

Genome-scale Reconstruction of *Schizosaccharomyces pombe* metabolic model and *in silico* analyses

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The fission yeast *Schizosaccharomyces pombe* has been used as a model eukaryotic for a variety of applications, including, but not limited to the studies of cell cycle regulation and ethanol production. Its mechanism for cell division is very similar to cell division observed in higher eukaryotes compared to other yeast which divide through budding. It has the smallest number of protein encoding genes in its genome, making it an ideal model for studying minimal cells. Here, we present the genome-scale metabolic reconstruction of the fission yeast *S. pombe* and analysis of its metabolic network with the intent to employ it for further elucidation of the yeast's characteristics. Through this analysis of the metabolic network, we attain a better understanding of its inner working and unique metabolic characteristics. [This work was supported by the Technology Development Program to Solve Climate Changes (systems metabolic engineering for biorefineries) (NRF-2012-C1AAA001-2012M1A2A2026556) and by the Intelligent Synthetic Biology Center of Global Frontier Project (2011-0031963) from the Ministry of Education, Science and Technology (MEST)]