## Developing the yeast Kluyveromyces marxianus as a thermotolerant bioproduction host

Ian Wheeldon,1\* (wheeldon@ucr.edu), Xuye Lang1, Mengwan Li1, Pamela Besada-Lombana2, Danielle Bever-Sneary2, Nancy Da Silva2

1University of California, Riverside; and 2University of California, Irvine

## Project Goals: This systems and synthetic biology project seeks to understand and engineer the native stress tolerance phenotypes of the yeast *Kluyveromyces marxianus* with the goal of developing a new synthetic biology chassis for fuel and chemical production.

The non-conventional yeast *Kluyveromyces marxianus* is one of the fastest growing eukaryotes, is thermotolerant to temperatures upward of 50°C, and has the capacity to assimilate a wide range of C5 and C6 sugars. These traits make K. marxianus an attractive host for the industrial production of biochemicals. However, in comparison to the common yeast synthetic biology chassis, S. cerevisiae, there is a clear lack of genome editing tools and standardized genetic parts for biosynthetic pathway construction. In this work, we expand the synthetic biology toolbox by identifying and characterizing a set of 25 different promoters and apply these new genetic parts to engineer the overproduction of a native metabolite, 2-phenylethanol, and a heterologous product, triacetate lactone (TAL). We first developed a one-step markerless multigene integration system that can effectively integrate three unique expression cassettes in a single round of strain engineering. We used this new technique to rapidly create a 27-member strain library that varied the expression of Shikimate pathway genes ARO4, ARO7, and PHA2. This refactoring experiment identified an engineered strain with a five-fold increase in 2phenylethanol production and demonstrated new capabilities in the rapid engineering of K. marxianus. We have also developed a new high-efficiency CRISPR system for our toolbox. Using this system, new pathway knowledge, and computer predictions (using the OptKnock algorithm/K. marxianus genome-scale model), we can rapidly engineer metabolic pathways for increased synthesis of TAL from various carbon sources. Initial gene knockouts or heterologous gene integrations have resulted in up to four-fold increases in TAL production from xylose or glycerol. Taken together, the genetic engineering tools and metabolic engineering presented here demonstrate significant advancement in K. marxianus as a viable host of biochemical production.

This work was supported by DOE DE-SC0019093