

CsrA, the spider in a potentially huge web. Does its regulation depend on RNase P activity?

Bacteria have developed complex and effective counter-mechanisms against changes in their environment and outside threat. In order to survive and reproduce under environmental changes, adaptations must take place. The adaptation reflects reprogramming of gene expression, which is accomplished by what is known as a global regulator. Global regulators allow bacteria to strictly and accurately regulate the expression of operons and genes, with distinct roles, distributed all over the genome. One of these regulators is CsrA, a post-transcriptional regulator that affects translation of its target gene by binding to multiple sites of its mRNA leading region. This regulator controls a wide range of physiological processes, for example motility and biofilm formation as well as central carbon metabolism.

Global regulators are proteins that act on the transcriptional level. Recent studies on post-transcriptional regulators show that they influence gene expression globally. An extracellular signal such as temperature variation or exposure to certain chemicals is the starting point of a reaction. This leads to changing the phenotypic traits arising from the variety of gene expression in order to respond to extracellular signals.

CsrA is involved in complex regulatory pathways. It negatively regulates genes responsible for peptide transportation and glycogen metabolism respectively. It also positively regulates a gene responsible for flagella formation. CsrA is however dependent on the activity of small non-coding RNAs, it is also dependent on the activity of a membrane bound protein and RNA degrading enzymes.

Further investigation must be made to truly understand this regulatory cascade. This pathway is important to understand, as it may hold a solution to prevent bacteria from adapting to antibiotics and other drugs.