

Ag BioEnergy (ABE) Program

Bioenergy at the Western Regional Research Center and Plant Gene Expression Center

Improvement of Agricultural Feedstocks

Employ modern molecular, genomic and biotechnological strategies to enhance the value of energy crops, small grain cereals, and industrial crops such as castor, soybeans, and guayule.

Study processes and control of gene networks in appropriate models such as rice, Brachypodium and maize relevant to bioenergy (plant cell wall) and biobased products

Development of Athletic Biorefineries

Flexible or 'athletic' biorefining is under development whereby the total value of agricultural resources for biofuels and biobased products is captured.

Biomass from multiple sources abundant in area can be converted to ethanol or other fuels within a single processing facility employing both novel enzyme systems and novel separation technologies.



ABE- Feedstocks

Genomics and Gene Discovery Unit (GGD)

- Biotechnological improvement of switchgrass
- Acceleration of switchgrass domestication through the application of genomics
- Developing *Brachypodium distachyon* as a model grass
- Bioinformatics and genome structure of Triticeae

Crop Improvement and Utilization Unit (CIU)

- Proteomics approach to study starch biosynthesis in wheat and response to the environment
- Tools to minimize risk in genetically engineered crops-- novel promoters and recombination tools
- Modification of castor to serve as a safe feedstock for biodiesel in the U.S.
- Improvement of domestic rubber-producing industrial crops through metabolic engineering

Plant Gene Expression Center (PGEC)

- New maize lines with altered levels of lignin via EMS and transposon mutagenesis
- Circadian clock coordination of cell wall genes

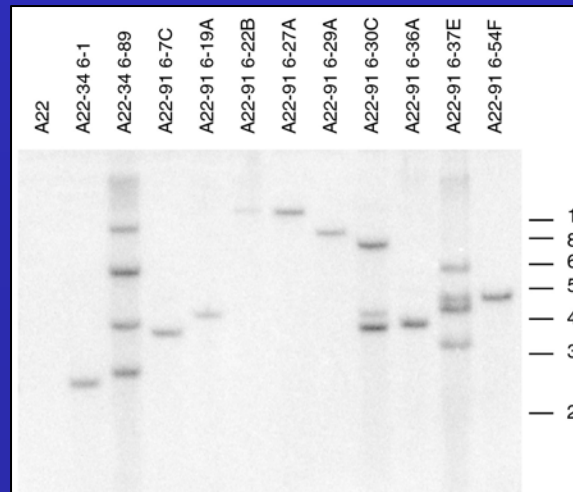
Switchgrass-Biotechnology

- Transformation technology (Alamo and Kanlow genotypes)
- Alter cell wall composition by down-regulating lignin biosynthetic genes
- Edenspace CRADA (Cellulases)
- Ceres CRADA and Grant (Gene containment, Biomass)

