View metadata, citation and similar papers at core.ac.uk
brought to you by CORE
provided by Universidade do Minho: RepositoriUM

PS8: 8

Revealing new biotechnological potentialities of the riboflavin producer fungus *Ashbya gossypii* by means of the construction and analysis of its metabolic network

Daniel Gomes, Óscar Dias, Lucília Domingues, Isabel Rocha
IBB - Institute for Biotechnology and Bioengineering, Centre of Biological Engineering, University of Minho

Systems biology has recently arisen as a promising and powerful tool for process development and optimization. The fast-growing number of sequenced genomes may have contributed to this phenomenon since sequenced genome is the starting point from where it is possible to associate by homology a specific function to the genes of a microorganism. From this entire set of functions we can disclose the main metabolic pathways of a specific microorganism. One of the genomes already sequenced is from the fungus *Ashbya gossypii*, an industrially relevant microorganism intensively used for industrial riboflavin production. Despite the high similarity with *Saccharomyces cerevisiae* genome *A. gossypii* presents a lower level of complexity containing only 4726 protein-coding genes distributed over seven chromosomes. The aim of this work is to construct a metabolic model from which we can retrieve valuable information concerning specific metabolic pathways and the optimum conditions for the production of other compounds besides riboflavin.The initial stage of this process, being performed at present, consists in collecting the all set of metabolic-relevant genes through a manual re-annotation of *A. gossypii* genome. Despite being a manual procedure, this step is made using the user-friendly software – MERLIN – that provides an automatic annotation for each gene, which speeds up the entire process. The user should then analyze the function automatically assigned by this application, accepting or suggesting another one. Each metabolic gene is assigned to an Enzyme Commission (EC) number that corresponds to a specific enzyme. For such procedure several databases are used such as UniProt, SGD, AGD, ExPASy and BRENDA. At the end of this phase we should obtain an extended set of EC numbers that represent the reactions possibly occurring on the cell. In a next stage some factors will be considered in order to elaborate a final mathematical model: reaction stoichiometry; distribution of reactions by different cell compartments; biomass formation; energy requirements; other constraints.

The authors thank the financial support of Fundação para a Ciência e aTecnologia (FCT), Portugal: project AshByofactoryPTDC/EBB-EBI/101985/2008.