USDA-DOE
Plant Feedstock Genomics for Bioenergy

BERAC
Thursday, June 7, 2012

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Plant Feedstock Genomics for Bioenergy

Joint competitive grants program initiated in 2006

• DOE Office of Science
  Office of Biological and Environmental Research

• USDA National Institute of Food and Agriculture
  (formerly USDA-CSREES)
  Agriculture and Food Research Initiative (AFRI)
  Competitive Grants Program
Goal:

Genomics-based research leading to improved use of biomass and plant feedstocks for the production of fuels such as ethanol or renewable chemical feedstocks:

- Improve biomass characteristics, biomass yield, or sustainability, water and nitrogen use efficiency
- Understand carbon partitioning and nutrient cycling in feedstocks
- Enhance fundamental knowledge of structure, function, and organization of feedstock plant genomes
- Enable plants to be efficiently bred or manipulated for such use

[Logos of U.S. Department of Energy and USDA National Institute of Food and Agriculture]
USDA-DOE Joint Program supports basic research:

• Regulation of:
  • gene networks
  • proteins
  • metabolites

• Comparative genomics

• Systems biology

• Integration of genomics with more traditional approaches
The program scope has evolved:

2006-2007

Regulatory mechanisms: lignocellulose, cell wall
Genetic markers
Genome organization
Model plants

Regulatory mechanisms: feedstock manipulation
-Sustainability, environmental stresses
-Comparative analyses, bioinformatics

Regulatory networks: C partitioning, nutrient cycling

Phenotyping for gene/allele discovery
Phenomics (genotype-to-phenotype)
The program scope has evolved:
Regulatory mechanisms: lignocellulose, cell wall
Genetic markers
Genome organization
Model plants

2008
Regulatory mechanisms: feedstock manipulation
-Sustainability, environmental stresses
-Comparative analyses, bioinformatics

Regulatory networks: C partitioning, nutrient cycling

Phenotyping for gene/allele discovery
Phenomics (genotype-to-phenotype)
The program scope has evolved:

Regulatory mechanisms: lignocellulose, cell wall
Genetic markers
Genome organization
Model plants

Regulatory mechanisms: feedstock manipulation
- Sustainability, environmental stresses
- Comparative analyses, bioinformatics

2009-2010
Regulatory networks: C partitioning, nutrient cycling

Phenotyping for gene/allele discovery
Phenomics (genotype-to-phenotype)
The program scope has evolved:

Regulatory mechanisms: lignocellulose, cell wall
Genetic markers
Genome organization
Model plants

Regulatory mechanisms: feedstock manipulation
-Sustainability, environmental stresses
-Comparative analyses, bioinformatics

Regulatory networks: C partitioning, nutrient cycling

2011-2012
Phenotyping for gene/allele discovery
Phenomics (genotype-to-phenotype)
Project Management

Jointly managed between USDA-NIFA and DOE-BER

Competitive, peer-reviewed

Annual PI meetings, concurrent with DOE-BER Awardee Meeting (DC area, odd years) or Plant and Animal Genome Conference (PAG-San Diego, even years)
**Portfolio of Feedstocks:**

Poplar  
Medicago  
Foxtail millet  
Sorghum  
Switchgrass  
Brachypodium  

Rice  
Miscanthus  
Sunflower  
Prairie Cordgrass  
Maize  
Energy Cane  
Soybean

**Processes and Resources:**

Small RNAs  
Plant-microbe interactions  
Cell wall biosynthetic pathways  
Database development
Projects are located across the US:
Allocations by Crop:

- Populus
- Brachy
- Sorghum
- Switchgrass
- Rice
- Grasses
- Miscanthus
- Medicago
- Maize
- Foxtail millet
- Sunflower
- Soybean
- Energy cane
- Wheat
- Prairie cordgrass
Allocations by Research Area:

- Basic Sciences
- Genomics/ Genetics/ Breeding
- Resource Development
96 pubs and counting!

