

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**



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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:

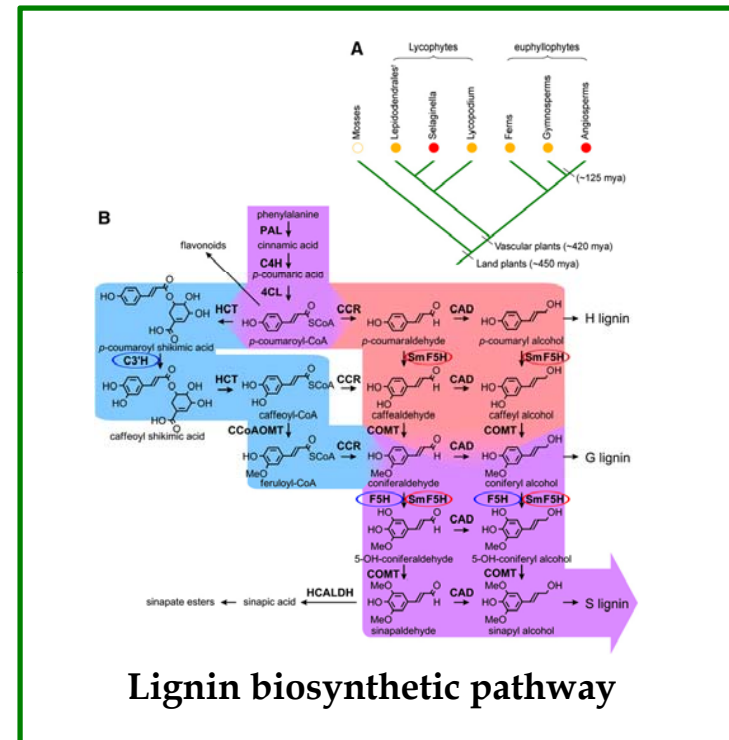
- **Improve biomass characteristics, biomass yield, or sustainability, water and nitrogen use efficiency**
- **Understand carbon partitioning and nutrient cycling in feedstocks**
- **Enhance fundamental knowledge of structure, function, and organization of feedstock plant genomes**
- **Enable plants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



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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)



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Regulatory mechanisms: lignocellulose, cell wall

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Model plants

2008

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-Sustainability, environmental stresses

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The program scope has evolved:

Regulatory mechanisms: lignocellulose, cell wall

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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)



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Regulatory networks: C partitioning, nutrient cycling

2011-2012

Phenotyping for gene/allele discovery

Phenomics (genotype-to-phenotype)



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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)



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Portfolio of Feedstocks:



