Plant Feedstock Genomics for Bioenergy
Joint Awards

http://GenomicScience.energy.gov/research/DOEUSDA/

U.S. Department of Agriculture

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Integrating the U.S. Department of Energy's (DOE) capabilities in genomic sequencing and analysis for production of biofuels with the U.S. Department of Agriculture's (USDA) long experience in crop improvement, DOE and USDA are working together to fund projects that accelerate plant breeding programs and improve bioenergy feedstocks. Investigators in these projects are characterizing the genes, proteins, and molecular interactions that influence lignocellulosic biomass production.

Significant advances in breeding, molecular genetics, and genomic technologies provide an opportunity to build upon the existing knowledgebase of plant biology to be able to confidently predict and manipulate their biological function for bioenergy resources. Some areas of interest are:

- Elucidation of the regulation of gene networks, proteins, and metabolites to improve plant feed-stock productivity and sustainability, and to advance understanding of carbon partitioning and nutrient cycling.

- Comparative approaches to enhance fundamental knowledge of the structure, function, and organiza-tion of plant genomes, leading to innovative strate-gies for feedstock characterization, breeding, or manipulation.

- Characterization of plant germplasm collections and advanced breeding lines of bioenergy crops to discover and deploy valuable alleles for key bio-energy traits.

- Fundamental research to enhance translation of genomic information for bioenergy crops into culti-var improvement ("phenomics").

Since 2006, dozens of projects have been funded by the DOE-USDA Plant Feedstock Genomics program, which is jointly supported by the Office of Biological and Environmental Research within DOE's Office of Science and the USDA National Institute of Food and Agriculture. This program supports fundamental research in biomass genomics to provide the scientific foundation for the use of lignocellulosic materials, either primary material or agricultural residues, for bioenergy and biofuels.

Switchgrass image courtesy of Lawrence Berkeley National Laboratory.

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More details including Co-PIs and funding amounts are on the web at http://GenomicScience.energy.gov/research/DOEUSDA/

2011 Awards
Ten Projects Selected for Awards Totaling $12.2 Million

Association Mapping of Cell Wall Synthesis Regulatory Genes and Cell Wall Quality in Switchgrass

• Laura E. Bartley, University of Oklahoma, Norman

Goal: Identify natural genetic variation in switchgrass that correlates with lignocellulose-to-biofuel conversion qualities. Most plant dry matter is composed of lignocellulose, and because switchgrass yields high amounts of this material and tolerates drought and other stresses it is an attractive candidate for development into a biofuel crop. This project should enhance understanding of the qualities that critically impact the conversion efficiency of lignocellulose into biofuels.

Functional Interactomics: Determining the Roles Played by Members of the Poplar Biomass Protein-Protein Interactome

• Eric Beers, Virginia Polytechnic and State University, Blacksburg

Goal: Identify key interactions between proteins associated with wood formation in poplar, a woody biomass crop. Wood characteristics result from the coordinated actions of enzymes and structural proteins in the cells, which typically interact with other proteins to perform their roles. This project will uncover the potential of the biomass protein-protein interactome to contribute to the development of poplar trees with superior biomass feedstock potential

Functional Genomics of Sugar Content in Sweet Sorghum Stems

• David M. Braun, University of Missouri, Columbia

Goal: Improve sucrose accumulation in sweet sorghum through investigating the mechanisms regulating carbon allocation to stems. A rapidly growing, widely adaptable crop, sweet sorghum accumulates in the stem high concentrations of sucrose that can be efficiently converted to ethanol, making this a valuable candidate bioenergy feedstock. This research will use a combination of approaches to identify bioenergy-relevant genes and to understand their functions in carbon partitioning in sweet sorghum.

Creation and High-Precision Characterization of Novel *Populus* Biomass Germplasm

• Luca Comai, University of California, Davis

Goal: Provide new genomic tools for poplar breeders to identify germplasm with unique genotypes and increased biomass yields, and develop techniques for creating poplar hybrids with unique combinations of chromosomal regions. Because such properties can confer faster growth, this project addresses a challenge posed by the long generation

time of trees through fast and cost-effective nontransgenic genetic manipulation.

