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Surmising Alterations in Fermentation Process Utilizing Photonic Sculpting Pathway of Fructose Disk Space Under Active Biomass Situations

Badal Saha*

Department of Bioengineering, Worcester Polytechnic Institute, Massachusetts, USA

Abstract

Microbial metabolism is heavily influenced by environmental factors. While these can be well controlled in the laboratory, large-scale bioreactors are distinguished by inhomogeneities and, as a result, dynamic conditions for the organisms. The mechanistic response of Saccharomyces cerevisiae to frequent perturbations in industrial bioreactors is still unknown. To investigate the adaptations to prolonged dynamic conditions, we used previously published repeated substrate perturbation regime experimental data, supplemented it with proteomic measurements, and combined the two for modeling approaches. Data from multiple sources, including quantitative metabolize, enrichment, and flux quantification, were combined. Kinetic metabolic modeling was used to investigate the dynamics of the relevant intracellular metabolic response. A previously developed model of yeast central carbon metabolism was expanded, and various subsets of enzymatic kinetic constants were estimated.

Keywords: Organism • Kinetic • Metabolize • Investigate

Introduction

Microbial metabolism is heavily influenced by environmental factors. While these can be well controlled in the laboratory, a large-scale approach based on combinatorial enzyme selection and regularization was developed to identify and predict the minimum enzyme and parameter adjustments from steady-state to dynamic substrate conditions. This method predicted proteomic changes in hexose transport and phosphorylation reactions, which were validated by proteome measurements. Nonetheless, the modeling suggests a previously unknown kinetic or regulatory phenomenon. Some intracellular fluxes, such as hexose transport and intracellular trehalose activity during substrate perturbation cycles, could not be reproduced by mechanistic rate laws [1].

Saccharomyces cerevisiae, also known as baker's yeast, has been used by humans for thousands of years to produce beverages, foods, and chemicals. Despite its widespread use in industry, scaling new *Saccharomyces cerevisiae* production processes to industrial scale presents a number of intriguing and fundamental challenges. Most challenges are caused by spatial inhomogeneities caused by mixing limitations in large-scale bioreactors, resulting in gradients throughout the reactor. As a result, a cell dispersed in the reactor is subjected to rapid changes in its extracellular environment, which has an impact on intracellular metabolic regulation. Similarly, oscillations in the natural habitat are common in response to changes in environmental conditions such as temperature, pH, and substrate availability [2].

Despite the fact that dynamic conditions are encountered in industrial applications and environmental habitats, many physiological studies on yeast are conducted under (pseudo-) steady-state conditions. Clearly, steady-state experiments are very useful in quantifying intracellular fluxes due to the vast amount of available reference data, reliable measurements, and reproducibility. However, dynamic metabolic experiments are required to identify in vivo kinetic parameters. Dynamic perturbation experiments can be used to bridge this gap, and many studies have focused on elucidating the metabolic response from single pulse (SP) experiments [3].

Literature Review

While this SP approach is very useful for identifying kinetic parameters of networks adapted to the pre-perturbation limited steady-state, it does not describe adaptations that may occur under industrial conditions. A system of periodic substrate perturbations was created to simulate such an environment. This regime generates time-dependent substrate concentration gradients, allowing for accurate and reproducible sampling of intracellular metabolism. The in vivo metabolic activity was monitored using this repeated substrate perturbation setup during cycles of At this timescale, it is assumed that the metabolic response within one cycle is primarily governed by metabolic interactions, as enzyme concentrations are assumed to be relatively constant during these. Feed was administered in a cycle in blocks of 20 seconds [4].

Saccharomyces cerevisiae cultures exhibit different metabolic phenotypes under such dynamic substrate conditions than SP or SS cultures. Following a pulse in the repeated substrate perturbation regime, there was an increase in ATP rather than a decrease, no ethanol production, and no accumulation of glycolytic metabolites. These metabolic response differences point to a proteomic adaptation induced by the prior dynamic growth conditions. Translational regulation, in particular, can result in condition-specific proteome compositions. Under changing glucose availability conditions, distinct proteome compositions have been observed, both for sugar transporters and intracellular enzymes, and distinct is enzymes have different kinetic properties that can include glucose sensitivity. However, the mechanisms underlying this adaptation remain unknown [5].

Discussion

Quantifying in vivo parameters, particularly for cyclic pathways such as the trehalose cycle, can be difficult because both in- and out fluxes influence concentration change and no in- or out flux is directly observable [6]. This

***Address for Correspondence:** Badal Saha, Department of Bioengineering, Worcester Polytechnic Institute, Massachusetts, USA, E-mail: badalsaha4@gmail.com*

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correlation, combined with the fact that networks are becoming larger, creates a risk of local minima and ill-conditioning, resulting in sloppy parameter estimates. The divide-and-conquer approach was developed to overcome this challenge and identify a minimal set of necessary changes in kinetic constants. A decomposition of the global estimation problem into independent sub problems is used in this case. Furthermore, when taking into account the already known parameter values for the enzymes under investigation, L1 or Tikhonov regularization can favour a given parameter set as long as experimental data is properly reproduced [7].

Conclusion

In this paper, we combine data from the metabolize, fulsome, and proteome to create a metabolic model. We propose enzymatic reactions whose reaction kinetics adapt to dynamic substrate conditions and locations where our knowledge is limited based on detailed analyses. Testing various subsets of parameters for recalibration revealed that transporters and phosphorylation reactions were critical for adaptation. This in silico approach is similar to the experimental approach of metabolic reverse engineering, but it is much faster and less laborious because it does not require experiments with combinatorial genome modifications. The combinatorial approach can also be applied to other industrially relevant downscaling setups for quickly determining key parameter changes and further optimizing the bioprocess.

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Conflict of Interest

There is no conflict of interest by author.

References

1. Swinnen, Steve, Kristien Schaerlaekens, Thiago Pais and Jürgen Claesen, et al. "Identification of novel causative genes determining the complex trait of high ethanol tolerance in yeast using pooled-segregant whole-genome sequence analysis." *Genome Res* 22 (2012): 975-984.
2. Meijnen, Jean-Paul, Paola Randazzo, María R. Foulquié-Moreno and Joost van den Brink, et al. "Polygenic analysis and targeted improvement of the complex trait of high acetic acid tolerance in the yeast *Saccharomyces cerevisiae*." *Biotechnol Biofuels* 9 (2016): 1-18.
3. Slininger, Patricia J., Bruce S. Dien, Steven W. Gorsich and Zonglin L. Liu. "Nitrogen source and mineral optimization enhance D-xylose conversion to ethanol by the yeast Pichia stipitis NRRL Y-7124." *Appl Microbiol Biotechnol* 72 (2006): 1285-1296.
4. Levine, Barton S. and Jack W. Coburn. "Magnesium, the mimic/antagonist of calcium." *N Engl J Med* 310 (1984): 1253-1255.
5. van Voorst, Frank, Jens Houghton-Larsen, Lars Jønson and Morten C. Kielland-Brandt, et al. "Genome-wide identification of genes required for growth of *Saccharomyces cerevisiae* under ethanol stress." *Yeast* 23 (2006): 351-359.
6. Caspeta, Luis, Yun Chen and Jens Nielsen. "Thermotolerant yeasts selected by adaptive evolution express heat stress response at 30 C." *Sci Rep* 6 (2016): 27003.
7. Walker, Graeme M. and Roy SK Walker. "Enhancing yeast alcoholic fermentations." *Adv Appl Microbiol* 105 (2018): 87-129.

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