

ABSTRACT

Staphylococcus haemolyticus is one of the members of Coagulase negative-staphylococci (CoNS) and they play a major role in clinical infections. *S. haemolyticus* is a Gram-positive, haemolytic, commensal bacterium found as part of the normal skin flora and it is the second most frequently isolated CoNS from human blood streams. The identification of non-protein coding RNA (npcRNA) can help to understand the pathogenicity of *S. haemolyticus*. Transcriptome of *S. haemolyticus* was analysed to identify the possible npcRNAs using customized computational methods and the expression level of selected npcRNAs were confirmed through Northern blot analysis. Expression profiles were analysed at different stress and growth phases of bacteria such as oxygen limitation, oxidative stress, osmotic stress, acidic pH, cold shock, heat shock, lag, log and stationary phase to predict their possible functions. By analysing the transcriptome of *S. haemolyticus*, we found 109 un-annotated transcripts and 33 of these are possible novel small ORFs. By filtering through the BLASTp, ORF finder and Rfam databases, 63 of these were found to be potential novel npcRNAs. 15 possible npcRNAs that were species specific were selected for the confirmation of their expression during different growth phases of bacteria. Out of this 15 npcRNAs, ShaR-10 and ShaR-63 the direction were predicted by nocoRNAC and for the remaining npcRNAs the directions were established by Reverse Transcription PCR (RT-PCR). For ShaR-10 and ShaR-63, their expression were verified by Northern Blot analysis. Besides, the secondary structures and possible mRNA targets of these two novel npcRNAs were predicted using RNAFold web server and TargetRNA2 software. ShaR-63 was predicted to have a housekeeping role in gene regulation and ShaR-10 was predicted to play growth dependent regulatory function in bacteria.