Talk

Genome-Scale in silico Reconstruction of the Reactive Oxygen Species (ROS) Generating Metabolism in Pseudomonas putida KT2440 and Study of the role of ROS in Different Metabolic Processes

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ABSTRACT

The understanding of the genotype-phenotype relationship is a fundamental biological question widely studied, but still not understood in all its dimension. The existence of emergent systems' properties largely complicates the lineality of this relationship making it mandatory for the study of such properties to fully understand the biological systems. The robustness, understood as the porperty that allows the systems to maintain their functions despite external and internal perturbations, is a system-level phenomenom ubiquitously observed in living systems (Blanchini and Franco 2011). Metabolic networks can be affected by variables that have the power of modulating it as a whole and, most likely, of influencing the referred-to molecular mechanisms. Those variables, one of whihch being endogenous ROS generating metabolism, must be included in metabolic in silico models to study this robustness. We decided to model endogenous ROS generation in Pseudomonas putida KT2440 genome-scale model. P. putida is a model microorganism in biotechnology and possesses an extremely versatile metabolism, which makes it the perfect candidate to study complex metabolic processes (Belda et al. 2016). The objective of this project is to go deep in the understanding of endogenous ROS metabolism and to study the role of ROS in different metabolic processes. To do so, we built and validated the ROS generating genome-scale model and used it as a tool for two purposes: (1) to analyse, in silico, the main metabolic mechanisms to prevent the cell from ROS damage and (2) to generate hypothesis about the role of ROS in different metabolic processes that we approached experimentaly. As a result of this investigation, we have came up with (1) the theory that the main cellular mechanisms to fight back endogenous ROS generation are fuelled by NADH, and not by the activation of NADPH generating metabolic pathways, as we find in scientific literature (Mailloux, Lemire, and Appanna 2011). (2) We have also found that ROS plays an important role in different molecular mechanisms involving robustness, as the carbon flux deviation to the accumulation of polyhydroxyalkanoate; and also influenciate the global metabolic regulator gen crc.

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