Model driven re-programming of the *Pseudomonas putida* metabolic network in response to solvent stress

Pseudomonas putida is a non-pathogenic bacterium that is of great industrial interest due to its metabolic flexibility. In particular, some *P. putida* strains exhibit extreme solvent-tolerance and even survive bi-phase production processes. In this collabrative project between Leiden and Wageningen, we aim to get a deeper understanding in what makes some of these *P. putida* strains so solvent-tolerant. This will be achieved using a combination of computational (Wageningen) and experimental (Leiden) work. The computational part serves to acquire hypotheses on specific genes and clusters of genes that are to be involved in solvent-tolerance mechanisms. This can be achieved using metabolic modeling in combination with comparative genomics and transcriptomics analysis. The candidate genes will be further examined in the experimental part of the work by doing knock-out experiments in *P. putida* solvent tolerant strains.

Techniques used in this project include (amongst others): Bioinformatics to construct an *in silico* metabolic network and analysis of the network, cultivation of *P. putida* and genome editing, molecular biology techniques like knock-out construction, PCR, etc..

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