**Poplar
Medicago
Foxtail millet
Sorghum
Switchgrass
Brachypodium**

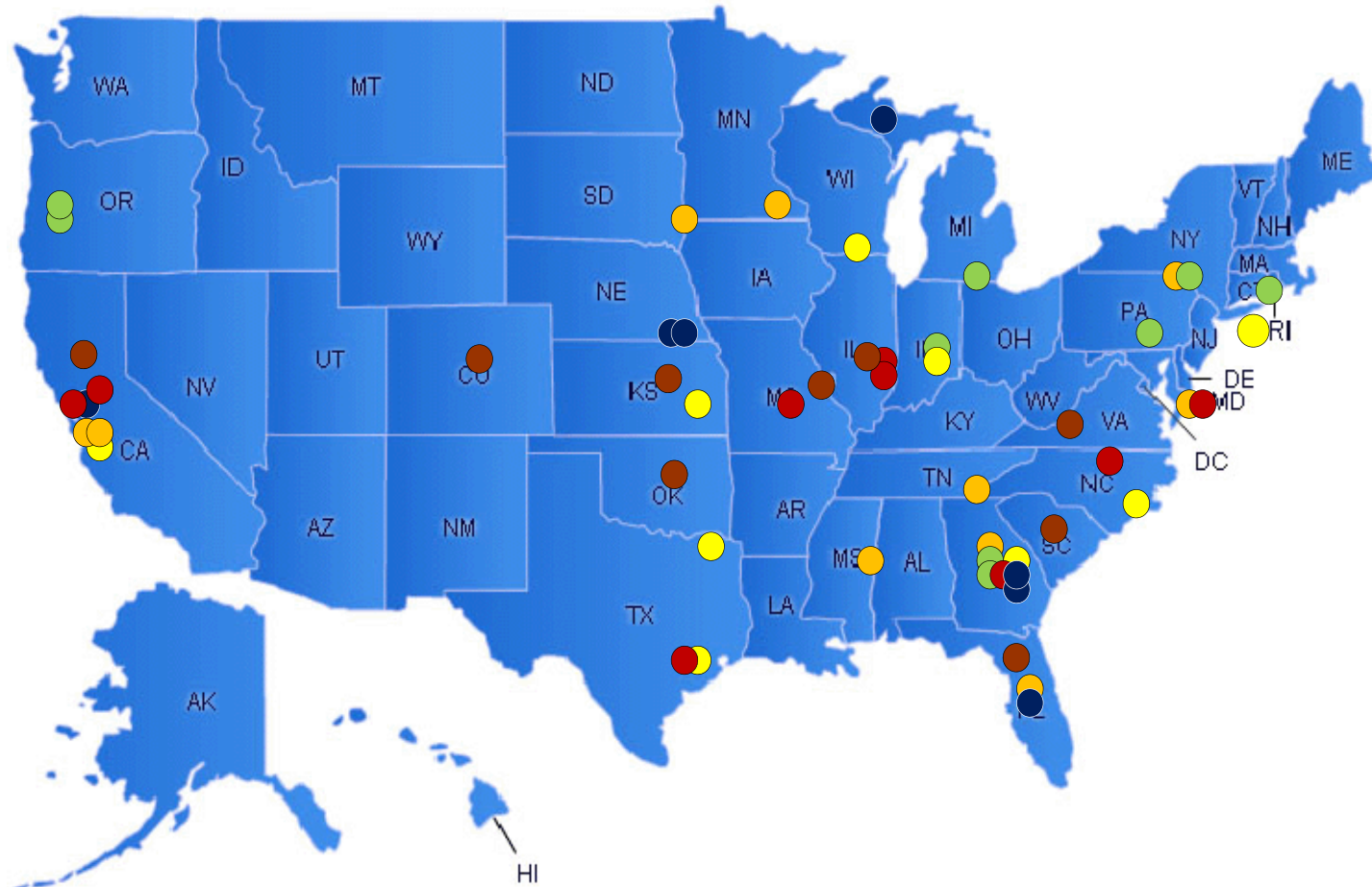
**Rice
Miscanthus
Sunflower
Prairie Cordgrass
Maize
Energy Cane
Soybean**

Processes and Resources:

**Small RNAs
Plant-microbe interactions
Cell wall biosynthetic pathways
Database development**

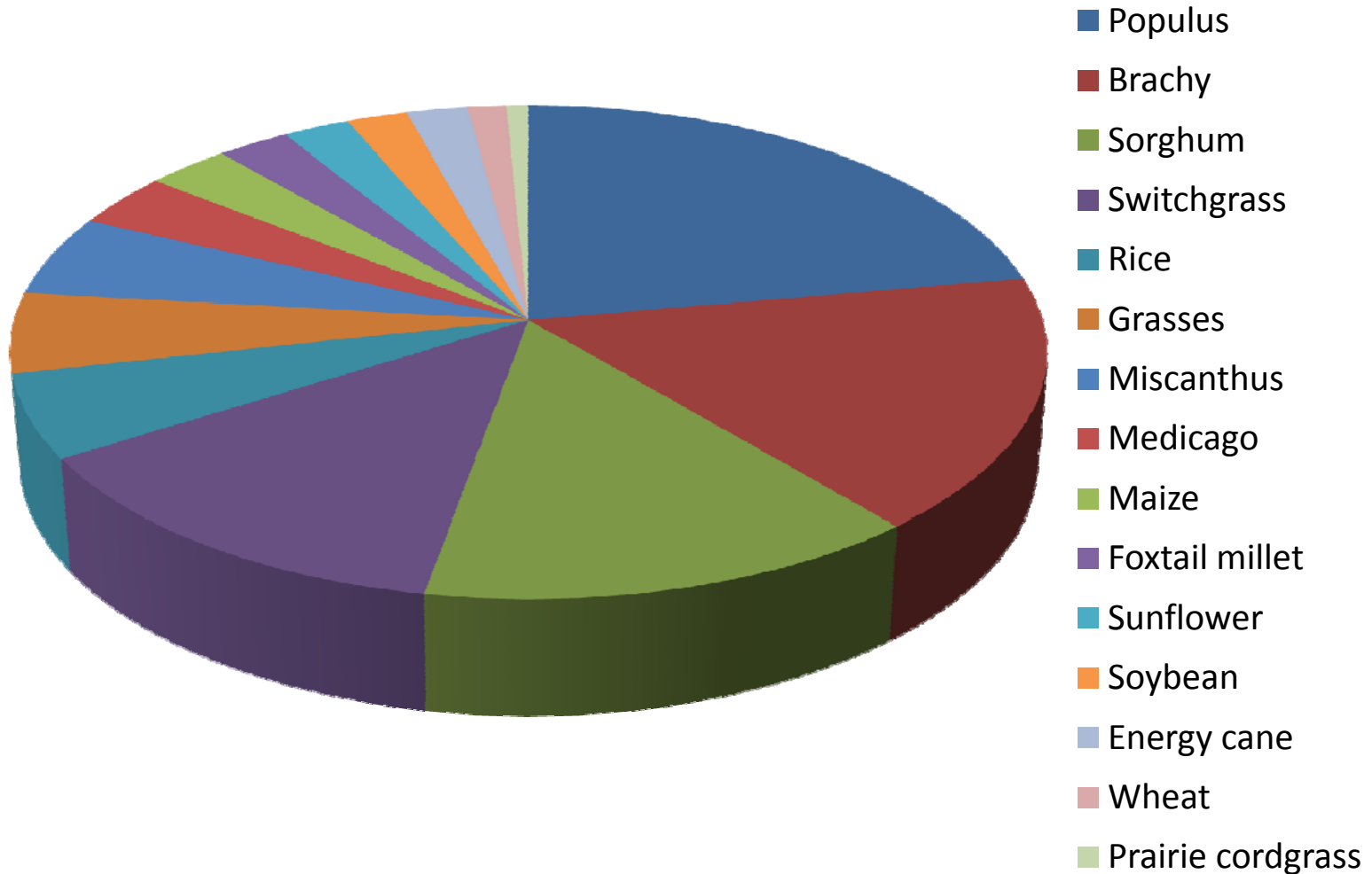


Projects are located across the US:

