Reference

265

Digging out Evidences on *Escherichia coli* stringent response from Scientific Literature

Carneiro, Sónia (1); Lourenço, Anália (1); Carreira, Rafael (1,2); Rocha, Miguel (2); Ferreira, Eugénio C. (1); Rocha, Isabel (1)

1: IBB - Institute for Biotechnology and Bioengineering, Centre of Biological Engineering, University of Minho, Portugal;
2: 2Departament of Informatics / CCTC, University of Minho, Portugal

E-mail: soniacarneiro@deb.uminho.pt

Keywords: *Escherichia coli*, Stringent Response, Literature Mining

Abstract

The study of microbial stress responses in model-organisms like *Escherichia coli* (*E. coli*) is expected to expand general knowledge on these systems. Stress responses take place when cells are subjected to a wide variety of environmental attacks, including nutrient starvation, heat shock and toxic compounds. After a sudden environmental change, all organisms, from the simplest bacterium to the most complex organism, sense and respond by increasing production of a certain class of molecules that buffer them from harm. As a result, organisms have developed and evolved mechanisms to survive stress.

Stringent response, caused by amino acid starvation, has remained a topic of interest during several years due to its role in microbial growth performance. Due to amino acid limitation, the rate of RNA synthesis and other cellular reactions is severely reduced. Experimental work has shown that this response is characterized by the accumulation of guanosine nucleotide, (p)ppGpp, maintained by RelA and SpoT proteins. However, most of the results coming from such research work lay in textual publications in peer-reviewed journals and as such, its computational analysis in view of a systems-level understanding of the phenomenon is not straightforward. The manual curation involved in searching stringent-related information in literature is a labour-intensive endeavour.

In our study of the mechanism of stringent response in *E. coli,* a Literature Mining computational system assisted the process of manual curation. Documents were retrieved from PubMed and an organism-specific dictionary supported automatic recognition of biological entities. Results corroborate that the guanosine nucleotide, RelA and SpoT proteins and the transfer and ribosome ribonucleic acids (tRNA and rRNA, respectively) are key players in the process. However, less reported players, such as the 50S ribosomal subunit protein L11, Fis transcriptional dual regulator and ribosome modulation factor were also identified. Whenever possible, entities were linked to additional database information and classified according to Gene Ontology functional annotation. Besides such immediate information gains, results show that literature mining processes are able to reduce manual curation and, at the same time, support the linkage of literature information with publicly available data. This is important for reconstructing more comprehensive regulatory networks and, ultimately, understanding stress-related mechanisms.