

Biological Systems Science Division Update

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U.S. DEPARTMENT OF
ENERGY

Office
of Science

Office of Biological
and Environmental Research

Update Outline

- *Completed Programmatic Actions*
- *Summary of FY 2012 Awards*
- *Workshops/Strategic Planning*
- *KBase Status*
- *Division Science Highlights*

Programmatic Activities

FY2012 Reviews of DOE National Laboratory programs – Completed

- ***Foundational Genomics***
 - Los Alamos National Laboratory
 - Oak Ridge National Laboratory
- ***Biofuels Research***
 - Lawrence Livermore National Laboratory
- ***Radiochemistry & Imaging***
 - Jefferson Laboratory

Upcoming Reviews in FY2013

- ***Bioenergy Research Centers (all three)***
- ***Biofuels Research***
 - Pacific Northwest National Laboratory
- ***Radiochemistry & Imaging***
 - Lawrence Berkeley National Laboratory
 - Oak Ridge National Laboratory

Summary of FY 2012 Awards

Genomic Science: Biosystems Design to Enable Next-Generation Biofuels (DE-FOA-0000640)

Systems biology research applications focused on the design of new biological systems for bioenergy production.

Eight awards made in FY12

Microbial systems design for biofuels

- ❖ Metabolic modeling and engineering an oleaginous yeast
- ❖ Next level of genome engineering in *E. coli*
- ❖ Genome-scale metabolic modeling and engineering in diatoms
- ❖ Engineer macroalgae-associated microbes



Plant systems design for bioenergy

- ❖ Modeling and engineering the shikimate and phenylpropanoid/phenylalanine pathways in *Arabidopsis*
- ❖ Engineering drought and planting density tolerance in the C4 model grass *Setaria viridis*
- ❖ Engineering CAM photosynthesis in poplar and *Arabidopsis*
- ❖ Engineering double haploid switchgrass and *Brachypodium sylvaticum* for improved drought tolerance and nutrient use efficiency.



Summary of FY 2012 Awards Cont'd

Plant Feedstocks Genomics for Bioenergy (DE-FOA-0000598)



Nine Total Awards in FY12

- ❖ Functional understanding of genes affecting biomass yield and quality in poplar
- ❖ Abiotic stress gene networks between lowland and upland ecotypes of switchgrass
- ❖ Poplar interactome
- ❖ Genetics of Panicum grasses: developing a model system with diploid *Panicum hallii*
- ❖ **Genomics of bioenergy grass architecture [sorghum]**
- ❖ Understanding natural allelic variation in Switchgrass
- ❖ **Genetic architecture of sorghum biomass yield component traits identified**
- ❖ Genomic analysis of high-yielding triploid hybrids of willow (*Salix* spp.)
- ❖ Tubulin manipulation on *Populus* wood formation and drought tolerance



United States Department of Agriculture
National Institute of Food and Agriculture



Summary of FY 2012 Awards Cont'd

Integrated Nuclear Medicine Research and Training Projects of Excellence (DE-FOA-0000646)

Five University Applications Awarded Funding

DOE/SC (OBER)

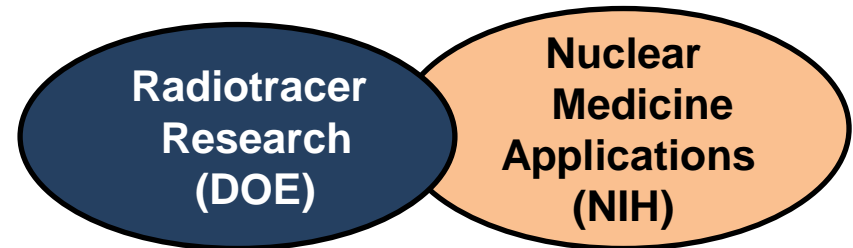
Investigator/Organization

- Sam Gambhir – Stanford
- Julie Sutcliffe – UC- Davis
- Jacob Hooker - Harvard
- Susan Lapi – Wash U.

