Super-fermenting fungus genome sequenced

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On the road to making biofuels more economically competitive with fossil fuels, there are significant potholes to negotiate. For cellulosic ethanol production, one major detour has being addressed with the characterization of the genetic blueprint of the fungus Pichia stipitis, by the U.S. Department of Energy Joint Genome Institute and collaborators at the U.S. Forest Service, Forest Products Laboratory.

The research, entailing the identification of numerous genes in P. stipitis responsible for its fermenting and cellulose-bioconverting prowess, and an analysis of these metabolic pathways, is featured in the March 4 advanced online publication of *Nature Biotechnology*.

P. stipitis is the most proficient microbial fermenter in nature of the five-carbon “wood sugar” xylose—abundant in hardwoods and agricultural leftovers, which represent a motherlode of bioenergy fodder.

“Increasing the capacity of P. stipitis to ferment xylose and using this knowledge for improving xylose metabolism in other microbes, such as Saccharomyces cerevisiae, brewer’s yeast, offers a strategy for improved production of cellulosic ethanol,” said Eddy Rubin, DOE JGI Director. “In addition, this strategy could enhance the productivity and sustainability of agriculture and forestry by providing new outlets for agricultural and wood harvest residues.”

Ligonocellulosic biomass, a complex of cellulose, hemicellulose, and lignin, is derived from such plant-based “feedstocks” as agricultural waste, paper and pulp, wood chips, grasses, or trees such as poplar,

recently sequenced by DOE JGI. Under current strategies for generating lignocellulosic ethanol, these forms of biomass require expensive and energy-intensive pretreatment with chemicals and/or heat to loosen up this complex. Enzymes are then employed to break down complex carbohydrate into sugars, such as glucose and xylose, which can then be fermented to produce ethanol. Additional energy is required for the distillation process to achieve a fuel-grade product. Now, the power of genomics is being directed to optimize this age-old process.

“The information embedded in the genome sequence of Pichia has helped us identify several gene targets to improve xylose metabolism,” said Pichia paper lead author Thomas W. Jeffries of the Forest Products Laboratory in Madison, Wisconsin. “We are now engineering these genes to increase ethanol production.” Jeffries said that yeast strains like Pichia have evolved to cope with the oxygen-limited environment rich in partially digested wood that is encountered in the gut of insects, from where the sequenced strain was originally isolated.

FPL has a Cooperative Research and Development Agreement (CRADA) in place with a New York City-based bioenergy company, Xethanol Corporation, which plans to integrate Dr. Jeffries’ findings into its large-scale biofuels production processes.

Source: DOE/Joint Genome Institute

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