

## ABSTRACT

*Pseudomonas aeruginosa* is a common environmental bacterium, which is able to assimilate many carbon sources, including polyethylene (PE). Small RNAs (sRNAs) are RNAs that are not translated into protein. It is also the key regulator for pathogenicity, stress response and regulation of metabolic pathways in response to environmental cues. The main aim of this study is to characterize and analyze the expression of ten sRNAs targets in *P. aeruginosa* AIMST-H2 strain, which have been previously identified via transcriptomic sequencing, during plastic biodegradation. Reverse transcription real-time PCR was performed to compare the expression of the sRNAs when the strain was grown in PE and glucose (control) supplemented media. Six housekeeping genes were evaluated and only four were used as reference genes for the normalization of real-time PCR data. Among the ten sRNA genes, six were over-expressed in PE culture conditions, which were *rnpB*, *ssrS*, candidate sRNA1, sRNA5, sRNA7 and sRNA9. On the other hand, sRNAs that showed lower expression in PE culture conditions were *rsmY*, PA1112.1, *prfF1*, and candidate sRNA8. Target prediction analysis for each sRNA revealed the possible interacting mRNA, which may be involved in the PE biodegradation pathway. Besides that, RLM-RACE PCR was performed on candidate sRNA5 to check the directionality of the transcript, which showed transcription from positive direction. The findings of this study provide us an insight into the role of the sRNAs as transcriptional regulators during PE biodegradation.