRSA) is a leading cause of healthcare-associated infections world-wide. The aim of the study was to characterize epidemiological structure of MRSA strains currently circulating in the Czech Republic.

Materials/methods: Between September 2017 and January 2018 non-duplicated (single patient) MRSA isolates were collected from 11 hospitals across the Czech Republic. Isolates causing infection or colonizing patients of both healthcare and community origin were characterized. Resistance to oxacillin and cefoxitin was confirmed by disk diffusion method. The presence of genes encoding Panton-Valentine Leucocidin (PVL) and mecA gene were detected by PCR. Isolates were assign to the known multilocus sequence type clonal complexes (CC) based on corresponding spa-types.

Results: Total of 441 MRSA isolates were characterized, 78% (n=343) of them belonged to a single clonal complex CC5 represented by spa-types t003 (n=136), t586 (n=92), t014 (n=81), t002 (n=20) and other (n=14). spa-types belonging to the CC5 were dominant (more than 50% of isolates) in all participating hospitals, with exception of one hospital where t008 (CC8) was one of the top three spa-types. Livestock-associated MRSA (CC398) was identified in 10 isolates (Figure 1). Except oxacillin and cefoxitin, the MRSA isolates were most frequently resistant to erythromycin (88.0%), clindamycin (84.8%), and ofloxacin (82.8%).

Conclusions: High prevalence of a limited number of spa-types, originating from healthcare-associated CC5 lineage (t003, t586, t014), was found in eleven Czech healthcare facilities suggesting spread and circulation of these strains within and between healthcare institutions in the Czech Republic.