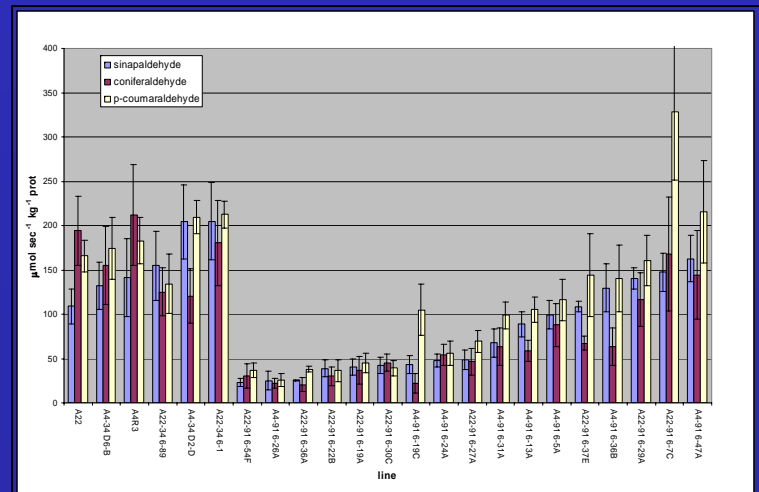
Hyg resistant embryogenic calli



Confirmation of lines by gDNA blot analysis



Analysis of CAD activity in replicated greenhouse trials



ABE-GGD

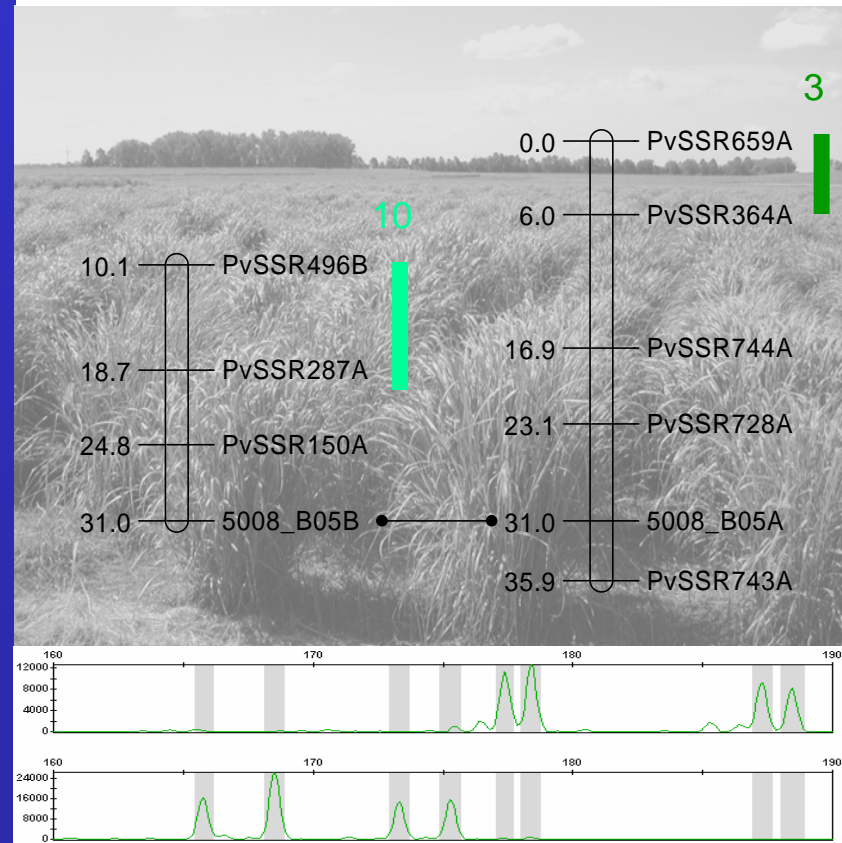
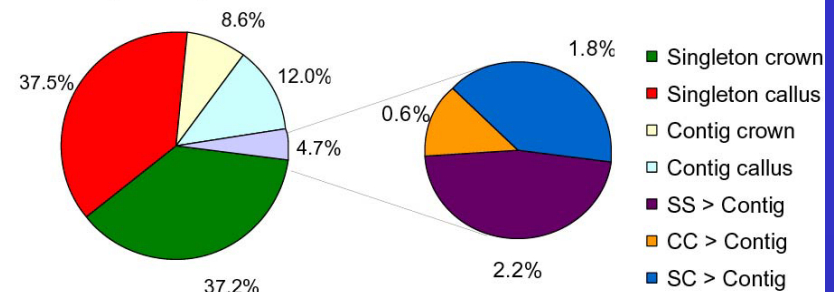
Switchgrass-Development of Resources for Breeding and Improvement

11,990 switchgrass Expressed Sequence Tags (ESTs) already generated

ARS/DOE collaborative project to sequence 500,000 ESTs at JGI has begun (PIs Tobias, Sarath). 250,000 clones paired 5' and 3' reads

- Gene Inventories
- Multiallelic-codominant marker systems
- Linkage/QTL analysis in lowland x lowland F1 population
- Intraspecific relationships
- Genetic Diversity

