Wednesday, August 1, 2012

total sugar, with most varieties doubling between 90 and 120 days, but the differences between the last two harvests were not significant. We have previously shown that biomass and total sugar are the best predictors of ethanol yield, so these data indicate that 350FS, M81E, and Sugar T can all be harvested at 150 days, 30 days earlier than predicted by plot flowering, and Dale harvested at 120 days after planting.

Specified Source(s) of Funding: Sun Grant, Western Region

(109) Exploration of Simple Sequence Repeat (SSR) Markers from *Miscanthus*

Young-In Choi

Chungnam National University, Daejeon; gjlee@cnu.ac.kr

Young-Ju Jeon Chungnam National University, Daejeon; gjlee@cnu.ac.kr

Do-Soon Kim

Seoul National University, Seoul; dosoonkim@snu.ac.kr

Geung-Joo Lee*

Chungnam National University, Daejeon; gjlee@cnu.ac.kr

The genus Miscanthus has been focused as an alternative bioenergy crop because of its higher productivity potential, non-food crop, marginal land use and stress resistance. However, despite the agronomic and economic significance, the whole genome and molecular markers study of the Miscanthus is primitive. Molecular markers associated with agriculturally important traits can be used for MAS (Marker Assisted Selection) at early stage to accelerate breeding of valuable cultivars. In the previous study, we obtained the ESTs (Expressed sequence tags) from the cDNA libraries using different tissue of leaf and rhizome in the M. sinensis (diploid) and M. sacchariflorus (tetraploid). In this study, we used a SSR search-module program 'SciRoKo' to find SSR markers. The number of SSR motif in the EST library was 1,158 for M. sacchariflorus (leaf: 549, rhizome: 609) and 1,724 for M. sinensis (leaf: 948, rhizome: 776). The most common repeat motifs were tri-nucleotide, while penta-nucleotide was lowest. Among the SSR markers detected, major tri-nucleotide repeats were CCG and AGC. Based on the ORF Predictor to screen the SSR location in the genome, the majority of the SSR motifs were located in the ORF regions than untranslated regions (UTR). Even though the tri-nucleotides were localized in the ORF region highly, di- and tetra-nucleotides were more frequent in UTR regions. We will use those SSR markers to identify enhanced biomass Miscanthus genotype and to map the quantitative trait loci (QTL) of interest.

Specified Source(s) of Funding: This work was supported by grants from the Next-Generation BioGreen 21 Program, RDA and from the IPET, MFAFF of Korea.

(110) Assessment of Glucose and Stem Dry Weight among 16 *Crotalaria juncea* Accessions for Potential Cellulosic Ethanol

Brad Morris* USDA–ARS, Griffin, GA; brad.morris@ars.usda.gov George Anotnious

Kentucky State Univ., Frankfort, KY; george.antonious@kysu.edu

Sunn hemp, Crotalaria juncea L. is a tropical legume grown primarily for fiber, cover cropping, and as a green manure crop with the potential to contribute to sustainability. Sunn hemp stems are potentially high sources of cellulose for the production of cellulosic ethanol. Sixteen sunn hemp accessions were grown in Griffin, GA, during 2008 and examined for stem glucose and stem dry weight. The data were subjected to an analysis of variance and cluster analysis. Significant variation for both glucose and stem dry weight were found among these 16 sunn hemp accessions. We found that the accessions, PI 250487, PI 337080, and PI 219717 were the highest producers of glucose averaging 813 mg/g per accession while PI 468956, PI 234771, and PI 322377 stems weighed the most averaging 234 g per accession. Cluster analysis separated sunn hemp accessions into four groups (clusters) based on very high, high, medium, and low concentrations of glucose. Some of these sunn hemp accessions could be used for the production of cellulosic ethanol as well as parents in a hybridization program for enhancing glucose and stem weight.

(111) Chromosome Doubling and Fertility Restoration in *Miscanthus* × giganteus

Darren H. Touchell*

NC State University, Mills River, NC; darren_touchell@ncsu.edu

Thomas G. Ranney

NC State University, Mills River, NC; tom_ranney@ncsu.edu

Miscanthus \times *giganteus* is a highly infertile allotriploid (2n = 3x= 57) hybrid between a tetraploid *Miscanthus sacchariflorus* (2n = 4x = 76) and a diploid *Miscanthus sinensis* (2n = 2x = 38). This hybrid has considerable potential as a bioenergy crop; however, the lack of fertility has restricted the use of M. × giganteus for crop improvement through conventional breeding approaches. Chromosome doubling can be a viable approach for restoring fertility in interspecific hybrids. In the current study, oryzalinmediate in vitro chromosome doubling was used to develop hexaploid M. ×giganteus cytotypes which were assessed for fertility. Pollen viability staining increased up to 88% in the hexaploid cytotypes compared to 34% for triploid *M*.×*giganteus*. To further test fertility, reciprocal crosses between hexaploid M. ×giganteus and diploid M. sinensis were conducted. A total of 466 seed were obtained from approximately 4,000 individual florets from 8 hexaploid M. × giganteus inflorescences. Many seeds appeared to abort and contained little or no endosperm. Therefore in vitro embryo culture was utilized on MS media supplemented with 20 µM 6-benzylamino purine. Forty-six embryos germinated, however, only nine developed into plantlets that could be transferred to the greenhouse. Using flow cytometry, all recovered plants were determined to be tetraploid representing hybridization events between hexaploid M. ×giganteus and diploid M. sinensis. In contrast, all progeny from diploid *M. sinensis* were diploid, most likely arising from selfing. The restoration of fertility to M. × giganteus may allow this valuable germplasm to be incorporated into future breeding programs for bioenergy crop improvement.