Optimization of an Experimental Protocol to Reduce Gene Expression Variability in *S. epidermidis* Biofilms

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S. epidermidis is the most frequently bacteria isolated from human epithelia. Currently, this bacterium persist as a major cause of hospital and community-acquired infections and it is primarily associated with infections of indwelling medical devices, by the formation of a structure called a biofilm. Biofilms can quickly adapt to new conditions and consequently, can result in the appearance of infections that are resistance to many antibiotics and mechanisms of the host immune defense. The understanding of how bacteria quickly adapt to the new environment is crucial to devise better therapeutic solutions. Gene expression studies have been important in addressing these issues. However, a high variability of gene expression studies can often compromise the results and leads to a higher number of experimental repeats, with an increase in costs. In this work, we quantified the origin of gene expression variability, by isolating the individual steps included in the experimental set-up, namely biofilm growth, RNA extraction, reverse-transcriptase reaction and qPCR. Our results showed that biological sample was the key step introducing high variability. We devised a simple approach wherein we pooled 20 biofilms in each RNA extraction. This simply solution was able to reduce gene expression variability 2-3 fold. This was then confirmed in 3 independent clinical and commensal strains.

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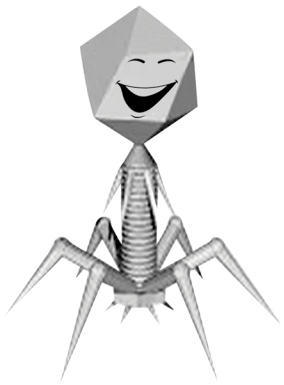

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ABSTRACTS

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