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Model plant: *Brachypodium*

*Brachypodium distachyon:*
- short life cycle; small genome

**Australian Plant Phenomics Facility (APPF), Adelaide**

Laser confocal microscopy of maize leaf.
Pink: mesophyll cells (high PSII activity);
purple: bundle sheath cells (low activity);
green: lignin

Chlorophyll fluorescence measures photosynthesis:
Arabidopsis (above, wheat (left).  Blue: high rate; red: low.

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*With ‘Phenomics,’ Plant Scientists Hope to Shift Breeding Into Overdrive.*
*Science (2009) 325:380-381*
Identification of an important component of the Sorghum Lignin Biosynthetic Pathway

Objective: Determine role of brown midrib (bmr6) gene on lignin biosynthesis in sorghum.

Approach
• Search for sorghum lignification gene homologs through comparative genomics.
• Putative cinnamyl alcohol dehydrogenase (CAD) gene identified, major component of lignin biosynthetic pathway.
• Cloning and subsequent molecular analysis confirmed identity as bmr6.

Results:
• bmr6 plants display reduced lignin content, relatively little effect on overall plant fitness.
• Identification of a major sorghum lignin biosynthetic gene will greatly facilitate development of new strategies to convert grass feedstocks to biofuels.

Genetic maps of *Miscanthus sinensis* and *M. sacchariflorus* reveal synteny with sorghum.

**Objective:** Generate genetic linkage maps to facilitate *Miscanthus* breeding programs.

**Approach:** EST-SSR-based map constructed using the progenitors of *Miscanthus x giganteus*; comparative genomic analysis with sorghum.

**Result/Impact:** Genome coverage with cDNA-derived SSR loci permitted alignment of *Miscanthus* linkage groups to sorghum chromosomes, and provides basis for well-saturated molecular linkage map to accelerate breeding.
Maize juvenility gene enhances biofuel production in bioenergy crops

Objective: Investigate biomass properties in maize *Corngrass1* (*Cg1*) mutant.

Approach:
- *Cg1* plants maintain juvenility, contain less lignin and more convertible starch.
- Transgenic switchgrass with *Cg1* has significantly higher glucose release without expensive pretreatment.
- Complete inhibition of flowering in *Cg1* plants prohibits transgene escape.

Result/Impact: Transferring *Cg1* gene to bioenergy crops could result in reduced recalcitrance and lowered conversion costs, offering promising new approach for improvement of dedicated bioenergy crops.

Multiple QTL—all with minor effects—for grain yield, lignin, glucose concentration, and glucose release after thermochemical treatment.

Higher selection gains for yield and stover quality when all markers, rather than markers with significant effects only, were used in selection.

Epigenetic modifications and gene expression in *Populus*

**Objective:** Investigate variation in genome-level cytosine methylation in poplar.

**Approach:** Methylated DNA (MeDIP) from seven *P. trichocarpa* tissues sequenced, mapped to reference genome; compared gene expression of methylated and unmethylated genes among tissues.

**Results/Impact:** First description of genome-scale epigenomic differentiation of tree or perennial plant species; foundation to understand heterosis and dioecy, facilitate Poplar improvement.

Database Resources for Bioenergy Feedstocks:

**Soybean KnowledgeBase (SoyKB):**


**Biofuel Feedstock Genomics Resource (BFGR) Genome Browsers:**

- Arabidopsis thaliana
- Brachypodium distachyon
- Oryza sativa
- Populus trichocarpa
- Sorghum bicolor
- Vitis vinifera
- Zea mays

A model plant more closely related to switchgrass than previously sequenced reference genomes. Also sequenced the wild relative green foxtail (*S. viridis*) and compared the two genomes.

Can be used to study switchgrass traits such as cell wall formation, and to learn how grasses can adapt and thrive under various environmental conditions.

2011: Ten Projects Selected for Awards Totaling $12.2M
($10.2M DOE, $2M USDA)
– Switchgrass, Populus, sorghum, Brachypodium, Miscanthus, energy cane

2012: DE-FOA-0000598 issued
November, 2011; proposals due February 24, 2012; currently under review
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http://genomicsscience.energy.gov/research/DOEUSDA/index.shtml