P58 - Towards an improved version of Kluyveromyces lactis genome-scale metabolic model

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Kluyveromyces lactis (*K. lactis*) is a Crabtree-negative yeast, which as the ability to metabolise lactose. Its complete genome sequence is available since 2004 [1], whereas we have published the genome wide metabolic annotation in 2012 [2] and the iOD907 metabolic model in 2014 [3].

For the initial construction of the iOD907 model, the iMM904 [4] baker's yeast model was used to overcome the lack of specific studies concerning the composition of the *K. lactis* biomass, providing the backbone of the biomass equation. This equation aims at mimicking the drain of building blocks and macromolecules to create more cells. Hence, the relative amounts of these compounds (carbohydrates, amino acids, nucleotides, lipids and cofactors), as well as the amount of ATP consumed for cell growth in the iOD907 model were all inferred from the baker's yeast model.

In this work we propose a new improved version of the *K. lactis* genome-scale metabolic model. These improvements come from the update of the biomass objective function. This reaction will be updated with information from wet-lab experiments in which the relative composition in terms of macromolecules and some building blocks were measured.

Moreover, according to a study of Xavier et al (submitted paper) there is a set of universal cofactors that should be present in all prokaryotes. Here, we also propose to add such cofactors to the biomass equation of *K. lactis*.

The outcome of this project is an improved version of the model, with enhanced predictive ability regarding the wild-type flux distribution, the prediction of essential genes and the activation of latent pathways for the production of the universal cofactors.

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