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Paper Poster Session
Staphylococcal pathogenesis

Detection of sasX, sesI, icaA, icaD and IS256 gene positivity of coagulase-negative staphylococci

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Background: SasX, newly described protein which is thought to play an important role in nasal colonisation and virulence of meticillin-resistant *Staphylococcus aureus* (MRSA). It is shown that *sasX* gene is located on a prophage. There is a very similar prophage in *Staphylococcus epidermidis* strains containing *sesI* gene which has sequence similarity with *sasX* gene indicating that *sasX* may be acquired from Coagulase Negative Staphylococci (CoNS) by horizontal gene transfer. And this gene may help in clarifying the relevance of the different adhesion mechanisms in the pathogenesis of infections associated with biofilm. The aim of the study was to investigate *sasX* and *sesI* gene positivity rates of invasive and non-invasive CoNS and its possible relationship between the genes which plays role in biofilm production.

Material/methods: A total of 180 CoNS strains were included in the study. Antimicrobial resistance profiles of all strains were studied by Kirby-Bauer disc diffusion method and for vancomycin Minimum Inhibitor Concentrations (MIC) were evaluated (CLSI, 2014).Polymerase chain reaction (PCR) was used to detect the presence of *sasX*, *sesI*, *mecA*, *icaA, icaD* and IS*256*.

Results: None of the isolates were found to be resistant to vancomycin, teicoplanin and linezolid. Of the 180 strains *mecA, sasX* and *sesI* genes were detected in 75%, 9.44% and 30.55%, respectively. The *sasX* / *sesI* genes were detected in 12.35% / 37.07%, 11.42% /37.14%, 7.69% / 34.61% and 0% /0% strains isolated from peripheral blood (n:89), catheter colonisation (n:35), nasal vestibules (n:26) and healthy hands (n:30), respectively (p=0.188 / p=0.001). Of the 17 *sasX* positive strains 18.75% (9/48) of them were *Staphylococcus haemolyticus*, 7.69% (1/13) *Staphylococcus capitis*, 6.66% (4/60) *Staphylococcus epidermidis*, 6.52% (3/46) *Staphylococcus hominis*, respectively (p=0.173). Of the 55 *sesI* positive strains 43.75% (21/48) of them were *Staphylococcus haemolyticus*, 31.66% (19/60) *Staphylococcus epidermidis*, 15.21% (7/46) *Staphylococcus hominis*, 46.15% (6/13) *Staphylococcus capitis*, respectively (p=0.020). The *mecA* gene was detected in 16 (94.11%) of 17 *sasX* gene positive isolates. The only strain which was *mecA* gene negative was a nasal coloniser isolate. Of the 180 strains, *icaA, icaD* and IS*256* genes positivity rates were found as 33 (18.33%), 57 (31.66%) and 72 (40%) respectively (p<0.001). Comparison of the IS*256* genes of *sasX* positive and negative isolates revealed that the former group had higher positivity rates (70.58% vs 36.8%) (p=0.007). Of the 17 *sasX* positive strains, at least one biofilm gene were detected in13 of them and neither in 4 which was peripheral blood isolates.

Conclusions: It is remarkable that *sasX* and *sesI* genes were found to be negative from strains isolated from healthy hands. Of the 17 *sasX* positive isolates 14 of them had also bands with *sesI* primers, this finding need to be investigated with sequence typing.