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BRANDL Julian (1), WORKMAN Mhairi (1), ARVAS Mikko (2), MEYER Vera (3), RAM Arthur Fj (4), ***ANDERSEN Mikael Rørdam*** *(1)*
(1) Department of Systems Biology, Technical University of Denmark, Kgs. Lyngby, Denmark
(2) Synthetic Biology Team, VTT Technical Research Centre of Finland, Esbo, Finland
(3) Technical University of Berlin, Berlin, Germany
(4) Institute of Biology Leiden, Leiden University, Leiden, The Netherlands

The development of a community consensus model for *Aspergillus niger*

Fungal primary metabolism is an essential part of fungal physiology and affects all phenotypic traits of the organism as well as carrying the biotechnological potential for the fungal host. While the study of individual pathways have gained essential knowledge and important scientific breakthroughs, a genome-scale view of metabolism is required to gain a holistic understanding of the cell. Mathematical models based on the stoichiometry of known enzymatic reactions have been developed in order to facilitate this approach and proven useful for guiding metabolic engineering in well characterized model organisms like *S. cerevisiae* and *E. coli*. With the sustained interest in *Aspergillus niger* as a potent host organism for citric acid and enzyme production, it was timely to improve on previous genome-scale modeling efforts. Here we have updated the genome-scale model by a combination of modeling, experimental work, and integration of the most recent literature information. In this new version of the model, the gene assignments have been improved by utilizing the genomes of the section *Nigri* being sequenced and analyzed in a community effort. Using these genomes in a comparative approach, we were able to identify shared isoenzymes and gene groups involved in primary metabolism between these closely related species in the section *Nigri*. In order to improve the coverage of our model in terms of nitrogen and carbon sources, we used Biolog plates for the screening of more than 270 carbon and nitrogen sources. Using this information we could identify missing substrates that have been subsequently added to the model as well as validated the presence of pathways already included in the model. In order to being able to simulate protein production we have included all enzymes that have been reported to be secreted in the literature thereby accounting for the natural catabolic activity of this fungus. Additionally we added all known pathways for the synthesis of secondary metabolites in order to enable the usage of the model to guide engineering of secondary metabolite cell factories. Here we present results from the modeling performance of said model and show an improvement over previous work. In conclusion this project has generated an experimentally validated community-consensus model of the *A. niger* metabolism being able to describe and predict beneficial modifications to the metabolic network in order to improve protein production on a variety of different substrates.