Reconstruction of a genome-scale metabolic model for the filamentous fungus *Ashbya gossypii*

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Metabolic models are an important tool for *in silico* simulation of cells’ behavior. Until now, a considerable number of metabolic models were released for several microorganisms. *Ashbya gossypii* is an industrially relevant fungus intensively used for riboflavin production with no model reported until now. Despite the high similarity with the *Saccharomyces cerevisiae* genome, *A. gossypii* contains only 4726 protein-coding genes and, contrarily to *S. cerevisiae*, has a filamentous growth. Here, we describe the first genome-scale metabolic reconstruction for *A. gossypii*. Initially, *A. gossypii* genome was re-annotated using several databases such as UniProt, SGD, AGD and BRENDA. A total of 1429 metabolic-relevant genes were assigned with the different enzymatic families: 35.4 % hydrolases; 35.8 % transferases; 28.8 % other families. 59 genes were assigned to multiple EC numbers and among these, 36 % were from different enzymatic families.

The next step in the reconstruction process was the compilation of the reactions set. For that purpose, re-annotation data were crossed with the models iMM904 and iIN800 from *S. cerevisiae*. BRENDA or Metacyc were used when data were not available and an in-house tool was used to predict the transport reactions from the *A. gossypii* genome. At the end of this step a set with 1755 reactions and 926 metabolites was obtained. This set was analyzed for critical gaps and those were filled adding specific reactions, leading to a model able to predict cell growth.

Despite its ability to predict growth, oxygen uptake was unattached to cell growth and for this reason, oxygen and ATP metabolism were inspected. All reactions from oxidative phosphorylation and those involving H+ were manually curated to ensure that an H+ gradient was being generated.

Current efforts aim the model validation with experimental data regarding specific growth rates, specific production rates for the main by-products (e.g. acetate, citrate, pyruvate), nutrient sources utilized and strategies of genetic engineering.

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