O178
Abstract (oral session)

Invasive Staphylococcus aureus isolates dominate within clonal complex (CC) 5, 8, 15 and 25

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S. aureus is a common bacterium with a clinical picture ranging from nasal carriage to invasiveness, sometimes with life-threatening bacteremia and hematogenous complications such as infective endocarditis (IE). The significance of different virulence factors has been investigated in previous studies with partly contradictory results. The aim of this study was to clarify if there was an association between S. aureus invasiveness and bacterial genotype in terms of clonality and genes encoding potentially important virulence and adhesion factors using DNA microarray analysis. S. aureus isolates (n=134), all MSSA, from 3 clinical groups (nasal carriage n=46, bacteremia n=88, of which 33 had concomitant IE) were analyzed. DNA microarray-based genotyping (Alere StaphyType DNA microarray) covering 185 distinct genes for detection of clinically relevant virulence factors, MSCRAMMs, capsule type, and resistant determinants were used. The isolates were also assigned to different clonal complexes (CCs) and sequence types (STs). The isolates represented 18 different CCs. The dominating were CC5, CC8, CC15, CC25, CC30 and CC45 and constituted together 113/134 (84%). Of isolates belonging to CC5, CC8, CC15 and CC25 37/46 (80%) were of invasive origin. Seven out of 11 isolates representing CC5 originated from patients with IE. All isolates were assigned to capsule type 5 or 8 following CCs affiliation. Analysis within capsule group showed a predominance of invasive isolates within capsule type 5(79% compared with 21%in the nasal carriage group). Of 15 examined MSCRAMM genes, fib, fnbB and sasG were more common among invasive isolates. The presence of fib and sasG were in concordance with CCs affiliation. Regarding leukocidins and other virulence genes, lukD/lukE as well as splA and splB were more prevalent among invasive isolates. Among the enterotoxin genes, the most common were those of the enterotoxin gene cluster, but there were no difference in frequency between isolates of different origin. The haemolysins were found in almost all isolates while the exfoliative toxins were rare. Our study concludes a predominance of invasive isolates within CC5, CC8, CC15 and CC25. Regarding CC5 most of the isolates were isolated from patients with concomitant IE. There was also a correlation between invasiveness and capsule type as well as genes encoding some adhesion factors. In most cases, however, this was in accordance with affiliations to CCs.