

**Genomics and Gene Discovery (GGD) Research Unit
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NP307

***Development of Biotechnological Resources for Biofuels
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NP301

***Molecular Basis of Key Cereal Grain Traits
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***Genomics and Bioinformatics of Small Grains
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Development of switchgrass genome resources and unique genetic stocks for improvement of biomass yield and composition.

Breeding progress in switchgrass is slow and efficient breeding techniques taking advantage of genome sequence information are needed. In collaboration with scientists at Tifton GA, we have established a switchgrass linkage mapping population that has been planted at multiple field locations in collaboration with the Forage Breeding Division of the Samuel Roberts Noble Foundation. We will collect morphological and phenotypic data that will help to identify genetic loci affecting traits relevant to biomass production. Many molecular markers developed from existing sequence information are being used to genotype this population and not only associate markers with phenotypes, but also to compare genetic maps of other grasses. New marker development is underway through the organization of a large scale EST-sequencing project with the Department of Energy. This will provide useful data for switchgrass improvement.

Working with polyploid species such as switchgrass complicates identification of beneficial genes and gene combinations that will affect biomass traits. We have identified a single switchgrass line that has been confirmed as diploid. Until the present, diploid switchgrass lines have been unavailable. Availability of such lines is extremely useful in several respects. Whole genome sequencing has become more feasible. Genetic map construction will be simplified, and population structure with regard to origins of polyploidy can now be determined. Breeders will be able to exploit this diploid line using a number of established breeding techniques to manipulate desirable traits.

***Brachypodium distachyon* genome resources.**

A simple model for studying grass cell walls is needed to allow more rapid progress in understanding the potential to alter the properties of cellulosic biomass. We have collaborated with scientists at the University of California, Davis to generate a physical map of the entire genome of the model grass species *Brachypodium distachyon*. Knowledge of the genome sequence of *Brachypodium* and the linear order of genes in the

genome relative to other grasses will help to make this species useful to researchers studying important agricultural traits in energy crops and grain species.

Expanding available genetic resources for *Brachypodium*.

A simple model for studying grass cell walls is needed to allow more rapid progress in understanding the potential to alter the properties of cellulosic biomass. We have collaborated with scientists at Namik Kemal Univ. in Turkey to collect novel accessions of the model grass species *Brachypodium distachyon* from diverse environments and have utilized molecular markers to measure genetic diversity. A mutagenized population has also been created to provide additional genetic resources. These lines can be used to study grass cell wall structure and other traits important for the production of cellulosic biomass.

***Brachypodium* mapping and marker development.**

To identify the underlying genes that are responsible for traits relevant to biomass production in grasses, markers and linkage maps are needed to delimit relevant regions of the genome. We have collaborated with scientists from St. Paul, Minnesota in marker development and linkage map construction through concerted genotyping efforts. Microsatellite markers were developed from existing sequence information and used to score a mapping population. In addition, a project to create 1,000 single nucleotide polymorphism (SNP) markers that will be used to link the genetic and physical maps of *Brachypodium* has been initiated. To date 234 SNP markers have been identified. These markers will help to produce a dense linkage map and enable map-based cloning approaches in this species.