

Transcriptome and metabolome analysis of the oleaginous yeast *Rhodosporidium toruloides* uncovered new gene targets for metabolic engineering

Anshu Deewan* (deewan2@illinois.edu), Sujit Sadashiv Jagtap, Jing-Jing Liu, Hanna Walukiewicz, Matthew Plutz, and **Christopher V Rao**

Institute for Genomic Biology, University of Illinois at Urbana-Champaign

<http://www.scs.illinois.edu/rao/index.php>

Project Goal: The goal of this project is to engineer the oleaginous yeast *Rhodosporidium toruloides* for the production of biofuels and bioproducts from plant based sugars and lipids. We are also interested in understanding the mechanism of substrate utilization, metabolite identification, and identification of the key genes governing the lipogenesis process.

Oleaginous yeasts are promising hosts for producing biofuels and bioproducts such as biodiesel, organic acids, polyols, jet fuels, and alcohols from renewable lignocellulosic biomass¹⁻². *Rhodosporidium toruloides* IFO0880 naturally accumulate lipids from multiple simple sugars when some other essential nutrient such as nitrogen is limiting³. Recently, we have engineered *R. toruloides* for increased lipid production during growth on glucose⁴⁻⁵. In addition to lipid-based chemicals, *R. toruloides* also produces a number of sugar alcohols at high titers. For example, during growth on xylose in nitrogen-rich medium, *R. toruloides* produced D-arabitol⁶. D-arabitol is listed by the Department of Energy as one of its top value-added chemicals from biomass.

We have performed transcriptome and metabolome analysis of *R. toruloides* during growth on glucose, xylose, acetic acid, and lipids. The principle component analysis (PCA) of the transcriptome and metabolome data showed a clear separation between different carbon sources in *R. toruloides*. We mapped the gene expression and metabolite concentrations on the metabolic pathways of *R. toruloides*. These results revealed that different metabolite pathways are activated under different carbon sources. The results provide a better understanding of the mechanism of

substrate utilization and the identification of the key genes governing the lipogenesis process. We also identified and functionally characterized a few putative sugar transporters from *R. toruloides* in *Saccharomyces cerevisiae*. The integration of the metabolite data of central carbon metabolism with gene regulation offers us a better understanding of the metabolic response of *R. toruloides* on different substrates. These results could provide the future directions for metabolic engineering of oleaginous yeasts for the production of biofuels and bioproducts.

References

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