A community-driven reconstruction of the Aspergillus niger metabolic network - DTU Orbit (18/11/2018)

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Aspergillus niger is an important fungus used in industrial applications for enzyme and acid production. To enable rational metabolic engineering of the species, available information can be collected and integrated in a genome-scale model to devise strategies for improving its performance as a host organism. In this paper, we update an existing model of A. niger metabolism to include the information collected from 876 publications, thereby expanding the coverage of the model by 940 reactions, 777 metabolites and 454 genes. In the presented consensus genome-scale model of A. niger iJB1325, we integrated experimental data from publications and patents, as well as our own experiments, into a consistent network. This information has been included in a standardized way, allowing for automated testing and continuous improvements in the future. This repository of experimental data allowed the definition of 471 individual test cases, of which the model complies with 373 of them. We further re-analyzed existing transcriptomics and quantitative physiology data to gain new insights on metabolism. Additionally, the model contains 3482 checks on the model structure, thereby representing the best validated genome-scale model on A. niger developed until now. Strain-specific model versions for strains ATCC 1015 and CBS 513.88 have been created containing all data used for model building, thereby allowing users to adopt the models and check the updated version against the experimental data. The resulting model is compliant with the SBML standard and therefore enables users to easily simulate it using their preferred software solution. Experimental data on most organisms are scattered across hundreds of publications and several repositories. To allow for a systems level understanding of metabolism, the data must be integrated in a consistent knowledge network. The A. niger iJB1325 model presented here integrates the available data into a highly curated genome-scale model to facilitate the simulation of flux distributions, as well as the interpretation of other genome-scale data by providing the metabolic context.

General information
State: Published
Organisations: Department of Biotechnology and Biomedicine, Department of Chemical and Biochemical Engineering, Section for Synthetic Biology, Network Engineering of Eukaryotic Cell factories, Utrecht University, Technical University of Berlin, VTT Technical Research Center of Finland, Leiden University, Concordia University
Number of pages: 16
Publication date: 2018
Peer-reviewed: Yes

Publication information
Journal: Fungal Biology and Biotechnology
Volume: 5
Article number: 16
ISSN (Print): 2054-3085
Original language: English
Keywords: Aspergillus niger, Genome-scale model, Primary metabolism, Secondary metabolism, Biotechnology, TP248.13-248.65
Electronic versions:
s40694_018_0060_7.pdf
DOIs:
10.1186/s40694-018-0060-7

Bibliographical note
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Source: FindIt
Source-ID: 2439623360
Research output: Research - peer-review › Journal article – Annual report year: 2018