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Abstract title	TOWARDS A GENOME-SCALE METABOLIC MODEL FOR THE KLUYVEROMYCES LACTIS YEAST
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Background

The interest in *Kluyveromyces lactis* (*K. lactis*) has begun in academia due to its ability to metabolize the beta-glycoside (1). Since then, this yeast has been considered a model organism for studies in genetics and physiology (2). This yeast had its genome sequenced back in 2004 (3) and recently we have published a full metabolic re-annotation of its genome (4). This re-annotation can be used, among other applications, to reconstruct genome-scale metabolic models.

These models allow anticipating a given organism's phenotype from its genome sequence. The reconstruction of biochemical networks is, currently, a valid alternative to microorganisms modelling as the output provided by the *in silico* simulations permits focusing on experiments with promising results.

Thus, we propose a new fully compartmentalised genome-scale metabolic model for *K. lactis*, the *i*OD1759 which comprises 1759 metabolic genes.

Aims

The main goal of this work is the reconstruction of the genome scale metabolic model for the *K. lactis* yeast. Using this model several tasks are performed, namely:

The behaviour of the microorganism is simulated under different environmental conditions, this way decreasing the number of experiments to be performed;

The nutritional needs of the organism is identified and therefore growth media can be rationally defined;

The metabolic capabilities of the organism are evaluated regarding the maximum production yields on products already obtained using this organism but also for novel products identified as interesting target;

Metabolic engineering approaches are evaluated, *in silico*, for improving the production capabilities of the organism.

Methods

The reconstruction of this model is being performed using *merlin 2.0* (5), a software tool we have previously developed for the reconstruction of metabolic models. This application includes tools to identify and annotate enzymes and transport proteins encoding genes, as well as the generation of transport reactions for such carriers. Tools for the compartmentalisation of the model are also provided

The simulations and optimization of the model are performed using OptFlux (6), an open-source and modular software designed to perform *in silico* metabolic engineering tasks.

Results

The uncurated draft model has approximately 1277 reactions (1152 enzymatic reactions and 125 spontaneous or non-enzymatic reactions). However, the number of reactions changes with the curation, as new reactions are added (e.g. biomass reaction, transport reactions) and some reactions are removed such as superfluous transport reactions.

Summary/conclusions

The ongoing reconstruction of the *K. lactis* metabolic model allows performing comparative studies with other published models, namely *S. cerevisiae*, and to simulate *in silico* the behaviour of the microorganism under different environmental and genetic conditions. Therefore, this model represents an important tool in metabolic engineering, envisaging the determination of the metabolic capabilities of this organism regarding potentially interesting chemicals.

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