A. library comparison-crown and callus



ABE-GGD

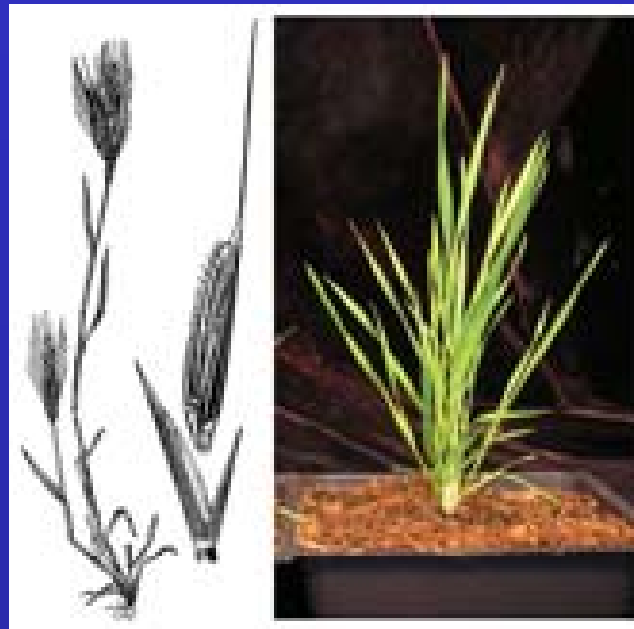
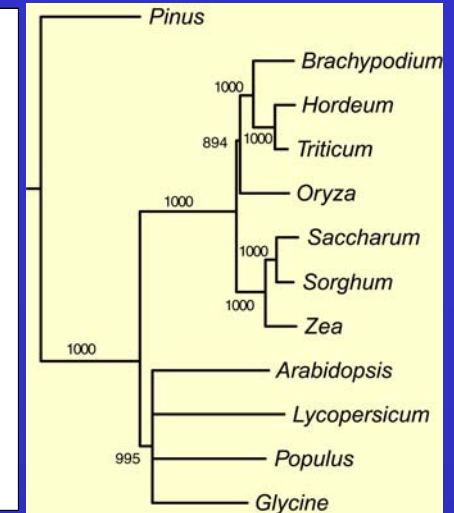
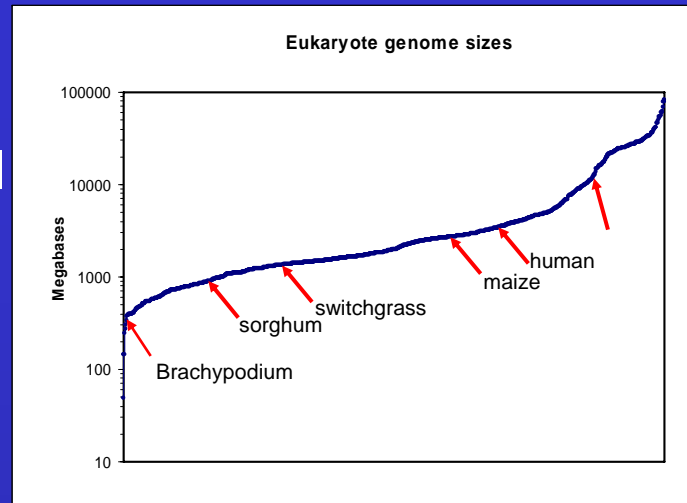
Brachypodium distachyon (Purple False Brome)

Ideal for modern high-throughput molecular genetic approaches (small size, small genome, short generation time, self fertile etc.)

Suited for rapidly testing strategies and study of global processes like cell wall biosynthesis, carbon flux, nutrient uptake, plant architecture

DOE model for energy crops
“Breaking the Biological Barriers to Cellulosic Ethanol”

