Small RNA-Controlled Gene Regulatory Networks in Pseudomonas putida - DTU Orbit
(30/09/2019)

Small RNA-Controlled Gene Regulatory Networks in *Pseudomonas putida*

Bacteria commonly encounter stressful conditions during growth in their natural environments and in industrial biotechnology applications such as the biobased production of chemicals. As the coordinated regulation of gene expression is necessary to adapt to changing environments, bacteria have evolved numerous mechanisms to control gene expression in response to specific environmental signals. In addition to two-component systems, small regulatory RNAs (sRNAs) have emerged as major regulators of gene expression. The majority of sRNAs bind to mRNA and regulate their expression. They often have multiple targets and are incorporated into large regulatory networks and the RNA chaperone Hfq in many cases facilitates interactions between sRNAs and their targets. Some sRNAs also act by binding to protein targets and sequestering their function. In this PhD thesis we investigated the transcriptional response of *Pseudomonas putida* KT2440 in different conditions via identification of differentially expressed mRNAs and sRNAs. *P. putida* is a soil bacterium with a versatile metabolism and innate stress endurance traits, which makes it suitable as future cell factory for the production of valuable compounds. Detailed insights into the mechanisms through which *P. putida* responds to different stress conditions and increased understanding of bacterial adaptation in natural and industrial settings were gained. Additionally, we identified genome-wide transcription start sites, and many regulatory RNA elements such as sRNAs and riboswitches. Further, the sRNAome during the growth of bacteria was investigated and compared to the strain without Hfq protein. Hfq has a big impact on sRNAs and gene expression in *P. putida*, hence many Hfq-associated sRNAs and mRNAs were found. Together, the results reported here significantly increase the knowledge of adaptation mechanisms in *P. putida*, as well as its transcriptome and regulatory networks. This will likely benefit the design and optimization of future cell factories.

**General information**
Publication status: Published
Organisations: Novo Nordisk Foundation Center for Biosustainability
Contributors: Bojanovic, K.
Number of pages: 214
Publication date: 2016

**Publication information**
Place of publication: Kgs. Lyngby
Publisher: Novo Nordisk Foundation Center for Biosustainability
Original language: English
Electronic versions:
KBojanovic_PhD_thesis_2016.pdf
Source: PublicationPreSubmission
Source ID: 126444498