This research will contribute to fueling the world as the population increases. Fossil fuels will eventually be depleted and switchgrass can serve as a “greener” energy source. This can help keep other crops, such as corn and sugar cane, in the food industry.

Methylome sequencing and DNase-seq: Genome-wide groundwork for switchgrass (*Panicum virgatum*) for use as renewable biofuel source

Who cares and why?

In 2050, it's expected that the demand for energy will double. By the same year, food production is also expected to double. With the increase in food demand, biofuel production is needed to shift from being derived from edible crops to those that are grown specifically for their high biomass conversion ratios [The Lancet, 2007]. If the requirement for food and energy doubles, while production lags behind, this will undoubtedly cause people to go without. The most affected will be the world’s poorest populations [The Lancet, 2007].
The use of biofuels derived from grasses addresses the impending energy crisis, food crisis, and greenhouse gas and climate change issues [Energy.gov]. Switchgrass has become a desirable crop to grow as a renewable source of energy (see Fig. 1). Switchgrass has been shown to have the capacity for long-term high productivity in a variety of environments. There is high genetic diversity among switchgrass genotypes. The lowland ecotype is generally tetraploid and grows better in non-drought environments, while the upland ecotype is composed of tetraploid, hexaploid, and octaploid genomes and are more drought-tolerant [Zhang *et al*., 2011]. Switchgrass thrives in soils of poor quality and is highly efficient in biomass conversion with minimal nutrient input, making it an excellent candidate as a source of renewable biofuel.

What has the project done so far?

The switchgrass genome has recently been made publicly available online. This is a key step for targeting genes of interest to breed switchgrass for use as an efficient biofuel crop. Our lab has conducted chromatin immunoprecipitation sequencing (ChIP-seq) to understand how genes are controlled in the genome by studying protein-DNA interactions. The current study is concerned with methylome sequencing, as methylation patterns are a determinant of gene expression. Methylation of cytosines in the genome acts as an “off switch” for genes. Methylation patterns will be detected using two methods, including methylated DNA immunoprecipitation sequencing (MeDIP-seq) and whole genome bisulfite sequencing. To get a better picture of the global control of gene expression, DNase-sequencing (DNase-seq) will also be used. DNase-seq, a technique where nuclear DNA is subjected to an enzyme, which degrades DNA (called DNase), will allow us to identify regulatory elements in the switchgrass genome. Comparison of identified regulatory elements and methylated genes among different genotypes of switchgrass allows for potential production of more favorable characteristics in crops produced to meet the increasing energy demand.

Impact Statement

Sources of sustainable energy are essential to continue fueling and feeding the world's population.

Switchgrass is a plant native to North America, which grows in a variety of environments and has proven to be an excellent candidate for biofuel production.

Our studies are helping to lay the groundwork for more in-depth studies in regards to genes of interest. This will allow for breeding of more efficient biofuel production using switchgrass.

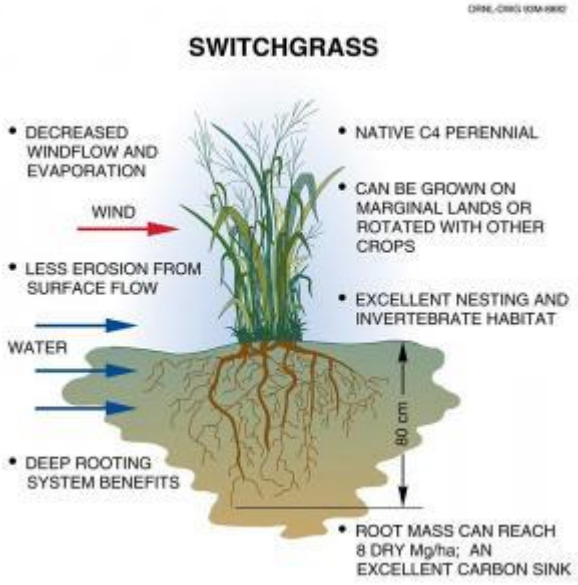

Figure 1.
http://www.iowaswitchgrass.com/benefits~onfarmbenefits.html

What research is needed?

Further research featuring the comparisons of different genotypes in regards to DNA methylation, DNase-sequencing and the other techniques mentioned above are necessary. Transciptome data would be helpful for breeding purposes to compare differentially expressed genes among different genotypes.

Want to know more?

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Strategic Priority: Renewable Energy; biofuels

Additional links

http://www.thelancet.com/journals/lancet/article/PIIS0140-6736(07)61427-5/fulltext
http://naldc.nal.usda.gov/naldc/download.xhtml?id=56377&content=PDF

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