

Dynamic community-level metabolic modeling for fermentation kinetics and metabolic interactions of the yogurt starter culture based on metagenomic analysis

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Abstract

Genome-scale metabolic models (GSMMs) and flux balance analysis (FBA) have been extensively used to model and design bacterial fermentation. However, FBA-based metabolic models designed for simulating the dynamics of co-culture with quantitative accuracy are still uncommon, which is particularly true for lactic acid bacteria (LAB) used for yogurt fermentation. To investigate metabolic interactions in yogurt starter culture of *Streptococcus thermophilus* (ST) and *Lactobacillus delbrueckii subsp. bulgaricus* (LB), this study built a dynamic community-level GSMM based on metagenomic analysis. We first assessed the accuracy of the model by comparing predicted bacterial growth, consumption of lactose and production of lactic acid with reference experimental data, and then used it to predict the impact of different initial ST:LB inoculation ratios (gDW/gDW) on acidification. The dynamic simulation demonstrated the mutual dependence of ST and LB during the yogurt fermentation process. The modeling pipeline presented in this work provided a basis for the computer-aided process design and control of the production of fermented dairy products, contributing to the development of precision fermentation in the food industry.

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