Genomic and Breeding Foundations for Bioenergy Sorghum Hybrids

• Stephen Kresovich, University of South Carolina, Columbia

Goal: Build the germplasm, breeding, genetic, and genomic foundations necessary to optimize cellulosic sorghum as a bioenergy feedstock. This project will facilitate breeding sorghum lines optimized for energy production and selected to maximize energy accumulation per unit time, land area, and/or production input.

An Integrated Approach to Improving Plant Biomass Production

• Jan Leach, Colorado State University, Fort Collins

Goal: Expedite discovery of genes controlling biomass productivity in switchgrass by leveraging results from rice, a well-studied model grass. Switchgrass and other perennial grasses are promising candidates for bioenergy feedstocks; however, the genetic resources necessary to develop these species are currently limited. This work will greatly expand the research tool box for switchgrass and advance its improvement as an energy crop.

Modulation of Phytochrome Signaling Networks for Improved Biomass Accumulation Using a Bioenergy Crop Model

• Todd C. Mockler, Donald Danforth Plant Science Center, St. Louis

Goal: Identify genes involved in light perception and signaling in the model grass *Brachypodium distachyon* to increase yield and improve the composition of bioenergy grasses. Plant growth and development, including biomass accumulation, are affected by the light environment. Finding key genes involved in modulating light perception could be useful in targeted breeding or engineering efforts for improved bioenergy grass crops.

Quantifying Phenotypic and Genetic Diversity of *Miscanthus sinensis* as a Resource for Knowledge-Based Improvement of *M. × giganteus (M. sinensis × M. sacchariflorus)*

- Erik J. Sacks, University of Illinois, Urbana-Champaign

Goal: Facilitate development of *Miscanthus* as a bioenergy crop by acquisition of fundamental information about genetic diversity and environmental adaptation. *Miscanthus* is among the most promising cellulosic biofuel crops, but its improvement as a feedstock will require a broader genetic base. Identification of molecular markers associated with traits of interest will improve *Miscanthus* breeding efforts.

Discovering the Desirable Alleles Contributing to the Lignocellulosic Biomass Traits in *Saccharum* Germplasm Collections for Energy Cane Improvement

- Jianping Wang, University of Florida, Gainesville

Goal: Improve energy cane by identifying the genetic components contributing to biomass production. Energy cane (*Saccharum* complex hybrids) holds great potential as a bioenergy feedstock in the southern United States. This project will produce foundational genetic resources for energy cane breeders to efficiently develop cultivars with increased biomass production and reduced input requirements.

Sorghum Biomass Genomics and Phenomics

- Jianming Yu, Kansas State University, Manhattan

Goal: Integrate key genomics-assisted approaches into biomass sorghum research, and combine with high-throughput and traditional field-based phenotyping methods to enable advanced breeding strategies. By both exploiting genetic diversity and understanding the genotype-phenotype relationship, predictive approaches for efficient and cost-effective breeding can be developed.

2010 Awards
Nine Projects Selected for Awards Totaling $9 Million

Genome-Wide Analysis of miRNA Targets in *Brachypodium* and Biomass Energy Crops

- Pamela J. Green, University of Delaware, Newark

Goal: Identify the targets of MicroRNAs (miRNAs) in different organs and under adverse environmental conditions in the model grass *Brachypodium* and in the energy crops switchgrass, *Miscanthus*, and sorghum. miRNAs are important regulatory molecules that repress selected "target" genes to enable normal development, stress responses, and other processes. This project should enhance understanding of regulatory networks and may suggest new strategies for improving biomass energy crops.

Organ and Tissue-Specific Sucrose Transporters: Important Hubs in Gene and Metabolite Networks Regulating Carbon Use in Wood-Forming Tissues of *Populus*

- Scott A. Harding, University of Georgia, Athens

Goal: Investigate how sucrose transporter proteins (SUTs) function to facilitate the distribution of sucrose for transient storage and biosynthetic use among different pathways in the developing wood matrix. Wood for lignocellulosic feedstocks is synthesized from sucrose that is exported from leaves and then processed in the wood-forming organs. SUTs mediate the export and efficient movement of sucrose from source leaves to sink organs in all plant species.