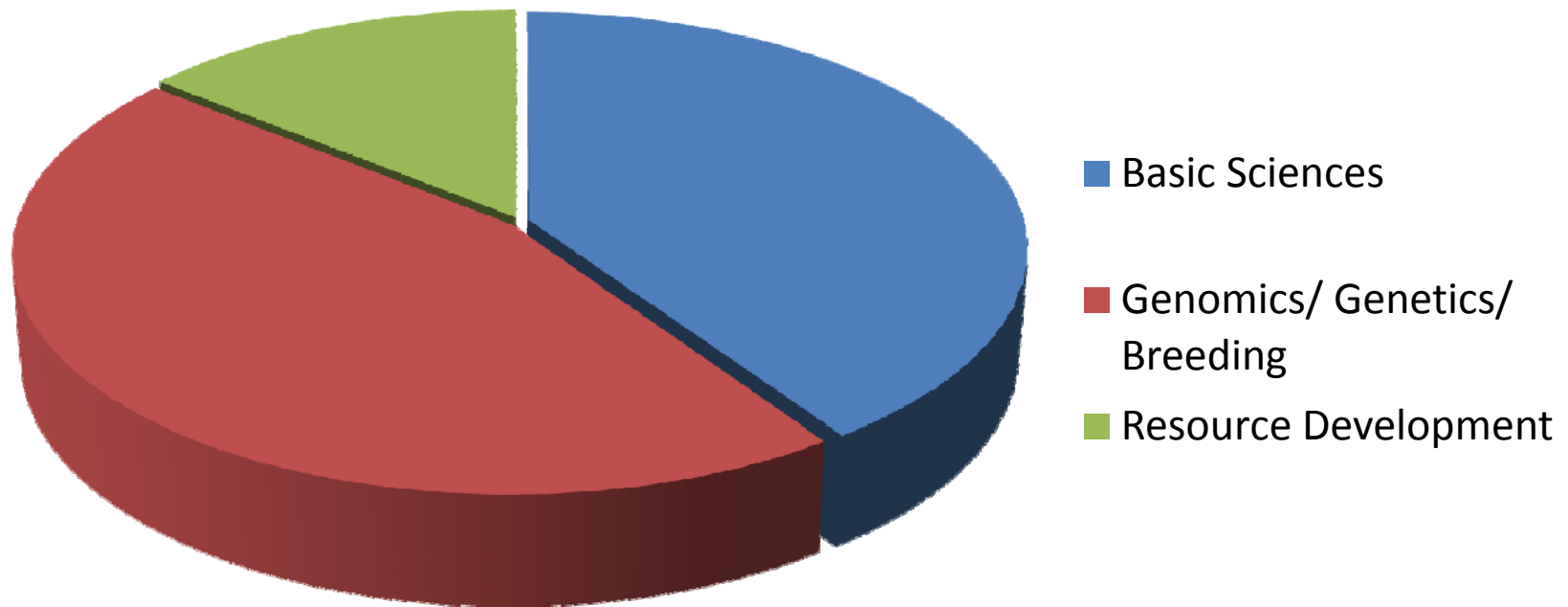


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Allocations by Crop:



Allocations by Research Area:



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96 pubs and counting!

Plant Cell	Planta	Crop Science
Theoretical and Applied Genetics	Current Opinion Plant Biology	Nature Biotechnology
PLoS ONE	BMC Bioinformatics	Science
Nature Genetics	BMC Plant Biology	Nature
Crop Science	Bioenergy Research	Plant Physiology
J Proteome Research	BMC Genomics	PNAS
Plant Genome	Genetics	Plant Cell



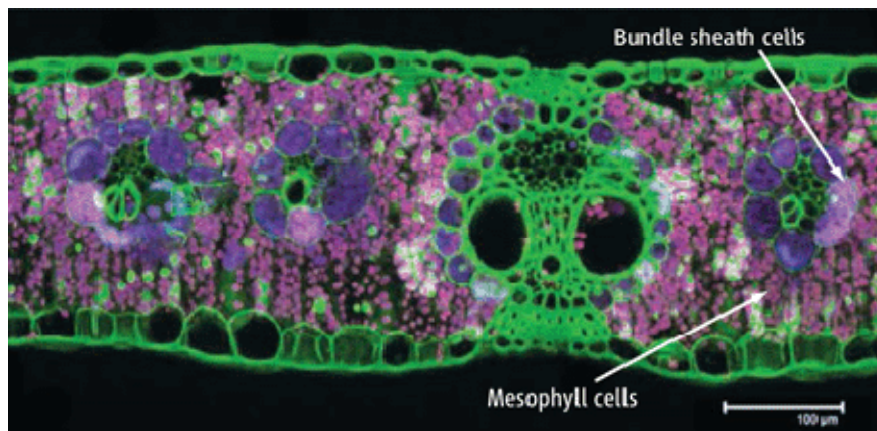
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Model plant: *Brachypodium*

