

Poster presentation

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A quantitative model for the GCN4 translational control in *Saccharomyces cerevisiae*

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Cells are capable of accommodating the environmental changes by reprogramming gene expression. In the yeast *Saccharomyces cerevisiae*, under the amino acid deprivation condition, the translational barrier primarily exerted on GCN4 mRNA is alleviated to enhance the production of Gcn4p, which subsequently induces the expression of nearly all genes involved in amino acid biosyntheses. Our Systems Biology project's goal is to construct a dynamic mathematical model that accurately predicts the kinetic behaviour of the GCN Response in *S. cerevisiae*. Here, we report the mathematical formulations to describe the translational control exerted on the GCN4 mRNA. More importantly, the kinetic parameter estimation for this model indicates differential scanning rates of the 40S ribosomal subunit on the GCN4 mRNA 5' leader sequence under the amino acid replete and starvation conditions. This discovery is speculated to be attributable to the change in relative helicase activities under the two conditions.

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