

# Wine-making yeast shows promise for bioethanol production

May 13 2010

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Researchers from the Stanford University School of Medicine have identified a gene in the yeast *Saccharomyces cerevisiae* that might be important for ethanol production from plant material, providing insights into the bioethanol alternative to 'fossil fuels'. Combining new high-throughput genome sequencing technology with traditional genetic methods, this study highlights the previously unknown potential of natural *S. cerevisiae* strains to convert five-carbon sugars such as xylose into ethanol. Details are published May 13 in the open-access journal *PLoS Genetics*.

*S. cerevisiae* is the primary organism used in the fermentation process required for industrial bioethanol production. However, despite voraciously fermenting the six-carbon sugars, such as glucose, found in cornstarch or [sugar](#) cane, it was not thought to be able to ferment the five-carbon sugars that are abundant in agricultural wastes or dedicated crops like [switchgrass](#). As the industry moves towards plant-based ethanol, a strain of yeast that can ferment both types of sugar equally well is highly desirable.

Therefore, Jared Wenger and Katja Schwartz sought to identify previously unstudied *Saccharomyces* yeast strains with some ability to ferment xylose. They found a number of strains, primarily used in wine-making, which could metabolize this important sugar in order to grow slowly. They studied one strain in particular, applying a new genome sequencing technology to determine the genetic basis of its growth - the presence of a single gene they named XDH1.

Although the ability of these naturally occurring yeasts to grow on this sugar is modest and they are still not as capable at using xylose as other, genetically-modified strains, this discovery may lead to the development of new, industrially-applicable strains of *S. cerevisiae* for use in large-scale bioethanol production.

**More information:** Wenger JW, Schwartz K, Sherlock G (2010) Bulk Segregant Analysis by High-Throughput Sequencing Reveals a Novel Xylose Utilization Gene from *Saccharomyces cerevisiae*. PLoS Genet 6(5): e1000942. [doi:10.1371/journal.pgen.1000942](https://doi.org/10.1371/journal.pgen.1000942)

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