The Role of Small RNA in Biomass Deposition and Perenniality in *Andropogoneae* Feedstocks

- Matthew E. Hudson, Energy Bioscience Institute, University of Illinois, Urbana-Champaign

Goal: Investigate the role of small RNA molecules in biomass production and their importance in the regulation of cellulose and lignin biosynthesis. The tissues and organs of next-generation biofuel crops that provide biomass for energy production are primarily composed of lignin and cellulose. This research will focus on *Miscanthus* species as well as other biomass crops including switchgrass and prairie cordgrass.

Development of a Low Input and Sustainable Switchgrass Feedstock Production System Utilizing Beneficial Bacterial Endophytes

- Chuansheng Mei, The Institute for Advanced Learning and Research, Danville, VA

Goal: Understand the molecular and physiological mechanisms by which interaction with bacterial endophytes promotes growth in the promising bioenergy crop switchgrass. The use of naturally occurring beneficial bacterial endophytes with switchgrass represents a practical and feasible way to develop a low-input and sustainable feedstock production system.

Functional Analysis of Regulatory Networks Linking Shoot Maturation, Stem Carbon Partitioning, and Nutrient Utilization in Sorghum

- Stephen Moose, University of Illinois, Urbana-Champaign

Goals: Determine if changes in the Glossy15 gene system of sorghum might contribute to current physiological differences among grain, sweet and biomass sorghums, and whether this gene can be used to convert superior sorghum grain hybrids to cultivars enhanced for bioenergy production.

Genomics of Energy Sorghum Biomass Accumulation

- John Mullet, Texas A&M University, College Station

Goal: Identify the genetic and biochemical basis for increasing yield and improving the composition of high-biomass cellulosic energy sorghum. Select genotypes will be analyzed for stem biomass yield, structure, and composition. The resources developed will enable analysis of the genes that modulate these traits and facilitate improvement of energy sorghum and other bioenergy grasses.

Identification and Genetic Characterization of Maize Cell-Wall Variation for Improved Biorefinery Feedstock Characteristics

- Markus Pauly, University of California, Berkeley

Goal: Identify and characterize maize lines with enhanced biorefinery feedstock characteristics, particularly those containing higher yields of fermentable sugars. Stover, the material from the corn plant that remains after removal of the grain, consists primarily of cellulose, hemicellulose, and lignin. Because corn stover is generated by U.S. agriculture in significant amounts, this lignocellulosic residue is desirable to use as a biofuel source.

Systems View of Root Hair Response to Abiotic Stress

- Gary Stacey, University of Missouri, Columbia

Goal: Gain insight into the impacts of variations in temperature and water availability on nutrient uptake by root cells. Root hair cells function to increase root surface area and to mediate water and nutrient uptake. The data obtained in this project should provide a better understanding of the impacts of climate change (heat and water limitation) on plant root physiology.

Insertional Mutagenesis of *Brachypodium distachyon*

- John Vogel, USDA Agricultural Research Service, Albany, CA

Goals: Generate 30,000 additional insertional mutants in the model grass *Brachypodium distachyon* and sequence DNA flanking the insertion sites. Insertional mutants are powerful research tools that allow researchers to rapidly determine the function of specific genes. Mutants from outside collaborators will be integrated into this collection and made available through a public database.

2009 Awards
Seven Projects Selected for Awards Totaling $6.3 Million

Improving Alfalfa as a Biofuel Feedstock

- E. Charles Brummer, University of Georgia, Athens

Goal: Develop in the long term biofuel-ready alfalfa cultivars that have improved yield and quality. Biofuel crops must maximize the production of energy, which requires a high yield of biomass with optimum fuel quality. In this project, molecular markers that are associated with optimal biofuel characteristics will be identified in alfalfa and directly integrated into traditional field-oriented alfalfa breeding programs.

