[P143] PROBING FOR RNA SEQUENCING DATA IN SEARCH FOR POSSIBLE DIAGNOSTIC MARKERS FOR STAPHYLOCOCCUS EPIDERMIDIS INFECTIONS

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Staphylococcus epidermidis is a commensal inhabitant of healthy human skin and mucosae that can originate important infections such as medical device-associated bloodstream infections. However, the current inability to discriminate between true bacteraemia caused by *S. epidermidis* and contaminated blood cultures often leads to misdiagnosis, resulting in a significant increase in patient morbidity and in health care costs. A fast diagnosis is, therefore, essential to reduce the clinical and economic impact associated with *S. epidermidis* infections. Several DNA-based molecular strategies have been tested before but, so far, no RNA-based strategy has been attempted to unravel possible differences in gene expression profiles of invasive and contaminant strains. Hence, our goal was to identify possible RNA-based molecular markers for the diagnosis of *S. epidermidis* biofilm-related infections. For that, the transcriptome of three clinical and three commensal isolates exposed to human blood was sequenced using RNA-seq technology. Freely available bioinformatics tools were used to analyse and compare the RNA-seq data obtained in order to rank potential markers for the diagnosis of *S. epidermidis* infections. We identified and selected eleven genes that were differentially expressed in clinical and in commensal isolates. To confirm this analysis, gene expression was validated by quantitative PCR using the same set of isolates and multiple blood donors. We found that the transcription levels of three of the previously selected genes had a potential to discriminate clinical from commensal isolates, making them good candidates for the diagnosis of *S. epidermidis* infections.