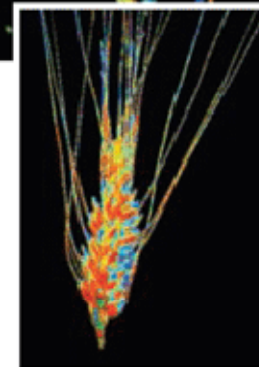
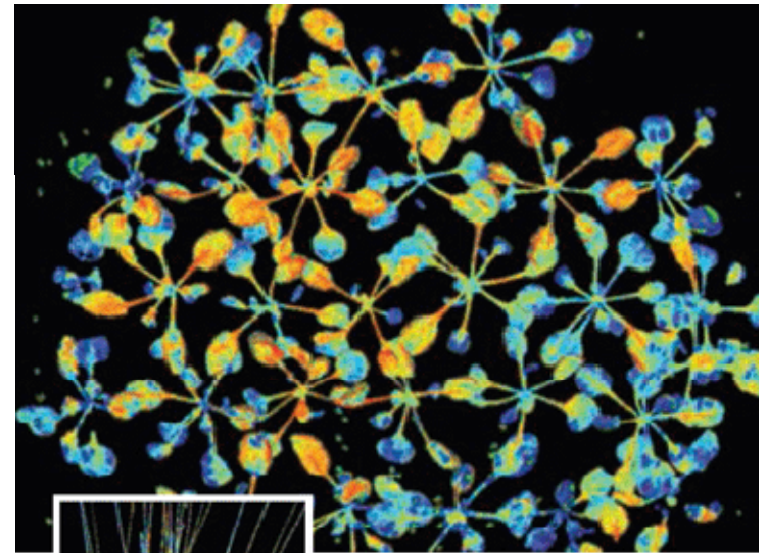
Brachypodium distachyon:

- 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.

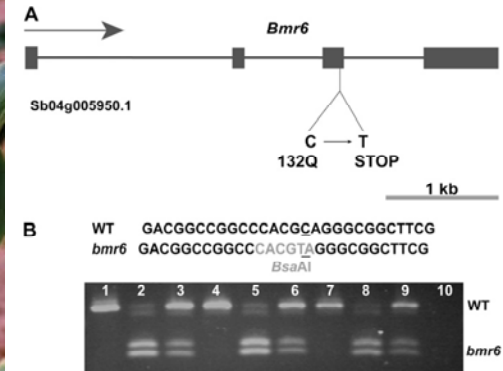
With 'Phenomics,' Plant Scientists Hope to Shift Breeding Into Overdrive.
Science (2009) 325:380-381

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:

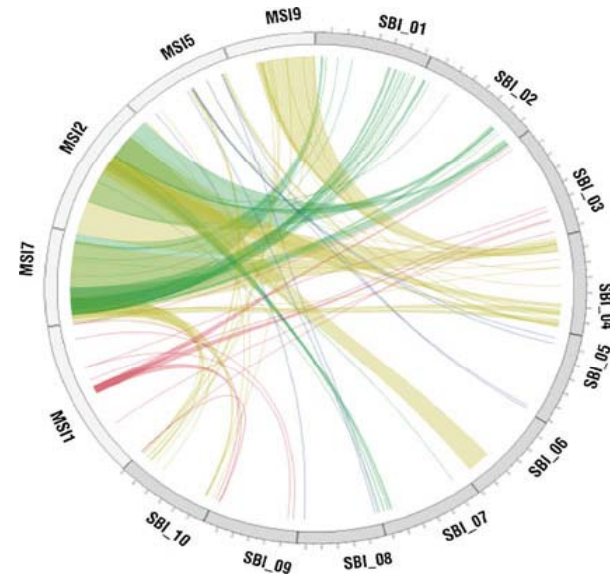
- *bmr6* plants display reduced lignin content, relatively little effect on overall plant fitness.
- Identification of a major sorghum lignin biosynthetic gene will greatly facilitate development of new strategies to convert grass feedstocks to biofuels.

Sattler et al (2009), Plant Physiol 150:584-595; Saballos et al (2009), Genetics 181:783-795

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.

Kim et al. 2012. SSR-based genetic maps of *Miscanthus sinensis* and *M. sacchariflorus*, and their comparison to sorghum. *Theor Appl Genet* doi 10.1007/s00122-012-1790-1.