A Systems Biology Approach to Elucidate Regulation of Root Development in *Populus*

- Victor Busov, Michigan Technological University, Houghton

Goal: Identify key regulators of root architecture in relation to nitrogen and water use in the bioenergy crop *Populus* using an integrated systems biology approach. This research will generate resources and innovations that can enable robust biomass productivity under marginal conditions for sustainable lignocellulosic biomass production.
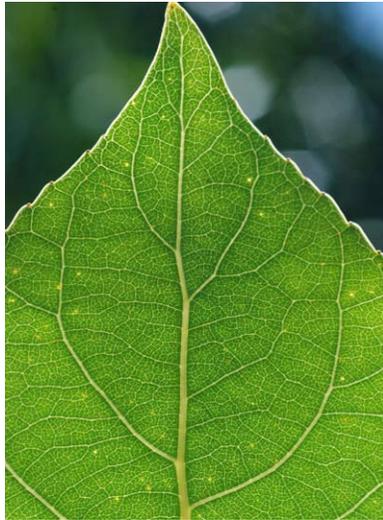
Poplar leaf image courtesy of the DOE Joint Genome Institute.

Characterization of Nitrogen Use Efficiency in Sweet Sorghum

- Ismail Dweikat, University of Nebraska, Lincoln

Goal: Enhance the ability of sweet sorghum to utilize nitrogen, increasing its potential as a leading and cost-effective bioenergy crop. This project will identify novel nitrogen use efficiency alleles in wild sorghum germplasm that can be used to improve sweet sorghum.

Sorghum image courtesy of Lawrence Berkeley National Laboratory.

Mechanism of Carbon Partitioning Regulation by cpg13 in the Bioenergy Woody Crop Poplar

- Matias Kirst, University of Florida, Gainesville

Goal: Characterize genes that regulate the balance of carbon going to cellulosics or lignin, leading to the development of plant materials that are more suitable for biofuel production.

Accelerating the Domestication of *Miscanthus* for Biofuel Production

- Andrew H. Paterson, University of Georgia, Athens

Goal: Provide genomic tools and resources for a promising cellulosic biofuel crop, *Miscanthus*, that will (a) foster innovative strategies for its improvement and (b) develop comparative and bioinformatic approaches to enhance fundamental knowledge of *Miscanthus* genome structure, function, and organization.

The Hunt for Green Every April: Factors Affecting Fitness in Switchgrass

- Gautam Sarath, USDA Agricultural Research Service, Lincoln, NE

Goal: Investigate winter survival in switchgrass populations and individual plants specifically selected for greater yields and with known differences in winter survival. Molecular events occurring in the crowns and rhizomes will be studied over two growing seasons and winters. The project will make a significant and lasting contribution to the future improvement of switchgrass as a bioenergy crop it also will directly benefit researchers working on developing other perennial grasses into biomass energy crops.

Phenomic Analysis of Natural and Induced Variation in *Brachypodium distachyon*

- John Vogel, USDA Agricultural Research Service, Albany, CA

Goal: Conduct high-throughput phenotypic analysis (phenomics) of homozygous T-DNA mutants and natural accessions of the model grass *Brachypodium distachyon* to accelerate the understanding of the basic biology underlying traits that control the utility of grasses as energy crops.

2008 Awards
Ten Projects Selected for Awards Totaling $10.8 Million

Development of Genomic and Genetic Tools for Foxtail Millet, and Use of These Tools in the Improvement of Biomass Production for Bioenergy Crops

- Jeff Bennetzen, University of Georgia, Athens

Goal: Generate a variety of genomic and genetic tools for foxtail millet, including SNPs, BAC libraries, optimized foxtail millet transformation technology, and a high-density QTL and genetic map of foxtail millet for significant biomass traits. These resources will complement the DOE Joint Genome Institute whole-genome sequencing of foxtail millet, enhancing its value as a functional genomic model for second-generation bioenergy crops such as switchgrass.

