

'Genetic road map' of biofuels crop drafted by researchers

February 1 2011

The first rough draft of a "genetic road map" of a biomass crop, prairie cordgrass, is giving scientists an inside look at the genes of one of the crops that may help produce the next generation of biofuels.

The study already has produced the "transcriptome" of the species, said plant geneticist Jose Gonzalez of South Dakota State University. He said the transcriptome can be used somewhat like a map — it records the [genes](#) the plant uses to reach certain goals.

A transcriptome is the small portion of the DNA of an organism that is transcribed into molecules of ribonucleic acid, or RNA. When DNA is transcribed into what is called "messenger RNA," it enables the organism to carry out instructions about building and maintaining cells. Scientists can decode those instructions to determine what particular DNA sequences do.

In an article in the September 2010 issue of *The Plant Genome*, Gonzalez and his colleagues discussed one of the first studies of the prairie cordgrass transcriptome. Prairie cordgrass is being viewed as a species suitable for producing biomass to make biofuels. One of the reasons scientists are interested in prairie cordgrass is because it yields extraordinarily well while tolerating wet conditions, high salinity or poorly aerated soils in low areas unsuitable for growing conventional [crops](#). But it can also survive in open arid prairies.

Gonzalez said one obvious benefit from studying the transcriptome of a

plant such as prairie cordgrass is to enable plant breeders to use marker-assisted selection in order to deliberately include gene sequences that confer desirable traits.

In the study, scientists used four tissues of prairie cordgrass to produce 556,198 expressed sequence tags, or portions of expressed genes. Overlapping DNA segments, totaling more than 26,000, were then assembled.

“We calculated probably 40 percent of the genes in prairie cordgrass, or more than 20,000,” Gonzalez said. “We’re starting to be able to look at the genes involved in particular traits. For example, for biofuels, for cellulosic ethanol production, cell wall composition is very important. We can actually look at the genes that are related to that cell wall composition so that we can study the variations of those genes. It can help the breeders eventually to select populations of prairie cordgrass with better composition.”

Gonzalez said cell walls — primarily made up of cellulose, hemicellulose, and lignin — are largely what remains when prairie cordgrass or some other biomass grass has been harvested and allowed to dry.

Cellulose and hemicellulose are carbohydrates that can be transformed into simple sugars that can be fermented. Lignin can’t be broken down by fermentation, though it can be isolated by other treatments.

The genes involved in the lignin biosynthesis pathway have been very well studied in other grasses, and the genes across the grasses are very similar. That will be one area of ongoing research for Gonzalez and his colleagues.

The synthesis of cellulose or hemicellulose is much more complex and

involves many more enzymes. That is also an area of further research for the group, though those pathways will take longer to unravel, he said.

Scientists are also interested in the morphological development of the plant because that's what supports the yield of the plant through many seasons — how the plant develops underground and starts growing at beginning of the season, how it goes into dormancy in fall, how it reactivates itself next season.

That is why current research efforts to decipher the plant's genetic information are so important, Gonzalez said.

Provided by South Dakota State University

Citation: 'Genetic road map' of biofuels crop drafted by researchers (2011, February 1) retrieved 26 April 2024 from <https://phys.org/news/2011-02-genetic-road-biofuels-crop.html>

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