MPA_23

Reconstruction of a genome-scale metabolic model for *Actinobacillus succinogenes*

Sónia Carneiro[1], Joana Miguel[1], Rafael Carreira[1], Paulo Vilaça[1] and Isabel Rocha[2]

[1]*SilicoLife, Braga, Portugal*

[2]*University of Minho, Braga, Portugal*

Actinobacillus succinogenes, a gram-negative bacterium, is one the most promising natural producers of succinate. This chemical has been well established as a bio-based chemical platform to produce bulk chemicals (e.g. 1,4-butanediol) and other biomaterials, but the costs associated with the bioproduction of succinate are still discouraging. One of the reasons is that succinate is often produced together with other fermentative products like formate, acetate and ethanol under anaerobic conditions, which reduces the cost-effectiveness of this fermentative bioprocess[1]. Systems biology approaches may be required to provide valuable insights into the metabolism underlying the homofermentative production of succinate and contribute to new developments in the bio-based production of succinate[2]. A genome-scale model of the metabolism of *A. succinogenes,* accounting for 500 genes, 930 reactions, and 690 metabolites, was reconstructed and validated against published experimental data. Flux Balance Analysis and Flux Variability Analysis were used to investigate flux distributions within the metabolic network. A thorough model-driven analysis was performed to explore the metabolism under hetero- and homo-fermentative conditions. The model provided valuable insights into the metabolism of this bacterium and has the potential to predict the phenotypes of perturbed metabolic networks that promote the homo-fermentative production of succinate. Acknowledgements: This work was supported by BRIGIT (FP7 project) and PEM co-funded by the ERDF under the Operational Programme for Competitiveness Factors (COMPETE).

References: 1. Mckinlay, J. B., et al. Appl. Environ. Microbiol. 71, (2005). 2. McKinlay, J. B. et al. BMC Genomics 11, 680 (2010).