

## DOE JGI Director highlights the genomics of plant-based biofuels in the journal Nature

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Genomics is accelerating improvements for converting plant biomass into biofuel—as an alternative to fossil fuel for the nation's transportation needs, reports Eddy Rubin, Director of the U.S. Department of Energy Joint Genome Institute (DOE JGI), in the August 14 edition of the journal *Nature*. In "Genomics of cellulosic biofuels," Rubin lays out a path forward for how emerging genomic technologies will contribute to a substantially different biofuels future as compared to the present corn-based ethanol industry—and in part mitigate the food-versus-fuel debate.

"The Apollo moon shot and the Human Genome Project rallied support for massive R&D efforts that created the capabilities to overcome obstacles that were not contemplated at the outset of these initiatives," says Rubin. "Similarly, today's barriers to improving biofuels are significant, but genetics and genomics can catalyze progress towards delivering, in the not-too-distant future, economically-viable and more socially acceptable biofuels based on lignocellulose."

While Rubin acknowledges that this strategy is in its infancy, rapid progress is being made.

"Over the past 10,000 years, wild plant species were selected for their desirable traits resulting in today's highly productive food crops. We simply don't have thousands of years in the face of the energy and climate challenges, so by applying the power of genomics to these problems, we are seeking to speed up the domestication of energy crops

and the technologies for converting them to suitable biofuels as a more carbon-neutral approach to meeting part of our transportation needs."

In the Nature Review, Rubin describes the processes entailed in biofuel production from lignocellulose: the harvesting of biomass, pretreatment and saccharification, which results in the deconstruction of cell wall polymers into component sugars, and then the conversion of those sugars into biofuels through fermentation. Each step, he says, offers an opportunity for genomics to play a significant role.

"With the data that we are generating from plant genomes we can home in on relevant agronomic traits such as rapid growth, drought resistance, and pest tolerance, as well as those that define the basic building blocks of the plants cell wall—cellulose, hemicellulose and lignin. Biofuels researchers are able to take this information and design strategies to optimize the plants themselves as biofuels feedstocks—altering, for example, branching habit, stem thickness, and cell wall chemistry resulting in plants that are less rigid and more easily broken down."

For microbial biomass breakdown, Rubin says that many candidates have already been identified. These include Clostridia species for their ability to degrade cellulose, and fungi that express genes associated with the decomposition of the most recalcitrant features of the plant cell wall, lignin, the phenolic "glue" that imbues the plant with structural integrity and pest resistance. The white rot fungus *Phanerochaete chrysosporium* produces unique extracellular oxidative enzymes that effectively degrade lignin by gaining access through the protective matrix surrounding the cellulose microfibrils of plant cell walls.

Another fungus, the yeast *Pichia stipitis*, ferments the five-carbon "wood sugar" xylose abundant in hardwoods and agricultural harvest residue. Rubin says that *Pichia*'s recently sequenced genome has revealed insights into the metabolic pathways responsible for this process, guiding efforts

to optimize this capability in commercial production strains. Pathway engineering promises to produce a wider variety of organisms able to ferment the full repertoire of sugars derived from cellulose and hemicellulose and tolerate higher ethanol concentrations to optimize fuel yields.

Rubin also touches on the emerging technology of metagenomics—characterizing, without the need for laboratory culture, the metabolic profile of organisms residing in an environmental sample—for the identification of enzymes suitable for industrial-scale biofuel production.

"Using this prospecting technique, we can survey the vast microbial biodiversity to gain a better picture of the metabolic potential of genes and how they can be enlisted for the enzymatic deconstruction of biomass and subsequent conversion to high energy value fuels."

As an example, Rubin cites an analysis of the hindgut contents of nature's own bioreactor, the termite, (published in *Nature* (450, 560-565 [22 November 2007]), which has yielded more than 500 genes related to the enzymatic deconstruction of cellulose and hemicellulose.

The *Nature* Review goes on to list the feedstock genomes, microbial "biomass degraders," and "fuel producers" completed or in progress. These include the first tree genome completed—that of the poplar *Populus trichocarpa* and other plants in the sequencing queue, such as soybean, switchgrass, sorghum, eucalyptus, cassava, and foxtail millet. In addition, Rubin points to oil-producing algae as an alternative source for biodiesel production—with the alga *Chlamydomonas reinhardtii*, as just one of several algal species that has been characterized for their ability to efficiently capture and convert sunlight into energy.

"Given the daunting magnitude of fossil fuel used for transportation, we

will likely have to draw from several different sources to make an appreciable impact with cellulosic biofuels, all of which will in some significant way will be informed by genomics," says Rubin.

"Toward this end, rapid new sequencing methods and the large-scale genomics previously applied to sequencing the human genome are being exploited by bioenergy researchers to design next-generation biofuels, higher-chain alcohols and alkanes, with higher energy content than petroleum and more adaptable to existing infrastructure."

Source: DOE/Joint Genome Institute

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