

Making tomorrow's bioenergy yeasts strong

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Cornstalks, wheat straw, and other rough, fibrous, harvest-time leftovers may soon be less expensive to convert into cellulosic ethanol, thanks to U.S. Department of Agriculture (USDA) scientists' studies of a promising new biorefinery yeast.

The yeast-*Saccharomyces cerevisiae* strain NRRL Y-50049-successfully ferments [plant sugars](#) into cellulosic ethanol despite the stressful interference by problematic compounds such as furfural (2-furaldehyde) and HMF (5-hydroxymethyl-2-furaldehyde) in fermenters, according to molecular biologist Zonglin Lewis Liu with USDA's Agricultural Research Service (ARS). Liu works at ARS' National Center for Agricultural Utilization Research in Peoria, Ill.

ARS is USDA's principal intramural scientific research agency. Liu's research supports the USDA priority of developing new sources of bioenergy.

The troublesome compounds, created during dilute acid pre-treatment of the crop leftovers, inhibit [yeast](#) growth and reduce ethanol yields. In particular, they damage yeast cell walls and membranes, disrupt yeast [genetic material](#) such as DNA and RNA, and interfere with yeast enzymes' fermentation abilities.

In research that began in 2003, Liu and coinvestigators have worked with dozens of strains of *S. cerevisiae*, a species already used to make ethanol from plant starch. Using a laboratory approach known as "evolutionary engineering," the scientists speeded up the microbe's natural adaptation

to the hostile environment created by the inhibitors. NRRL Y-50049 was one result of these studies.

The scientists are discovering more about the genes and the multiple networks of genes that are likely responsible for the notable tolerance that this yeast has shown in laboratory tests with a 2-liter fermenter.

Their research suggests that, of the nearly 7,000 genes in the *S. cerevisiae* genome, more than 350 may be involved in counteracting stress. For instance, Liu and colleagues determined that a gene called YAP1 acts as a [master gene](#), orchestrating interactions of many related [genes](#), so that they work together to reduce the impact of furfural and HMF.

More information: Peer-reviewed articles in *Applied Microbiology and Biotechnology*, *Molecular Genetics and Genomics*, and other scientific journals document the studies.

Provided by United States Department of Agriculture

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