

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

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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 ceftiofuran was confirmed by disk diffusion method. The presence of genes encoding Panton-Valentine Leucocidin (PVL) and *mecA* gene were detected by PCR. Isolates were assigned 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 ceftiofuran, 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.

