

iAD 824: AN IMPROVED GENOME-SCALE METABOLIC NETWORK MODEL FOR *SCHEFFERSOMYCES STIPITIS*

*Andrew Damiani*¹, *Q. Peter He*², *Thomas Jeffries*³, *Jin Wang*¹

1. Auburn University, Department of Chemical Engineering
212 Ross Hall
Auburn, AL 36849, USA
2. Tuskegee University, Department of Chemical Engineering
Tuskegee, AL 36088, USA
3. University of Wisconsin at Madison, Madison, Department of Bacteriology
Madison, WI 53706, USA
E-mail: wang@auburn.edu
Oral Presentation

Suggested Session: Models and Metrics

Funding Agency: Sun Grant, NSF, NSF-IGERT

Due to its important role in the production of lignocellulosic ethanol, *Scheffersomyces stipitis* has drawn tremendous research interest in the last few decades. The complete genome of *S. stipitis* has been sequenced, which provides the foundation for genome-scale metabolic network reconstruction. Recently, two genome-scale models, iSS884 and iBB814 were published, which represent significant steps forward in gaining a systematic understanding of cellular metabolism of *S. stipitis*. However, both models have certain limitations. For example, neither of them predicts the production of xylitol under any condition, aerobic, microaerobic or anaerobic. It is well-known that xylitol is a key byproduct produced by *S. Stipitis* under microaerobic condition, so being able to predict xylitol production is very important for a model to identify candidates for balancing cellular redox potential.

In our previous work, we have conducted comprehensive evaluation of the two genome-scale models by applying a system identification based framework to extract the knowledge embedded in the genome scale model. We found that even though model iBB814 show worse agreement with quantitative experimental results, it agrees better with existing biological knowledge, and was chosen as the base model for further improvement.

In this work, guided by the findings obtained through the system identification framework, we developed a modified genome-scale model for *S. stipitis*, named iAD824. The new model not only shows better agreement with various quantitative and qualitative experimental results than iBB814 and iSS884, but also predicts the xylitol production which is in good agreement with reported experimental value under different conditions.