

Integrating Transcriptomic and Metabolomic Analysis of the Oleaginous Yeast *Rhodospiridium toruloides* IFO088o During Growth under Different Carbon Sources

Background/objective

Rhodospiridium toruloides is an oleaginous yeast capable of producing a variety of biofuels and bioproducts from diverse carbon sources. Despite studies showing its promise as a platform microorganism, little is known about its metabolism and physiology. We investigated the central carbon metabolism in *R. toruloides* IFO088o using transcriptomics and metabolomics during growth on glucose, xylose, acetate, or soybean oil.

Approach

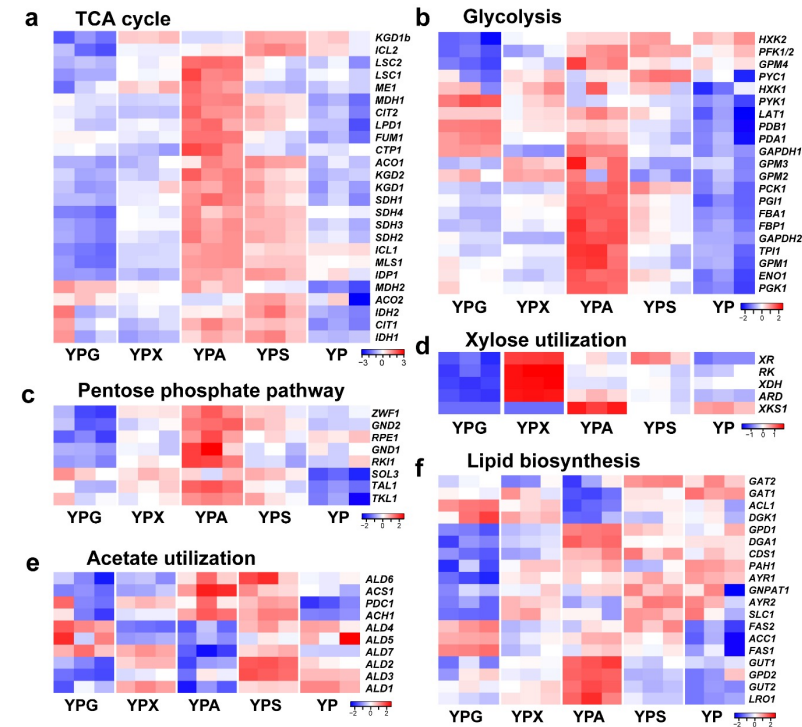
- ❖ Substrates were chosen to represent potential substrates for bioconversion by *R. toruloides*.
- ❖ To understand the metabolism of these substrates, changes in gene expression were measured using RNAseq and changes in intracellular metabolites were measured using GC-MS. These data were mapped onto the central carbon metabolic pathways of *R. toruloides* in order to understand how they are regulated during growth on different carbon sources.

Results

- ❖ Most of the changes in gene expression and metabolite concentrations are consistent with the metabolism of these substrates.
- ❖ Growth on xylose resulted in increased expression of the genes involved in xylose metabolism, with the notable exception of xylulokinase.
- ❖ Reduced expression of xylulokinase induces a bypass leading to arabitol production using xylose.

Significance

These results further our understanding of central carbon metabolism in *R. toruloides*, and the associated data sets might help metabolic engineers further exploit the ability of *R. toruloides* to make diverse fuels and chemicals. They also might aid in the development of genome-scale models.



Transcriptional changes in pathways associated with central metabolic pathways (a-f) in *R. toruloides* IFO088o grown on glucose (YPG), xylose (YPX), acetate (YPA), soybean oil (YPS) and yeast peptone (YP).