Identifying Genes Controlling Ferulate Cross-Link Formation in Grass Cell Walls

- Marcia Maria de Oliveira Buanafina, Pennsylvania State University, University Park

Goal: Investigate the regulation of ferulic acid cross-linking in the cell walls of *Brachypodium distachyon* and generate a saturated EMS mutant population for forward genetic studies in this model bioenergy crop.

Computational Resources for Biofuel Feedstock Species

- C. Robin Buell, Michigan State University, East Lansing

Goal: Provide computational tools and resources for data-mining of genome sequence, genome annotation, and large-scale functional genomic datasets available for biofuel feedstock species. Such species include candidates within the *Poaceae*, *Pinaceae*, and *Salicaceae* families, for which a diversity of genome sequence resources currently exist, ranging from whole-genome sequences to modest EST transcriptome datasets.

Translational Genomics for the Improvement of Switchgrass

- Nick Carpita, Purdue University, West Lafayette, IN

Goal: Study the cell walls of grass species, performing bioinformatics analyses on cell-wall biosynthetic genes in maize, and annotate switchgrass orthologs. The project also will generate mutants in selected candidate cell wall–related genes, with direct analysis of saccharification of maize and switchgrass cell-wall mutants.

Identification of Genes That Regulate Phosphate Acquisition and Plant Performance During Arbuscular Mycorrhizal Symbiosis in *Medicago truncatula* and *Brachypodium distachyon*

- Maria Harrison, Boyce Thompson Institute for Plant Research, Ithaca, NY

Goal: Identify genes controlling arbuscular mycorrhizal symbiosis, as well as key factors regulating gene function and the acquisition of key nutrients such as phosphate. The results will provide mechanistic and molecular-level understanding of plant-fungal partnerships in natural ecosystems and their role in maintaining a terrestrial soil environment for sustainable biofuel production.

Systems-Level Engineering of Plant Cell-Wall Biosynthesis to Improve Biofuel Feedstock Quality

- Samuel Hazen, University of Massachusetts, Amherst

Goal: Identify and characterize cell-wall biosynthetic regulatory genomic binding sites using reverse and forward genetic approaches with candidate transcription factors in *Brachypodium* and *Arabidopsis*, two model plant systems. The results will contribute to our understanding of key tissue-specific and developmental regulators of plant cell-wall biosynthesis in monocot and dicot bioenergy crops.

Genomics of Wood Formation and Cellulosic Biomass Traits in Sunflower

Steven Knapp, University of Georgia, Athens

Goal: Develop genomic resources for woody biomass trait identification in hybrid sunflower, a species that is extremely drought tolerant. This fundamental knowledge will complement the existing body of work on this species with respect to oilseed production.

Identification of Genes that Control Biomass Production Using Rice

- Jan Leach, Colorado State University, Fort Collins

Goal: Provide an integrated breeding and genomics platform to identify biomass traits in rice, for translation to second-generation bioenergy grasses such as switchgrass and *Miscanthus*.

Rice image courtesy of the USDA Agricultural Research Service.

A Universal Genome Array and Transcriptome Atlas for *Brachypodium distachyon*

- Todd Mockler, Oregon State University, Corvallis

Goal: Develop an Affymetrix genome tiling array, based on the DOE Joint Genome Institute sequence *of Brachypodium distachyon*, and make the array available for broad community use. The investigators will use the array to generate an expression atlas representing major developmental stages or stress responses in *Brachypodium*, a model species for polyploid, perennial grasses with complex genomes, such as wheat and switchgrass.

Epigenomics of Development in *Populus*

- Steven Strauss, Oregon State University, Corvallis

Goal: Construct a study of the role of chromatin modification (epigenetics) in the regulation of development and dormancy induction in poplar and other woody species. The investigators will characterize changes in DNA methylation patterns on specific tissues during dormancy induction and poplar development.

