

Identification of novel non-coding RNA in *Enterobacter cloacae* by transcriptome analysis and their characterization

ABSTRACT

Non-coding RNAs (ncRNAs) are a complex class of regulatory molecules that play a critical role in bacterial gene regulation. In addition, they influence bacterial physiology including intermediary metabolism, bacterial cell to cell communication, biofilm formation and virulence. Recently, *Enterobacter cloacae* have emerged as multiple antibiotic drug resistance as infections caused by this nosocomial pathogen are difficult to control and has hinted mortality rate compared to other *Enterobacter* infection. In this study, novel ncRNAs were identified by using transcriptome analysis of *E. cloacae* which were further characterized by expression analysis that will give us a better understanding of this bacterium. A comparative analysis was carried out to identify the presence of known ncRNAs from Gram-negative bacteria as orthologous ncRNAs in *E. cloacae*. Total 295 ncRNAs candidates which were previously identified in 3 Gram-negative bacteria from *Enterobacteriaceae* family, namely *Salmonella typhimurium* – 68, *Escherichia coli* – 67, and *Salmonella typhi* – 160 were chosen for comparative analysis. Out of the total of 295 ncRNAs, only 64 ortholog ncRNAs were found to be conserved in *E. cloacae*. A total of 541 novel ncRNAs were identified in this transcriptome analysis study and nine ncRNAs were selected on the basis of high read per kilobase of transcript per million mapped reads (RPKM) for northern blot analysis. Differential expression of the five novel ncRNAs, EclR_44, EclR_1021, EclR_1219, EclR_1243 and EclR-1306 were observed by northern blot analysis remaining four did not show proper expression due to some reason and limitation. In this study, possible functions of these five ncRNAs were also predicted based on their differential expression during different growth phases, target mRNA prediction and their secondary structure analysis. This is a pioneering study in ncRNA identification in *E. cloacae* which further can help in well considerate of gene regulation during virulence and the multiple drug resistance of the bacteria.