

## Comparative fungal genomics for improved biofuel production

Audrey P. Gasch (agasch@wisc.edu)<sup>\*1,2</sup>, Trey Sato<sup>1</sup>, Dana Wohlbach<sup>1,2</sup>, Jeff Lewis<sup>1,2</sup>, Maria Sardi<sup>1,2</sup>, Nikolay Rovinskiy<sup>1,2</sup>, Kevin Myers<sup>1,2</sup>, Jeff Pietrowski<sup>1,2</sup>, Nick Riley<sup>1,3</sup>, Joshua J. Coon<sup>1,3</sup>

<sup>1</sup> Great Lakes Bioenergy Research Center, University of Wisconsin-Madison, Madison WI 53706

<sup>2</sup> Laboratory of Genetics, University of Wisconsin-Madison, Madison WI 53706

<sup>3</sup> Department of Chemistry, University of Wisconsin-Madison, Madison WI 53706

**Project Goals:** Our goal is to engineering *Saccharomyces cerevisiae* for efficient xylose fermentation in the presence of ligno-toxins present in plant hydrolyates. We are using comparative and functional genomics to first understand bottlenecks in xylose fermentation and ligno-toxin survival and then use this information to improve strains for industrial biofuel production.

**Abstract:** Plant cellulosic material represents an important source of biomass for biofuel production. However, native strains of *Sacchaomyces cerevisiae* – the current workhorse of bioethanol production – cannot use pentose sugars that comprise a significant fraction of hemicellulose. Furthermore, toxic byproducts generated during biomass pretreatment induce significant stress responses in yeast, limiting biofuel production. These bottlenecks exacerbate each other, since cells minimally engineered for xylose metabolism display a particular defect in xylose consumption in the presence of ligno-toxins, even when metabolism of glucose continues unabated.

We are using multi-omic analyses to understand these bottlenecks and implicate genes and processes for directed engineering for strain improvement. In this talk, I will summarize several complementary projects that are uncovering targets for directed engineering. A key feature of our approach is comparing and contrasting yeast strains with different capabilities through 1) Genome-wide association studies in hundreds of wild strains, 2) transcriptome analyses of stress-resistant wild strains responding to stresses relevant to biofuel production, and 3) transcriptomics and proteomic analysis of strains serially evolved for anaerobic xylose fermentation. The knowledge garnered through these collaborative projects is significantly expanding our understanding of xylose metabolism and stress tolerance, that will also foster improvement of other strains used in industrial processes.

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