2007 Awards
Eleven Projects Selected for Awards Totaling $8.3 Million

Towards a Map of the *Populus* Biomass Protein-Protein Interaction Network

- Eric Beers, Virginia Polytechnic and State University, Blacksburg

Goal: Map protein-protein interactions relevant to biomass production by focusing on proteins coexpressed in poplar xylem, site of the majority of lignocellulose synthesis and hence biomass accumulation in poplar.

Strategies for Using Molecular Markers to Simultaneously Improve Corn Grain Yield and Stover Quality for Ethanol Production

- Rex Bernardo, University of Minnesota, Minneapolis-St. Paul

Goal: Optimize the use of DNA markers to simultaneously breed for high corn grain yield (for nonenergy and energy uses) and high stover quality for ethanol production.

Developing Association Mapping in Polyploid Perennial Biofuel Grasses

- Ed Buckler, USDA Agricultural Research Service, Ithaca, NY

Goal: Undertake an association-mapping study of two important biofuel grasses, switchgrass and reed canarygrass, to identify molecular markers tightly linked to biomass-related trait loci. This will enable marker-assisted selection and greatly accelerate breeding programs for enhanced biomass production.

Resource Development in Switchgrass, an Important Bioenergy Crop for the U.S.A.

- Katrien Devos, University of Georgia, Athens

Goal: Construct a detailed genetic map of switchgrass based on simple sequence repeats and align it with maps produced in rice, maize, and sorghum. This will allow the exploitation of resources and sequence information generated for these well-studied cereals. The genetic maps also will serve as a framework for locating genes that control bioenergy traits.

Development of Genomic Tools to Improve Prairie Cordgrass (*Spartina pectinata*), a Highly Productive Bioenergy Feedstock Crop

- Jose Gonzalez, South Dakota State University, Brookings

Goal: Develop PCR markers for this species and construct an initial linkage map for prairie cordgrass, a native perennial high–biomass yielding grass.

Analysis of Small RNAs and mRNAs Associated with Abiotic Stress Responses in *Brachypodium distachyon*

- Pam Green, University of Delaware, Newark

Goal: Identify small RNAs related to stresses such as drought, temperature, and nutrient deprivation and relate them to the emerging genome sequence of *Brachypodium distachyon*, thus enhancing its value as a functional genomic model for energy crops and temperate grasses.

Identification of Cell-Wall Synthesis Regulatory Genes Controlling Biomass Characteristics and Yield in Rice (*Oryza sativa*)

- Zhaohua Peng, Mississippi State University, Mississippi State

Goal: Examine cell-wall synthesis in rice, a model grass bioenergy species and the source of rice stover residues, using reverse genetic and functional genomic and proteomic approaches.

Linkage Analysis Appropriate for Comparative Genome Analysis and Trait Selection in Switchgrass

- Christian Tobias, USDA Agricultural Research Service, Albany, CA

Goal: Create a comprehensive marker set for switchgrass based principally on simple sequence repeats, and initiate development of a linkage map.

A Functional Genomics Approach to Altering Crown Architecture in *Populus*: Maximizing Carbon Capture in Trees Grown in Dense Plantings

- Jerry Tuskan, Oak Ridge National Laboratory, Oak Ridge, TN

Goal: Gain a molecular understanding of phytochrome-mediated responses to competition in *Populus* and then use that knowledge to maximize carbon capture per unit of land area for increased biomass production.

Development of Brown Midrib Sweet Sorghum as a Dual-Source Feedstock for Ethanol Production

- Wilfred Vermerris, University of Florida, Gainesville

Goal: Maximize the amount of fermentable sugar in the whole sorghum plant by identifying and isolating genes that control the high stalk juice sugar trait and a decreased stalk lignin trait, with the aim of eventually combining both traits in a single germplasm.

Insertional Mutagenesis of *Brachypodium distachyon*

- John Vogel, USDA Agricultural Research Service, Albany, CA

Brachypodium distachyon image courtesy of Oregon State University.

Goal: Create a collection of insertional mutants in *Brachypodium distachyon*. This resource collection then can be used to identify mutations in genes predicted to affect biomass quality and agronomic characteristics of other perennial grass energy crops.

