

## ABSTRACT

Biofilm formation and inherent persistence of *Staphylococcus epidermidis* which is commonly regarded as dominant species of normal flora that lives on human skin, enlist it as a leading nosocomial pathogen. Identification and characterization of novel intergenic noncoding RNAs (ncRNAs), which do not translate into a protein, permit an insight into regulatory roles that these molecules involved in elucidation of pathogenicity in *S. epidermidis*. Comparative intergenic ncRNAs transcriptomes profile analysis across *S. epidermidis* in three different growth conditions (normal, biofilm and biofilm released cells co-incubation in human blood components) were evaluated *in silico* to identify the novel intergenic ncRNAs and its differential expression at its respective growth conditions based on *S. epidermidis* RP62A (ATCC35984) as a reference genome. Expression pattern of 4 of selected novel intergenic ncRNAs was experimentally validated via reverse transcription polymerase chain reaction method. Also, putative messenger RNA (mRNA) targets for 4 of the selected novel intergenic ncRNA was predicted via *in silico*. Present study reports the detection of 575 novel intergenic ncRNAs and its statistically significant differential expression patterns. Putative mRNA target for 4 of selected novel intergenic ncRNAs was done based on the RNA-RNA interaction upon minimum free energy profile. The expression pattern of novel intergenic ncRNAs shows that they are growth condition dependent. Hence, this study serves as a platform for preliminary understanding towards elucidating their potential role in the regulatory networks.

**Keywords:** Biofilm, Sepsis, noncoding RNA, *S. epidermidis*, Transcriptome