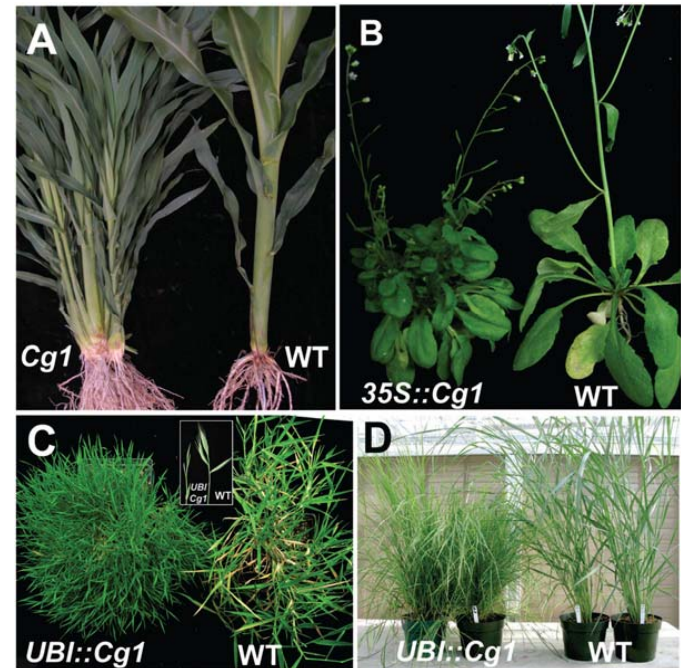
Maize juvenility gene enhances biofuel production in bioenergy crops

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

Approach:

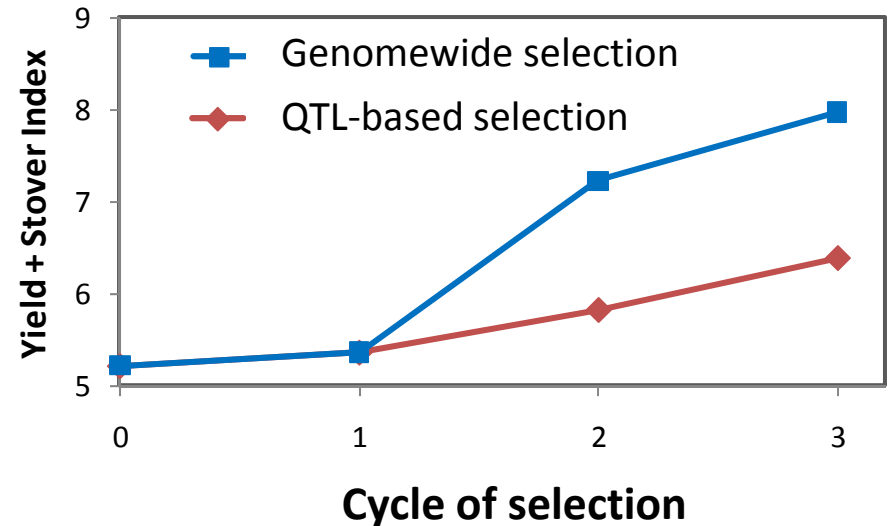
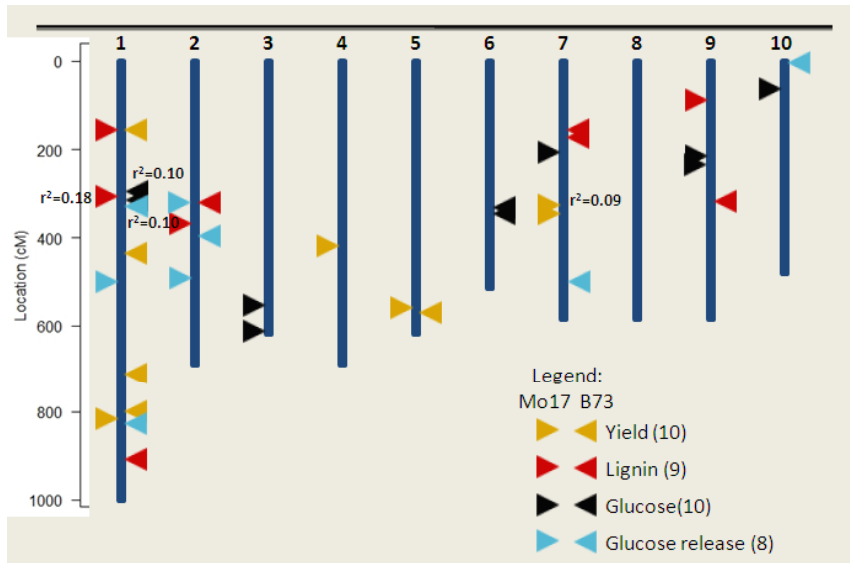
- *Cg1* plants maintain juvenility, contain less lignin and more convertible starch.
- Transgenic switchgrass with *Cg1* has significantly higher glucose release without expensive pretreatment.
- Complete inhibition of flowering in *Cg1* plants prohibits transgene escape.

