Characterisation of the SCCmec and ACME in *Staphylococcus epidermidis* isolated from prosthetic joint infections, compared with isolates from hands and nares

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**Introduction**

*Staphylococcus epidermidis* is considered to be the most important pathogen in infections related to implanted foreign body materials, especially prosthetic joint infections (PJIs), and an increasing number of isolates are methicillin resistant. Methicillin resistance emerges when *S. epidermidis* produces an alternative penicillin-binding protein (PBP2a), which is encoded by the *mecA* gene. Accordingly, identical resistance mechanism as observed in methicillin-resistant *S. aureus* (MRSA). The *mecA* gene is located within a mobile gene cassette called Staphylococcal Cassette Chromosome mec (SCCmec). SCCmec has been thoroughly studied in MRSA but not extensively in *S. epidermidis*.

A newly described genetic island in staphylococci is the arginine catabolic mobile element (ACME), which is believed to enhance the capacity of the staphylococci to colonize the human skin and mucosal surfaces. It is located in close proximity to the SCCmec and it is believed to use the recombination (cassillB) in SCCmec for its mobility. ACME contains two genetic clusters; arc - encoding a secondary arginine deiminase system and opp-3 – encoding an oligopeptide permease system.

The aim of this study was to characterise the SCCmec of *S. epidermidis* isolated from PJIs, and, if possible, assigning them to a SCCmec type, according to the nomenclature of MRSA, and to examine the isolates for the presence of ACME.

**Material and Methods**

Sixty-one *S. epidermidis* isolates obtained during revision surgery due to PJIs were analysed. In addition, 24 *S. epidermidis* from skin of hands and nares of healthy individuals were examined for comparison.

Detection of the *mecA* gene was performed using real-time PCR and all isolates containing the *mecA* gene were further analysed using both conventional and real-time PCR for detection of the ccr complex 1-4 and C and class A-C mec-complex.

Presence of ACME was examined using conventional PCR for detection of the *arc* and *opp-3AB* genes. The results were classified into three ACME allotypes depending on whether one or both genes were detected, type 1 *arcA* + *opp-3AB* +, type 2 *arcA* + *opp-3AB* –, and type 3 *arcA* - *opp-3AB* +.

**Results**

In 49 out of 61 (80%) PJI isolates and four out of 24 (17%) commensal isolates the *mecA* gene was possible to detect and the composition of the SCCmec were further analysed and, if possible, assigned a SCCmec type (n=23), according to the nomenclature for *S. aureus* (Table 1).

ACME could be detected in eight out of 61 (13%) PJI isolates and in 14 out of 24 (58%) commensal isolates representing all three ACME allelotypes (Table 1).

**Table 1.** Detection of *mecA*, mec-classes, ccr-types, SCCmec-type (when applicable), and ACME-type among 61 isolates from PJIs and 24 commensal isolates from hands (H) and nares (N). NA = Not Applicable.

**Conclusions**

The SCCmec of *S. epidermidis* is more complex compared to *S. aureus*. For many of the isolates it was not possible to assign an SCCmec type, according to the nomenclature for *S. aureus*, due to multiple ccr-complexes. ACME was detected more frequently in the commensal isolates than in the PJI isolates.