

研究简报

基元通量模式预测酵母生长现象

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摘要 本文通过EFM预测了基因突变后的酵母细胞生长现象, 模拟预测结果和实验结果吻合很好; 与FBA方法得到的模拟结果相比较, EFM方法能更好地把基因突变和其表型(生长)联系起来.

关键词 [预测](#) [基元通量模式](#) [啤酒酵母](#) [生长现象](#)

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Prediction of *Saccharomyces Cerevisiae* Growth Phenotypes Based on Elementary Flux Mode Analysis

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Abstract The purpose of this work is to illustrate the relationship between genotype and phenotype in the complex cellular network of *saccharomyces cerevisiae*. As a structure oriented method, using elementary flux mode(EFM) analysis can obtain its popularity in analysis of the robustness of the central metabolism, as well as network function of some organisms. However, this method has not been widely used for modeling gene deletion phenotype. By enumerating all the metabolic pathways, the EFM analysis presented herein can be used to identify the functional features and predict the growth phenotype of the *S. cerevisiae*. In comparison with the flux balance analysis(FBA), the performance of EFM analysis was superior to FBA in prediction of gene deletion phenotype. EFM analysis is demonstrated to be an effective tool for bridging the gap between metabolic network and growth phenotype.

Key words [Prediction](#) [Elementary flux mode](#) [Saccharomyces cerevisiae](#) [Growth phenotype](#)

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