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.



Chuck et al. 2011. "Overexpression of the maize *Corngrass1* microRNA prevents flowering, improves digestibility, and increases starch content of switchgrass" *Proc Nat Acad Sci* 10.1073/pnas.1113971108.

Breeding Research: Corn for both Food and Fuel



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.

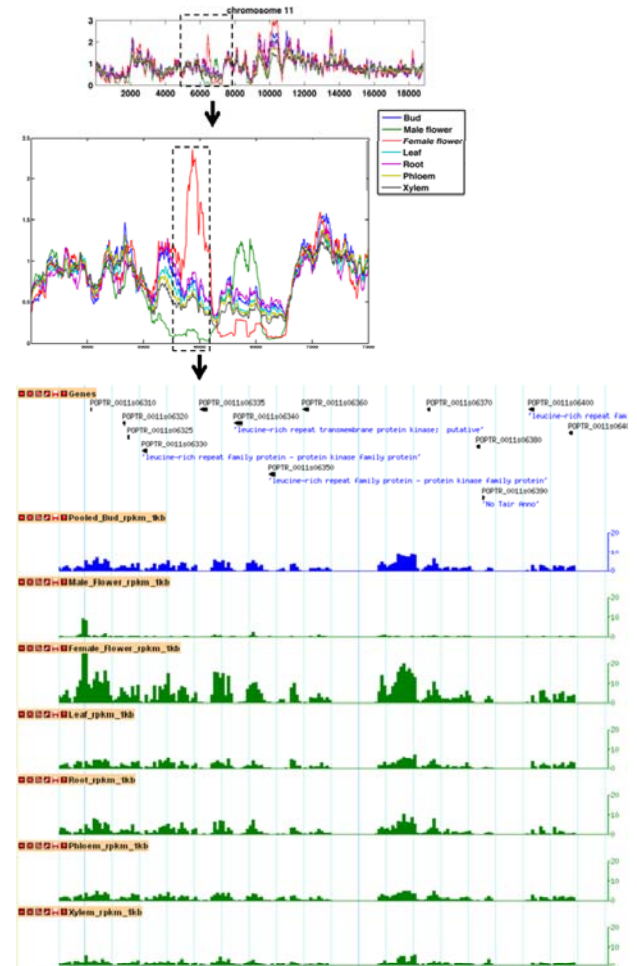
Lorenzana et al. 2010. Quantitative trait loci and trait correlations for maize stover cell wall composition and glucose release for cellulosic ethanol. *Crop Sci.* 50: 541-555.

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.



Vining et al. 2012. Dynamic DNA cytosine methylation in the *Populus trichocarpa* genome: tissue-level variation and relationship to gene expression. *BMC Genomics* 2012, 13:27.

Database Resources for Bioenergy Feedstocks:

Soybean KnowledgeBase (SoyKB):



Joshi et al. Soybean KnowledgeBase (SoyKB): a web resource for soybean translational genomics. *BMC Genomics* 2012, 13(Suppl 1):S15.

