Genomic diversity of *Staphylococcus epidermidis* isolates from the intensive care unit

We read with interest the article in *Clinical Microbiology and Infection* by Cafiso et al. [1], in which they described their findings when they assessed 40 isolates of *Staphylococcus epidermidis* from nosocomial infections for the presence of the ica operon and for genetic relatedness using pulsed-field gel electrophoresis (PFGE). Almost half (45%) of the isolates were positive for ica, but there were 30 different PFGE profiles. We have also studied detection of the ica operon as a possible marker for virulence [2], and wished to exclude the possibility that the findings could be explained by the presence of a predominant clone in the population of isolates studied. We used PFGE [3] to compare 18 previously characterised *S. epidermidis* isolates associated with device-related infection (DVI) and 13 contaminants. Genetic relatedness was determined by visual inspection using the criteria proposed by Tenover et al. [4]. Wide genomic diversity was detected among the 31 isolates, with 21 different PFGE patterns evident. Thus, although a significant association between the presence of ica and DVI had been noted previously [2], no specific PFGE type was associated with DVI, carriage of the icaADBC operon or biofilm-forming capacity. These findings suggest that a single clone of *S. epidermidis* with enhanced virulence is not responsible for DVIs. Therefore, our findings, and those of Cafiso et al. [1], indicate that many hospital strains have the potential to form biofilm because of the presence of ica and other potential virulence determinants, thus reflecting the diverse aetiology of infections involving this opportunistic pathogen.

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