2006 Awards
Nine Projects Selected for Awards Totaling $5.7 Million

Using Association Mapping to Identify Markers for Cell Wall Constituents and Biomass Yield in Alfalfa

- Charles Brummer, University of Georgia, Athens

Goal: Use genomics approaches to identify chromosomal regions, and ultimately genes, controlling the two most important bioenergy traits, biomass yield and composition, and develop genetic markers that can be used directly in applied plant breeding programs to improve the bioenergy qualities of alfalfa.

Manipulation of Lignin Biosynthesis to Maximize Ethanol Production from *Populus* Feedstocks

- Clint Chapple, Purdue University, West Lafayette, IN

Goal: Generate transgenic poplar up- or down-regulated for four enzymes known to impact lignin quantity and quality; develop metabolic profiling methods for poplar and their application to greenhouse- and field-grown wild-type and transgenic plants; conduct morphometric analysis of transgenic lines grown in field plots; and analyze cell-wall deconstruction for wild-type and lignin-modified transgenic lines.

Genomic Knowledgebase for Facilitating the Use of Woody Biomass for Fuel Ethanol Production

- Vincent Chiang, North Carolina State University, Raleigh

Goal: Establish a knowledgebase about the possible genes and transcription factor genes involved in lignocellulosic formation and those genes that may enable effective manipulation of lignocellulosic traits to facilitate ethanol production.

Systematic Modification of Monolignol Pathway Gene Expression for Improved Lignocellulose Utilization

- Richard Dixon, The Samuel Roberts Noble Foundation, Ardmore, OK

Goal: Determine which features of the lignocellulosic material (lignin content, lignin composition, or other factors) are most detrimental to the fermentation of biomass to ethanol and develop the crop plant alfalfa (*Medicago sativa*) as a model system for genomic studies on biomass utilization.

Genetic Dissection of the Lignocellulosic Pathway of Wheat to Improve Biomass Quality of Grasses as a Feedstock for Biofuels

- Bikram Gill, Kansas State University, Manhattan

Goal: Investigate the expression of ~80 candidate genes for lignin biosynthesis, their enzymatic activities, and lignin content and composition in different organs at different stages of diploid wheat plant; silence these 80 genes individually by VIGS; identify knockout mutants of these genes using TILLING; and characterize the silenced tissues and knockout mutants by metabolite profiling.

Biochemical Genomics of Wood Formation: O-Acyltransferases for Alteration of Lignocellulosic Property and Enhancement of Carbon Deposition in Poplar

- Chang-Jun Liu, Brookhaven National Laboratory, Upton, NY

Goal: Identify genome-wide acyl-CoA dependent acyltransferase genes from poplar genomics database; systemically explore the tissue-specific and stress-responsible expression patterns of O-acyltransferase genes to identify the enzymes specifically involved in lignocellulosic biosynthesis; and systemically characterize the biochemical functions of acyltransferases responsible for polysaccharide acetylation, lignol biosynthesis, and phenolic compound modification.

Streamlined Method for Biomass Whole-Cell-Wall Structural Profiling

- John Ralph, USDA Agricultural Research Service, Madison, WI

Goal: Provide the plant cell-wall and biomass research communities with improved methods for polysaccharide and lignin structural profiling, based on complete cell-wall solubilization and NMR. The aim is to develop and streamline procedures to allow 20 to 30 samples per day to be profiled.

Sorghum Biomass/Feedstock Genomics Research for Bioenergy

- William Rooney, Texas A&M University, College Station

Goal: Annotate genes, pathways, and regulatory networks identified in the sorghum genome sequence that are important for biomass generation, and identify, map, and clarify the function of trait loci that modulate accumulation and quality of biomass in sorghum.

Development of a Proteoglycan Chip for Plant Glycomics

- Chris Somerville, Carnegie Institute of Washington, Stanford, CA

Goal: Develop high-throughput methods and reagents that will facilitate the assignment of function to large numbers of glycosyltransferases and other glycan-modifying enzymes.