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The yeast *Saccharomyces cerevisiae* is one of the most widely used cell factories in industrial biotechnology. However, the development of optimized yeast strains for the production of novel compounds is a time-consuming process and represents a significant cost/time burden. Currently, genome-scale metabolic models play an important role to reduce cost and time in order to develop improved strains. Nevertheless, the existence of various genome-scale metabolic models for *S. cerevisiae*, with different metabolic information and predictability capabilities, increases the complexity of metabolic engineering studies. The MIYeastK is a web-accessible metabolic integrated knowledgebase (<http://193.137.11.210/yeast/>) that integrates the metabolic information of 10 genome-scale metabolic models of *S. cerevisiae*, not only between each other but also with external databases, such as KEGG and MetaCyc. An enhancement of the annotation of individual metabolites, reactions, genes and gene rules included in the models was also performed. Moreover, the gene information in the models is integrated with the myriad of information contained in SGD (*Saccharomyces* Genome Database) simplifying phenotype analysis. Hence, MIYeastK is valuable tool for users to compare and implement metabolic engineering strategies using yeast metabolic models.

Keywords: Integrated knowledgebase, Saccharomyces cerevisiae, genome-scale metabolic models



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