Understanding and Harnessing the Exceptional Robustness of *Yarrowia lipolytica* for the Conversion of Biomass Hydrolysate into Designer Bioesters.

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Project Goals: To elucidate and harness the exceptional robustness of novel, undomesticated *Y. lipolytica* isolates from genetic diversity screening as a bioenergy-relevant microbial platform for efficient conversion of undetoxified biomass hydrolysates into designer bioesters with continuous recovery using solvent extraction.

Abstract text. Robustness is an important phenotype for bioenergy microbes to acquire but is difficult to engineer. The oleaginous yeast, Yarrowia lipolytica, is an exceptionally robust microbe that can tolerate stressful environments, assimilate a wide range of substrates^{2,3} and produce high-value chemicals.4 In this study, we aim to understand and harness these robust characteristics of Y. lipolytica for the conversion of biomass hydrolysate into designer bioesters. Specifically, we aim to understand how these Y. lipolytica i) tolerate and effectively assimilate inhibitory biomass hydrolysates for superior lipid accumulation, ii) tolerate organic solvents that are required to produce bioproducts in a two-phase fermentation system and iii) endogenously degrade lipids to produce designer bioesters. From a screen of 57 undomesticated Y. lipolytica isolates, 5,6 we selected top-performing strains exhibiting robust growth and lipid accumulation in undetoxified biomass hydrolysate for comprehensive growth and multi-omics characterization. Comparative proteomic analysis of these robust Yarrowia strains revealed previously uncharacterized proteins that influence robust utilization of biomass hydrolysate sugars and transcription factors regulating lipid accumulation and degradation. We further engineered these strains to improve their robustness for effective conversion of these sugars for lipid production. Next, transcriptomic analysis of an exceptionally solvent-tolerant Yarrowia mutant identified genes conferring high solvent tolerance. These foundational insights provide key mechanisms and genetic targets to engineer robustness in Yarrowia strains for production of biofuels and bioproducts from lignocellulosic biomass.

References

- Walker, C., Ryu, S. & Trinh, C. T. Exceptional solvent tolerance in *Yarrowia lipolytica* is enhanced by sterols. *Metabolic Engineering* **54**, 83-95, doi:https://doi.org/10.1016/j.ymben.2019.03.003 (2019).
- 2 Ryu, S., Hipp, J. & Trinh, C. T. Activating and Elucidating Metabolism of Complex Sugars in *Yarrowia lipolytica*. *Applied and Environmental Microbiology* **82**, 1334-1345, doi:10.1128/aem.03582-15 (2016).
- Ryu, S. & Trinh, C. T. Understanding Functional Roles of Native Pentose-Specific Transporters for Activating Dormant Pentose Metabolism in *Yarrowia lipolytica*. *Applied and Environmental Microbiology* **84**, doi:10.1128/aem.02146-17 (2018).
- 4 Ryu, S., Labbé, N. & Trinh, C. T. Simultaneous saccharification and fermentation of cellulose in ionic liquid for efficient production of α-ketoglutaric acid by Yarrowia lipolytica. *Applied microbiology and biotechnology* **99**, 4237-4244, doi:10.1007/s00253-015-6521-5 (2015).
- Quarterman, J., Slininger, P. J., Kurtzman, C. P., Thompson, S. R. & Dien, B. S. A survey of yeast from the Yarrowia clade for lipid production in dilute acid pretreated lignocellulosic biomass hydrolysate. *Applied microbiology and biotechnology* **101**, 3319-3334, doi:10.1007/s00253-016-8062-y (2017).
- Walker, C. *et al.* Draft Genome Assemblies of Five Robust Yarrowia lipolytica Strains Exhibiting High Lipid Production, Pentose Sugar Utilization, and Sugar Alcohol Secretion from Undetoxified Lignocellulosic Biomass Hydrolysates. *Microbiol Res Announc* **7**, e01040-01018 (2018).

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