“Bacterial regulatory networks are extremely flexible in evolution”

Irma Lozada-Chávez & Julio Collado-Vides

Program of Computational Genomics. Center for Genomic Sciences, UNAM. México.
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INTRODUCTION

Evolution is the result of the variation and selection through time of the components and structure of the organisms, for example, the transcriptional basis of natural variation in microbial species.

Transcriptional regulation plays a prominent role because it controls the cellular processes through activity of proteins and the expression levels of genes for the response to environmental changes, such as nutritional status and several stresses.

An important idea emerging from works of Michael A. Savageau and Stuart A. Kauffman (around 70’s) is that the transcriptional regulation can be viewed as a complex network of interactions among diverse types of molecules like proteins, DNA and metabolites [1].

OBJECTIVE

In order to understand the plasticity of Transcriptional Regulatory Network [TRN] in bacteria, we studied the conservation of currently known TRNs of the two model organisms Escherichia coli K12 [4] and Bacillus subtilis [5] across complete genomes including Bacteria, Archaea and Eukarya through REGULOG [6] principle at three different levels:

1) Transcription Factors [TF] and Target Genes [TG]
2) Pairs of Interactions
3) Regulons (group of all genes regulated by a TF)

METHODOLOGY

We demonstrate that individual elements, interacting pairs and groups of interactions are not conserved, in fact even in closely related species.

Therefore, transcriptional regulation reflects that is more flexible than genetic component of the organisms to adapt to environmental changes in phenotypic speculation.

RESULTS

Transcription factors [TFs] evolve much faster than target genes [TGs] across phyla. Hence, TFs could be major players responsible for the evolvability of the TRNs.

There is only a small fraction of significantly conserved interactions in bacteria and there is no constraint on the elements of the interaction to co-evolve.

The majority of regulons (interactions) in bacteria are rapidly lost implying a high order flexibility in the TRNs.

REFERENCES

[1] Stuart A. Kauffman (around 70’s) is that the transcriptional regulation can be viewed as a complex network of interactions among diverse types of molecules like proteins, DNA and metabolites.
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