Brachypodium.org for more information



ABE-GGD

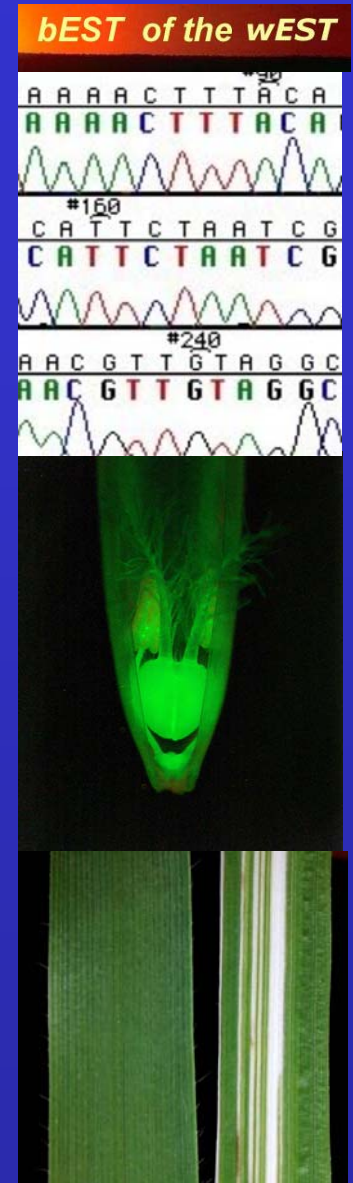
Brachypodium-System Development

Genome Sequencing, Assembly, and Annotation

- One of three PIs guiding genome project at DOE Joint Genome Institute. (J. Vogel, D. Garvin, M. Bevan)
- Submitted 20,440 ESTs to genbank, the first significant genomic resources for *Brachypodium*.
- Constructed three BAC libraries and are currently sequencing >50,000 BAC ends.
- Are creating a physical map by fingerprinting 70,000 BAC clones.
- JGI plans to shotgun sequence to 8X coverage in 2007

Molecular Genetic Resources

- Developed a high efficiency *Agrobacterium*-mediated transformation method.
- Are creating EMS and insertional mutant collections that will be screened for alterations in cell wall composition.
- Marker development and linkage mapping



ABE-GGD

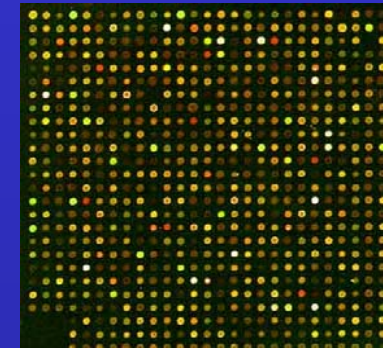
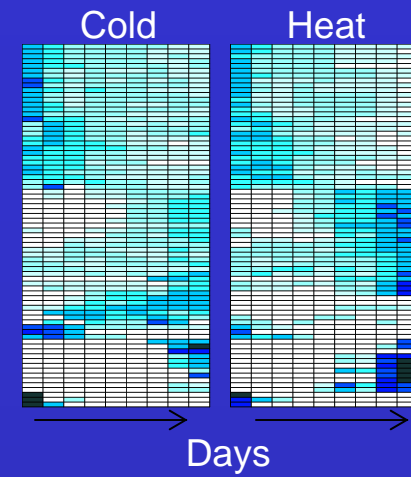
Bioenergy

Proteomics approach to study

- Starch biosynthesis in wheat and response to the environment
- Comparative analysis of seed proteins in wheat and Brachypodium

Tools to minimize risk in genetically engineered crops

- Novel promoters identified through global expression profiling
- Recombination tools for targeting gene insertions and elimination of antibiotic resistance



Bioproducts

- Modification of castor to serve as a safe feedstock for lubricants and biodiesel in U.S.
- Improvement of domestic rubber-producing industrial crops through metabolic engineering of isoprenoid pathway

guayule



bagasse



latex



ABE-Feedstocks

Major Collaborators

- Gautam Sarath, ARS, Lincoln, NE
- David Garvin, ARS, St. Paul, MN
- Michael Bevan, John Innes Centre, Norwich, UK
- Metin Tuna, Trakya University, Turkey
- Paul Twigg, Univ. of Nebraska, Kearney, NE
- DOE Lawrence Berkeley Labs-JGI
- U.C. Davis (BERG, Wheat Genome Sequencing Consortium)
- Jay Keasling, UC Berkeley
- Dave Shintani, Univ Nevada Reno

CRADA partners

- Edenspace Systems Corp.
- Ceres Inc.
- Yulex Inc.
- Dupont Inc.