

Discovery and profiling of small RNAs responsive to stress conditions in the plant pathogen *Pectobacterium atrosepticum*

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Abstract

© 2016 Kwenda et al. Background: Small RNAs (sRNAs) have emerged as important regulatory molecules and have been studied in several bacteria. However, to date, there have been no whole-transcriptome studies on sRNAs in any of the Soft Rot Enterobacteriaceae (SRE) group of pathogens. Although the main ecological niches for these pathogens are plants, a significant part of their life cycle is undertaken outside their host within adverse soil environment. However, the mechanisms of SRE adaptation to this harsh nutrient-deficient environment are poorly understood. Results: In the study reported herein, by using strand-specific RNA-seq analysis and in silico sRNA predictions, we describe the sRNA pool of *Pectobacterium atrosepticum* and reveal numerous sRNA candidates, including those that are induced during starvation-activated stress responses. Consequently, strand-specific RNA-seq enabled detection of 137 sRNAs and sRNA candidates under starvation conditions; 25 of these sRNAs were predicted for this bacterium in silico. Functional annotations were computationally assigned to 68 sRNAs. The expression of sRNAs in *P. atrosepticum* was compared under growth-promoting and starvation conditions: 68 sRNAs were differentially expressed with 47 sRNAs up-regulated under nutrient-deficient conditions. Conservation analysis using BLAST showed that most of the identified sRNAs are conserved within the SRE. Subsequently, we identified 9 novel sRNAs within the *P. atrosepticum* genome. Conclusions: Since many of the identified sRNAs are starvation-induced, the results of our study suggests that sRNAs play key roles in bacterial adaptive response. Finally, this work provides a basis for future experimental characterization and validation of sRNAs in plant pathogens.

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Keywords

3' UTR, 5' UTR, in silico prediction, *Pectobacterium atrosepticum*, Riboswitches, Small RNAs, Strand-specific RNA-seq, Transcriptome