

Novel gene increases yeast's appetite for plant sugars

25 July 2011

For thousands of years, bakers and brewers have relied on yeast to convert sugar into alcohol and carbon dioxide. Yet, University of Wisconsin-Madison researchers eager to harness this talent for brewing biofuels have found when it comes to churning through sugars, these budding microbes can be picky eaters.

Published online this week in the [Proceedings of the National Academy of Sciences](#), a Great Lakes Bioenergy Research Center team identified several new genes that improve yeast's ability to use xylose, a five-carbon sugar that can make up nearly half of available plant sugars. If researchers can coax yeast into using most of these sugars, they can improve the efficiency of producing renewable fuels from biomass crops like [corn stover](#) or switchgrass.

"Strains of yeast that are currently used for biofuel production convert xylose to ethanol slowly and inefficiently, and only do so after all the glucose is exhausted," says the study's lead author Dana Wohlbach, a postdoctoral researcher at UW-Madison. "For industrial purposes, the faster a yeast can consume the sugars, the better, since more sugar consumption means more ethanol."

The team partnered with the Department of Energy Joint Genome Institute and sequenced the genomes of two types of fungi that reside in the habitats of [bark beetles](#). Since [woody biomass](#) like bark contains a lot of xylose, these fungi were well adapted at using this type of sugar to both grow and also provide nutrients for the beetles.

Applying the power of [comparative genomics](#) to fungal ecology, scientists were able to rapidly identify genes that have potential for improving biomass conversion.

"By comparing the genome sequences and expression patterns of many yeasts -rather than just looking at one - we were able to identify

elements common to all xylose-fermenting yeasts, and elements absent from non-xylose fermenting yeasts," says Wohlbach.

The team then introduced several genes into *S. cerevisiae*, which cannot normally consume xylose. By introducing one gene in particular, named CtAKR, the researchers significantly increased xylose consumption, an important step for economic biofuel production from plant material.

"This research has provided us with a great genomic toolset," says Wohlbach. "We're excited to explore new ways to increase yeast's ability to consume xylose and improve ethanol production for cellulosic biofuels."

Provided by University of Wisconsin-Madison

APA citation: Novel gene increases yeast's appetite for plant sugars (2011, July 25) retrieved 18 September 2019 from <https://phys.org/news/2011-07-gene-yeast-appetite-sugars.html>

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