**Naturally occurring yeast strains applicable to bioenergy production have genetic determinants that are functionally linked to stress tolerance**

Most biological catalysts used for biofuel production have come from nature, where there is selective pressure to adapt to changes in the environment. As such, natural populations contain a diversity of genetic traits, some of which may be useful for bioenergy production. GLBRC researchers characterized three natural isolates of *Saccharomyces cerevisiae* shown to have robust growth in ammonia fiber expansion (AFEX™)-treated corn stover hydrolysates (ACSH) or were tolerant to increased temperature or ethanol concentrations, culturing conditions that are relevant to biofuel production and are known to impose physiological stress on microbes. To identify genetic determinants of stress tolerance, the genomes and transcriptomes of the isolates were sequenced and compared to a reference laboratory strain or condition. All three genomes were shown to be highly mosaic, containing genetic signatures from different strain lineages, suggesting that novel combinations of alleles may contribute to stress tolerance. In addition, they all possessed strain-specific gene sets, absent from the lab strain, that were functionally linked to tolerance phenotypes. Gene expression analyses of cultures grown in the absence or presence of stressors indicated physiological processes and enrichment of gene categories implicated in specific stress responses. Many of the responses occurred in pathways regulated by transcription factors that had signatures of positive selection, suggesting that these strains have undergone positive selection for stress tolerance. GLBRC yeast conversion research has centered on the use of these stress-tolerant strains as chassis strains for engineering, highlighting the value of environmental isolates and the potential to enhance biocatalyst performance.

**Reference:** Wohlbach DJ, Rovinskiy N, Lewis JA, Sardi M, Schackwitz WS, Martin JA, Desphande S, Daum CG, Lipzen A, Sato TK, Gasch AP (2014) Comparative genomics of *Saccharomyces cerevisiae* natural isolates for bioenergy production. Genome Biology and Evolution 6(9): 2557-2566.

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