Biofuel Feedstock Genomics Resource (BFGR) Genome Browsers:

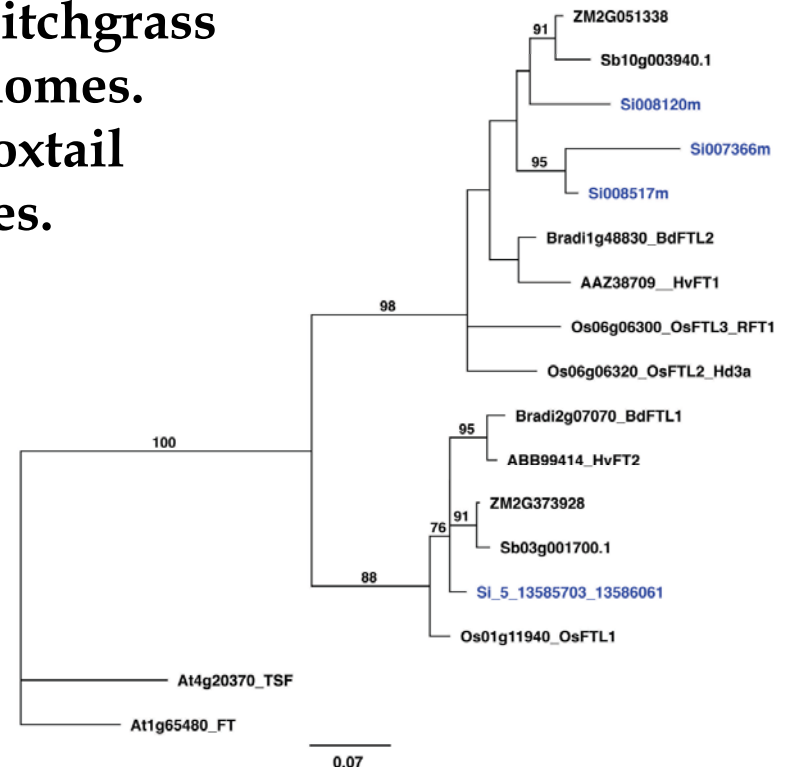
Arabidopsis thaliana
Brachypodium distachyon
Oryza sativa
Populus trichocarpa
Sorghum bicolor
Vitis vinifera
Zea mays

Childs et al. The Biofuel Feedstock Genomics Resource: a web-based portal and database to enable functional genomics of plant biofuel feedstock species. *Database* 2012; doi:10.1093/database/bar061..

Foxtail millet genome sequence: a collaboration with JGI, BESC, JBEI

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.



Bennetzen et al. 2012. Reference genome sequence of the model plant *Setaria*. Nature Biotech May 2012; doi:10.1038/nbt.2196.



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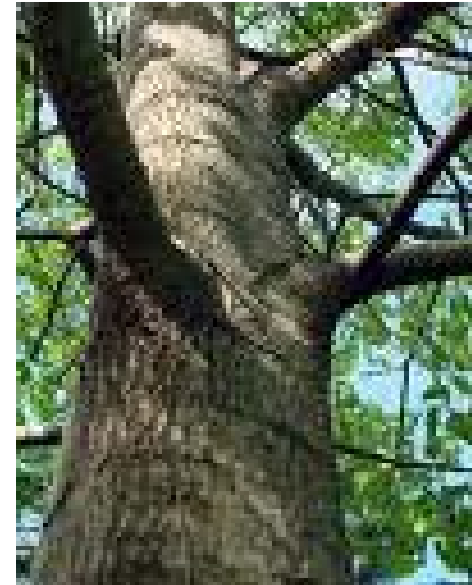


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2011: Ten Projects Selected for Awards Totaling \$12.2M (\$10.2M DOE, \$2M USDA)

– 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://genomicscience.energy.gov/research/DOEUSDA/
index.shtml](http://genomicscience.energy.gov/research/DOEUSDA/index.shtml)



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