O270
Oral Session
PCR and other molecular tests directly on blood: what is new?

MOLECULAR EPIDEMIOLOGY AND CHARACTERIZATION OF S. AUREUS BACTEREMIC ISOLATES DURING FOUR DECADES IN SWEDEN

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Objectives
According to the background of increased life expectancy, implementation of more advanced medical interventions and the emergence of antibiotic resistance, there might be an increased incidence of *S. aureus* bacteremia.
The aim of the present study was to investigate changes of the molecular epidemiology with regard to the assignment to clonal complexes (CCs), presence of virulence genes as well as antibiotic resistance genes of 400 invasive *S. aureus* isolates, all MSSA, collected during the last 4 decades.

Methods
A total of 400 *S. aureus* isolates collected as the first 100 consecutive episodes of *S. aureus* bacteremia each decade between 1980 and 2010, were retrospectively identified and analyzed using DNA microarray based genotyping (Alere StaphyType test).
Trends of change in prevalence per decade were expressed as incident rate ratio (IRR), estimated by Poisson regression analysis. P-values <0.05 were considered statistically significant.

Results
A majority of isolates (319/400) were distributed between 6 major CCs (5, 8, 15, 25, 30 and 45). During the study period an increasing trend was observed for CC5 (IRR=1.96; p=0.002) and CC15 (IRR=1.62; p=0.001), while the opposite was shown for CC8 (IRR=0.66; p=0.015), CC25 (IRR=0.44; p=0.001) and CC30 (IRR=0.79; p=0.015). CC45 comprised 106/400 isolates without changes over years (IRR=1.17; p=0.069).
Agr group I included 200/400 isolates, while only 12 isolates were assigned to *agr* group IV, with no changes over time. For *agr* group II an increasing trend over decades was observed (IRR 1.36; p=0.002), while *agr* group III decreased (IRR 0.81; p=0.021). Presence of the capsule polysaccharide (*cap*) gene 5 showed reduced prevalence over years (IRR=0.78; p=0.004). Both *agr* group and capsule type followed CC affiliation.
Of 15 analyzed MSCRAMM genes, *sasG* showed an increasing prevalence over decades (IRR=1.17; p=0.040), and gene carriage was in accordance with CC affiliations.
Genes encoding the PVL-toxin (*lukF-PV*, *lukS-PV*) were found in only 7 isolates originating from different decades.
Of enterotoxin genes, the *egc*-cluster was the most prevalent beeing found in 274/400 isolates with no significant changes over years.
Prevalence of the *sea*-gene declined over years (IRR=0.80; p=0.026) while the *sep* gene increased (IRR=1.89; p=0.001). Exfoliative toxin genes were rare while haemolysin genes were found in almost all isolates.
The antibiotic resistance was not increased during the study period, and with the exception of *blaZ* found in 295/400 isolates only occasional isolates harbored resistance genes.

Conclusion
We found a significant trend of changes regarding assignment to some of the major CCs, *agr* group II and III as well as CP type 5, of which some previously have been associated with invasive disease with haematogenous complications. Moreover, the antibiotic susceptibility pattern was unchanged during the study period and MRSA are in Sweden a much lesser problem than in other countries.