

Multi-Omics Integration Combined with Deep Learning Predicts High-Density Growth Regulatory Genes in *Saccharomyces cerevisiae*

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Abstract

Saccharomyces cerevisiae is the most widely used eukaryotic model chassis and core industrial workhorse in the fields of synthetic biology, metabolic engineering and green biomanufacturing. For industrial-scale bioproduction, high-density fermentation of this yeast is the core prerequisite for the large-scale manufacturing of bio-based chemicals, recombinant proteins and biofuels. Its high-density growth performance is the core trait that directly determines the upper limit of fermentation titer, production efficiency and comprehensive manufacturing cost of the yeast cell factories. However, traditional experimental screening and validation of high-density growth regulatory genes face inherent bottlenecks: long research cycles, high experimental costs, heavy dependence on prior knowledge, and low hit rate of functional targets, which severely restrict the rapid directed optimization of industrial yeast chassis. To address these gaps, this study aims to develop an efficient and accurate prediction method for high-density growth regulatory genes in *Saccharomyces cerevisiae* through multi-omics integration and deep learning, as multi-omics data can comprehensively cover the multi-dimensional information of genes from sequence to expression and function, while deep learning can effectively mine the hidden nonlinear regulatory relationships in high-dimensional omics data to make up for the shortcomings of traditional analysis methods. We integrated whole-genome, transcriptomic, proteomic and phenomic data to build a multi-dimensional panoramic gene feature set, and constructed a deep learning prediction model embedded with an attention mechanism to increase the accuracy and identify high-confidence regulatory genes links to yeast high-density growth. This study provides a low-cost, high-efficiency research strategy and a high-value candidate target library for the directed modification and performance optimization of industrial *Saccharomyces cerevisiae* chassis.

Keywords

Saccharomyces Cerevisiae, High-density Growth, Growth Regulatory Genes, Multi-omics Integration, Deep Learning