

## Quantification of Biofilm-Associated Genes in *Staphylococcus Epidermidis* Biofilms: Its Impact in Biofilm Formation and 3D Structure

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*Staphylococcus epidermidis* is a common commensal coloniser of the human skin and is currently the most frequent cause of biomaterial associated infections. Several studies have attempted to identify the determinants that distinguish invasive from commensals *S. epidermidis* strains. Its pathogenesis is directly related to its ability to establish multi-layered and highly structured biofilms, resistant to antimicrobial agents. This bacterium expresses several factors that are responsible for the development of the biofilm, including the contribution of specific factors (*icaA*, *aap* and *bhp* genes) in the accumulation phase. Recently, several research groups have been trying to understand the contribution of the genes involved in biofilm formation. Thus, the main goal was to analyse the gene expression of *icaA*, *aap* and *bhp* and compare with the formation of the biofilm structure. Two *S. epidermidis* strains, a clinical and a commensal were characterized at the level of biofilm formation, at different incubation times. According to our results both strains showed an increase of biomass production overtime, revealing the importance to use screening assays with more than 24 h of incubation. A biofilm structure analysis was also performed to detect the presence of poly-N-acetylglucosamine (PNAG), the major component of *S. epidermidis* biofilm matrix. The results revealed a higher production of PNAG only after 48 h for SECOMO034.A1. Finally, the gene expression at two different incubation times was determined, confirming the importance of the *icaA* gene in the accumulation stage, explaining the high production of biomass and PNAG. On the other hand, the *aap* and *bhp* expression levels raised some questions about their role in the biofilm process.



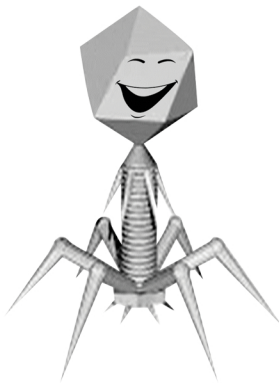
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# ABSTRACTS



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