ABSTRACT

Bacteria are well known for their fast adaptation to stress conditions. In order to sustain stress conditions, the bacteria modulate their gene expression. *Proteus mirabilis* undergo various stress conditions including oxidative stress during pathogenesis. Therefore, it is of prime importance to understand the adaptation mechanism and the role of npcRNAs in oxidative stress during bacterial pathogenesis. A transcriptome analysis was carried out to understand the differential gene expression of npcRNA and mRNAs of *P. mirabilis* in normal and oxidative stress condition. The total RNA was sequenced via Illumina HiSeq 2000 platform. The fastQ format transcriptome sequences were analysed using bioinformatics software tools. Unannotated intergenic regions were screened for the possible novel npcRNA candidates using Artemis. Besides that, comparative analysis was carried out to identify the npcRNAs with high sequence conversation in *P. mirabilis*. Differential expression of mRNAs and npcRNAs was analysed using HTSeq and DESeq softwares. A total of 207 possible novel npcRNA candidates were identified. By verifying the annotation in other bacteria and Rfam database, 52 were selected as potential npcRNAs. Interestingly, 23 npcRNAs were up-regulated, 22 npcRNAs were down-regulated during oxidative stress condition and 7 npcRNAs shown to have equal expression. The four genus specific npcRNAs that differentially expressed during normal and oxidative stress condition were experimentally validated by Northern blot analysis. The npcRNAs namely PmiR-19, PmiR-34 and PmiR-171 were shown to be down-regulated during oxidative stress condition. Only PmiR-137 was up-regulated in oxidative stress condition. Out of 3338 coding genes, 1662 and 1676 showed significantly up and down regulations, respectively. Most of the phage proteins and dimethyl sulfoxide reductase genes were up-regulated. The selected mRNAs were analysed for their involvement in metabolic pathways, revealed the involvement of different metabolic pathways during oxidative stress adaptation. The high expressions of *glmZ* and *isrC* npcRNAs contribute to the protection mechanism of *P. mirabilis* from the oxidative

damage. The differential expression of the npcRNAs and mRNAs in *P. mirabilis* suggested that the bacteria might be using biofilm formation to adapt to the oxidative stress condition.