

ADAPTATIONS OF THE GALACTOSE METABOLISM AND GENE NETWORK TO CHANGES IN EXTRACELLULAR GALACTOSE AND GLUCOSE

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Abstract

The galactose operon is one of the few gene networks studied in unicellular organisms, which improved our understanding of the regulatory mechanisms occurring at the genetic level. The key molecular players and processes have been already discovered, but experimental results of research groups are sometimes not fully understood or contradictory. We extend here a previous model of the galactose gene network in the yeast *Saccharomyces Cerevisiae*, by including relevant metabolic processes and glucose repressive reactions. After estimating parameters using computational tools and literature values, we employ bifurcation analysis to decipher the systems' properties. Various frequencies in the administration of the glucose medium are another type of environment that we study. What was previously described as a low-pass filter property revealed to be rather a decrease in the amplitude and in the mean transcription level, due to the combination of fast metabolic rates and slow regulatory dynamics. The interplay between an inducer and a repressor of the gene network are crucial in characterizing the systems' adaptive capacities to environmental changes, along with its sensitivity to genetic mutations and molecular instabilities.

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