A model for sigma factor competition in bacterial cells

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***Short Abstract* — Modulation of sigma factors and competition among them for core RNAP provide important mechanisms for the global switch of the transcriptional program. We study a theoretical model for sigma factor competition. Competition occurs when the number of free sigmas exceeds the number of free cores. Predictions of the model are in good agreement with in vitro sigma competition experiments. Within this framework we analyze the effects of some factors that modulate the competition such as anti-sigma factors and 6SRNA.**

***Keywords* — Systems biology, gene regulation, sigma factor competition.**

I. Introduction

BACTERIA respond to changing environmental conditions by switching the global pattern of expressed genes. In response to specific environmental stresses the cell activates several stress-specific molecules such as sigma factors. They reversibly bind the core RNA polymerase (RNAP) to form the holoenzyme and direct it towards the appropriate stress response genes. In exponentially growing E. coli cells, the majority of the transcriptional activity is carried out by the housekeeping sigma factor, sigma70, while stress responses are often under the control of six alternative sigma factors. It is believed that the modulation of their availability and competition among them for core RNAP provide important mechanisms for the global switch of the transcriptional program. Different genes remain coupled to the global state of the cell through the sharing of RNAP. The effect of this sharing on the mutual influence of the genes has not yet been completely understood. To shed light on these open problems we studied the influence of the competition on the gene expression using a theoretical approach.

II. Model and effect of competition

In the simplest case two species of sigma factors compete to bind the core RNAP to form two types of holoenzymes. To analyze this competition, we have developed a quasi-steady state model based on earlier work [1]. The relevant parameters are three measurable quantities: concentration of core RNAP and sigma factors and binding affinity between them. Simulations of the response of the system altering the amount of one sigma factor reveal that the competition takes place when the concentration of free sigmas exceeds the concentration of free cores. The analysis of the transcription rate points out that the reduce activity of one sigma can indirectly up-regulate the transcription of the genes that depend on the competing sigma. The predictions of our theory are in good agreement with a set of experimental data [2,3].

III. Applications of the model

The competition between sigma can be modulated by additional factors. Our model can be used to study their impacts. One example are anti-sigma factors that bind a sigma factor preventing the holoenzyme formation. Their effect is to shift the set-in of the competition. Another example is 6SRNA, a small non-coding RNA that sequesters RNAP holoenzymes with sigma70 preventing the transcription. In this case the set-in of the competition is unaffected.

IV. Conclusions

We have developed a simple model to describe the competition of sigma factors to bind the core RNA polymerase. The model shows that the passive regulation of the expression of a set of genes depending on a sigma factor is possible by acting on the availability of a second different sigma factor not coupled to these genes. We have included within the framework of the model some tuning effects of the competition such as anti-sigma factors, regulatory RNA and active transcription. The predictions of our theoretical work are in good agreement with in vitro experiments data here analyzed. The model suggests that competition between sigma factor has an impact on the global switch of the transcriptional program of the bacterial cell.

References

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