DOE/SC (OBER) - NIH (NIBIB)

Investigator/Organization

- Carolyn Anderson – U. Pittsburg



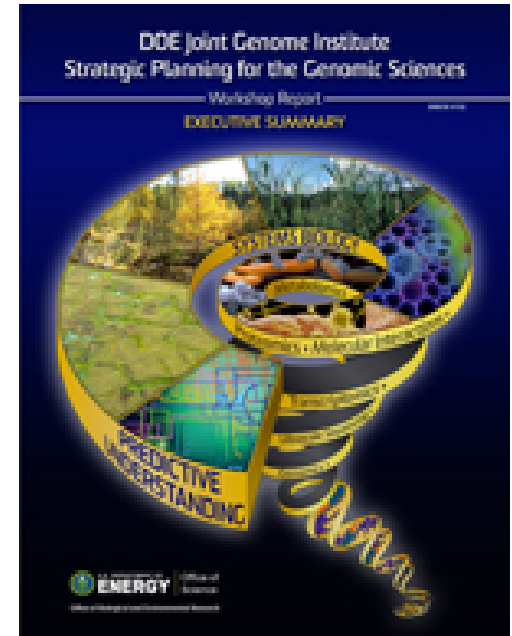
NIBIB National Institute of Biomedical Imaging and Bioengineering
National Institutes of Health
Leading the Development and Accelerating the Application of Biomedical Technologies to Improve Health

Workshops/Strategic Planning

DOE Joint Genome Institute Strategic Planning Workshop (May 30–31, 2012)

Major Themes and Needs:

- Continue to Sequence (New Genomes, Resequencing, Transcriptomes...)
- New Capabilities for High Throughput Functional Annotation of DNA
- Extended and Improved bioinformatics capabilities
- DNA Synthesis to Efficiently Build Genes, Pathways and Genomes
- Improved Automation of Biological Experiments to Match Sequencing Output
- Organize Communities Around Big Coordinated Projects



<http://genomicscience.energy.gov/userfacilities/jgi/futuredirections/index.shtml>

Workshops/Strategic Planning Cont'd



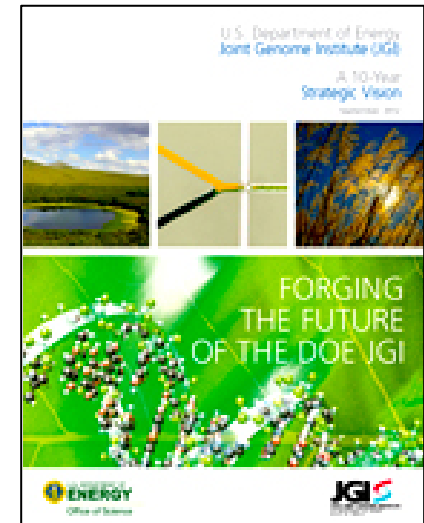
Completion of the JGI Strategic Plan

- ❖ A path to transform the JGI into a next generation genome science center
- ❖ An emphasis on providing high throughput functional information and analysis techniques to complement genomic data.
- ❖ Incorporate new capabilities and/or partners to enhance genotype to phenotype interpretations.

