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Project Goals: Long-term goal of this project is to understand the genetic basis of the key biofeedstock traits of biomass yield and composition in order to accelerate development of superior cultivars of switchgrass. The specific objectives are to: i) develop a nested association mapping (NAM) population of 2,000 plants and construct a genetic map for this population; ii) evaluate the population at multiple environments to identify QTLs and molecular markers associated with biomass yield, feedstock quality and other agronomically important traits; iii) validate marker-QTL associations in breeding populations as part of a marker-assisted breeding program. Validated markers co-segregated with key traits for biomass yield and composition will be used to initiate a marker-assisted and/or genomic selection program to develop improved switchgrass cultivar(s).

Switchgrass (Panicum virgatum L.) biomass yield and feedstock quality improvement are priority research areas for bioenergy feedstock development. Understanding the genetic basis of quantitative traits is essential to predictive crop improvement. Nested association mapping (NAM) is a technique especially designed for identifying and dissecting the genetic architecture of complex traits. NAM enables high power and high resolution in QTL detection through joint linkage-association analysis by capturing the best features of bi-parental and association mapping approaches. A switchgrass NAM population was developed by crossing 15 diverse genotypes with specific characteristics, selected from natural variants, to a recurrent parent, AP13, a genotype used for the genome sequencing. Confirmed F1s (n=10) from each cross were then chain-crossed and a final population of 2,000 progenies were developed.

A total of 2,350 genotypes (2000 progeny genotypes from 15 families, 30 ramets of AP13, three copies of grandparents, two copies of F1 parents and Alamo checks) were planted in the field at Knoxville, TN and Ardmore, OK following the Alpha Lattice design. Phenotypic data were collected on biomass yield and related traits. In 2014, Average plant height of different families varied from 64-300 cm. At Knoxville, average yield of grandparents was 0.75 kg plant-1, F1 parents was 0.83 kg plant-1 and AP13 was 0.44 kg plant-1. Average yield of progeny families varied from 0.17 to 0.82 kg plant-1. In 2013, the family average yield ranged from 0.06-0.12 kg plant-1. Wide variability was observed within each family. Several families produced more biomass than their parental genotypes. We just completed harvesting of the population at Ardmore, OK.

Grandparents of the NAM population have been sequenced at the JGI following the NGS technology. After quality filter, on average we received 28-66 Gb sequence data from each parent. Preliminary analysis of the sequence data revealed that 78-98 % of the sequence reads can be mapped to the reference switchgrass genome sequence. A total of 249 million reads from the parent CDV09_05 were mapped to the switchgrass genome. Number of reads assembled to each switchgrass chromosome varied from 10.3 to 20.6 million. Genomic DNA was extracted from the whole population and genotyping with exome capture is in progress at the University of Wisconsin.
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