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Abstract (poster session)

Genetic characterisation of community-acquired methicillin-resistant *Staphylococcus aureus* isolated in a low-endemic area using DNA microarray analysis

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Objectives: Methicillin-resistant *Staphylococcus aureus* (MRSA) is a well known nosocomial pathogen that has spread worldwide. Sweden is still a low-endemic area and the prevalence of MRSA has continued to be low, approximately 1%. However, a changing epidemiology has recently been observed, and community-associated (CA) MRSA is emerging. In 2010 a total of 1580 cases of MRSA were reported in Sweden and > 60% were CA-MRSA. The aim of the present study was to investigate the molecular epidemiology as well as the distribution of genetic characteristics such as virulence genes and resistance genes among CA-MRSA isolates obtained in a low endemic country using DNA microarray analysis. **Methods:** CA-MRSA isolates (n=114) obtained from clinical infections as well as from screening procedures (nares, throat and perineum/groin) in Örebro County, Sweden, (population approximately 280,000 inhabitants) were analyzed. DNA microarray-based typing was performed by the Alere StaphyType DNA microarray that includes 334 target sequences corresponding to approximately 170 distinct genes and their allelic variants. **Results:** The CA-MRSA isolates obtained from 114 index patients displayed 34 distinct clonal complexes (CC) or STs containing 1 to 26 isolates. The three dominating CCs were CC80-MRSA-IV European caMRSA Clone (n=26), ST8-MRSA-IV USA300 (n=10), and CC5-MRSA-IV Paediatric clone (n=10), comprising together 46/114 (40 %). The distribution of the SCCmec types were type I (n=2), type II (n=3), type IV (n=95), and SCCmec type V (n=14). PVL was found in almost all isolates. The genes encoding staphylococcal enterotoxins A, B and C were found in 14, 4 and 3 isolates, respectively, and 9 isolates harboured the *tst-1* gene. In general, the prevalence of genes encoding various antimicrobial resistance genes was low. The genes *aacA-aphD* encoding resistance against gentamicin and *aaD* encoding resistance against tobramycin were found in 14 (12%) and 9 (8%) isolates, respectively. The gene *mupR* encoding resistance against mupirocin was not found in any isolate. **Conclusion:** The CA-MRSA found in our low endemic area are heterogeneous and diverse displaying numerous genetic backgrounds. However, the known geographic background of some of the CCs found suggest a multiple and random importation of CA-MRSA from epidemic regions into Sweden.