New Call from JGI

Emerging Technologies Opportunities Program

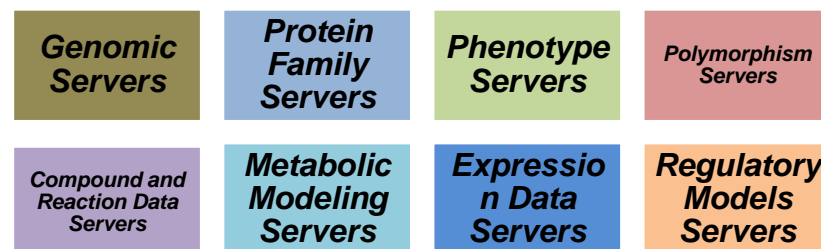
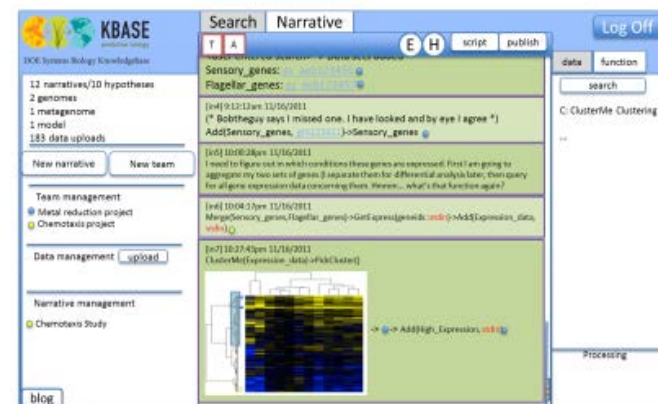
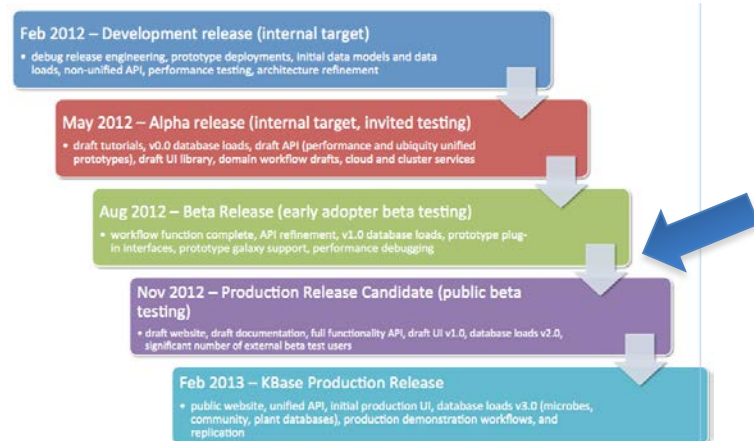
- ❖ Posted 10/4/12
- ❖ <http://www.jgi.doe.gov/programs/ETOP/index.html>
- **New Capabilities for High Throughput Functional Annotation of DNA**



<http://www.jgi.doe.gov/whoweare/10-Year-JGI-Strategic-Vision.pdf>

DOE Systems Biology Knowledgebase

- The **KBase Central Data Model (CDM)** focuses on genomes and includes annotation, expression, chemistry, and models and includes:
 - 7,830 genomes
 - 23,058,670 features
 - 12,620 regulons
 - 266,345 protein families
 - 16,196 compounds
 - 13,428 reactions
- Stood up **KBase network and User Interface** for cross cutting Science:
 - Interactive web scripting enable, for example, direct annotation and immediate inference of metabolic model from user's microbial genome sequence in a few easy steps.
 - New tutorials allow developers to begin to script using KBase functions and work with KBase infrastructure.
- **New partnerships** with JGI to enable metagenome assemble, analysis of sequencing-based gene function analysis and metabolic model reconciliation, and collaborative outreach and training.
- **Collaborative development** of joint Milestones with BRCs to meet their mission goals with planned KBase functionality.



Poplar Resequencing Suggests Enhanced Improvement Strategies



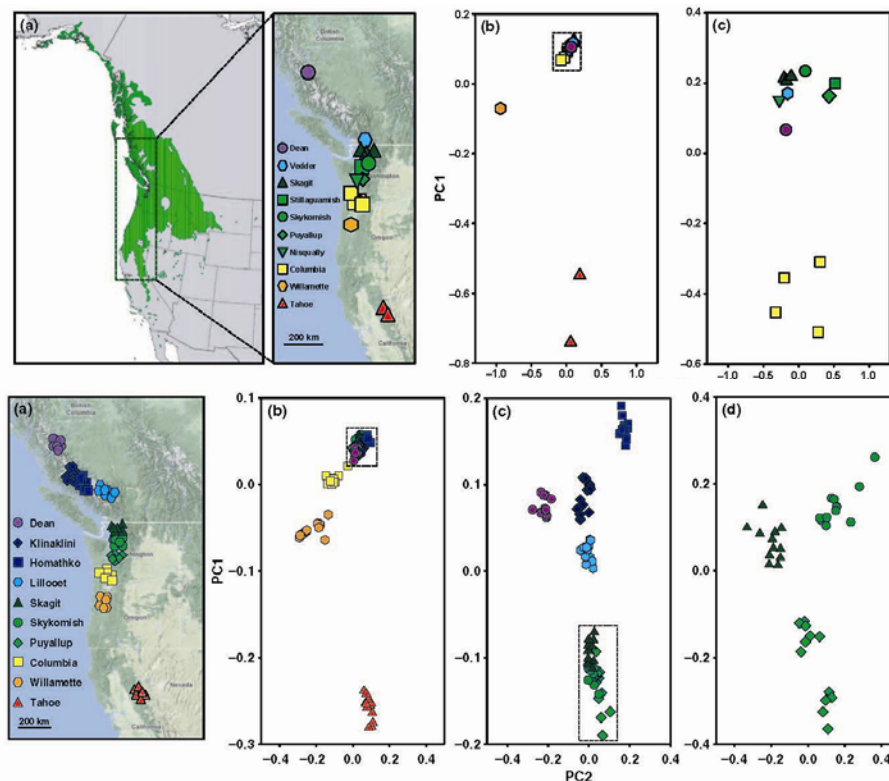
Objective: Investigate genetic and genomic structure in a natural population of *Populus* in relation to geographical location.

Approach:

- Resequenced genomes of 16 different native *P. trichocarpa* subpopulations across a broad north to south range.
- Determined population structure and genetic variation on a geographic scale.

Result/Impact:

- Strong correlation between latitude and genetic differentiation allows inference of phenotypic expression – genotype relationship.
- Presence of extensive linkage disequilibrium supports feasibility of genome-wide association studies, facilitating marker-assisted breeding through genomic selection and enhancing the potential for genetic improvement of *Populus* as a biofuel feedstock.



Slavov et al. 2012. "Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree *Populus trichocarpa*." *New Phytologist* 10.1111

A New High Temperature Cellulase Cocktail from Switchgrass Degrading Microbes

Objective:

Develop a new multi-cellulase cocktail that can be used deconstruct cellulose at high temperatures and is compatible with ionic liquid (IL) pretreated switchgrass.

Approach:

- Enrich a thermophilic microbial community on switchgrass and identify secreted cellulase enzymes with metaproteomics.
- Combine secreted enzymes with two purified high temperature cellulases to form a novel cocktail (JTherm) and apply to IL treated switchgrass.

Results/Impact:

- JTherm cocktail broke down IL switchgrass at temperatures from 50-79 C and in the presence of 10-20% of the ionic liquid [C2mim][OAc].
- Resulting hydrolysates were converted to biodiesel by an engineered *E. coli* strain, demonstrating low production of inhibitory compounds.



Whole Plant Cell Wall Characterization using 2-D NMR



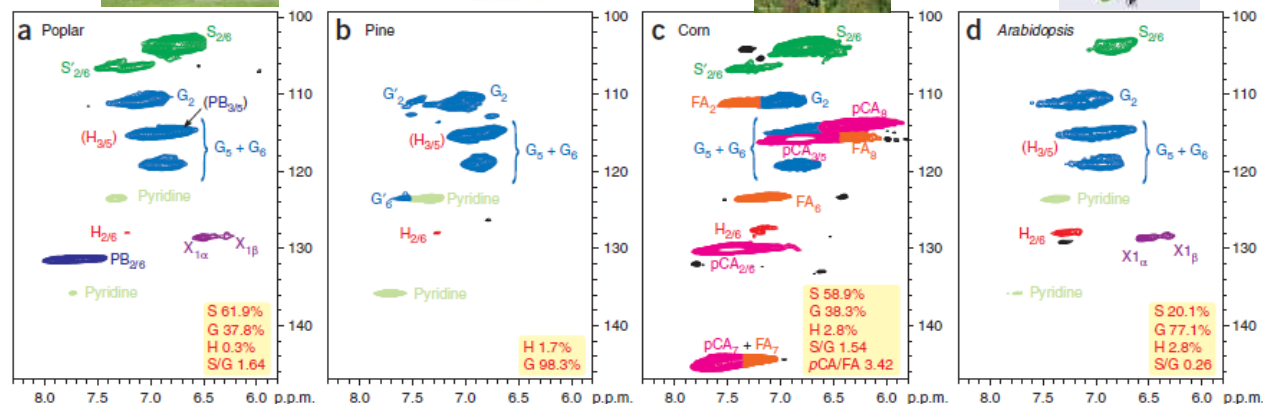
Objective: Develop a solution based protocol and analysis method to characterize the percent of S/G/H Lignin in plant cell walls

Approach:

GLBRC researchers describe a state of the art nuclear magnetic resonance (NMR) protocol to analyze the structural components of plant cell walls:

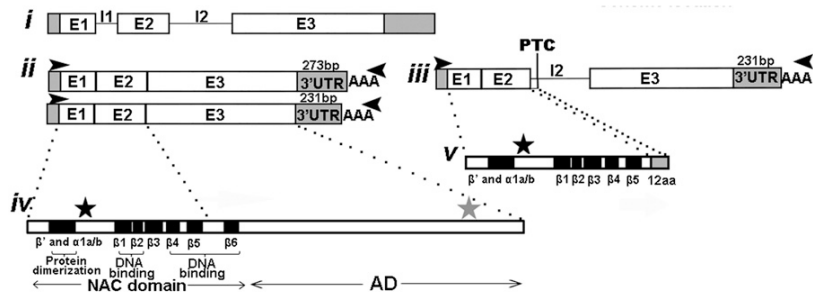
- Prepare and extract biological plant tissues
- Solubilize plant materials for composition analysis
- Perform 2D NMR spectroscopy and analysis for elucidating lignin composition and molecular profiling.

Result/Impact: The method outlined can be used to facilitate the structural analysis of plant cell walls and offers a means to visualize the chemical constituents of primary and secondary lignified cell walls from a diverse set of plant species.



Shawn D Mansfield, Hoon Kim, Fachuang Lu and John Ralph. 2012. "Whole plant cell wall characterization using solution-state 2D NMR", *Nature Protocols* 7(9) 1579-1589

Regulation of Wood Formation Characterized

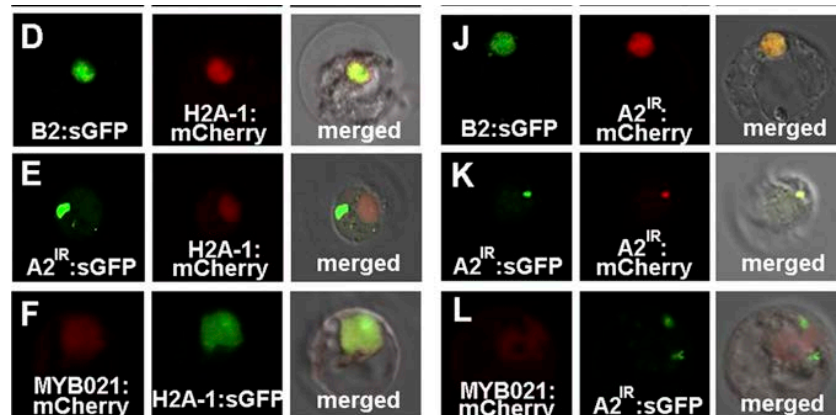


Objective: Investigate regulation of the gene expression cascade associated with lignin biosynthesis in Poplar.

Approach: Discovered a splice variant of a member of the PtrSND1 transcription factor gene family, whose members activate genes affecting secondary cell wall biosynthesis.

- Variant protein is localized outside the nucleus, then translocated into nucleus in presence of a non-variant PtrSND1 proteins where they bind.
- Newly created molecule then suppresses expression of the gene cascade.

Result/Impact: Repression of a TF family member by its splice variant has never before been seen in plants. This discovery helps define the process of wood formation at the molecular level, guiding research to optimize bioenergy production from biomass.



Li Q, Lin Y-C, Sun Y-H, Song J, Chen H, Zhang X-H, Sederoff RR, and Chiang VL. 2012. "Splice variant of the SND1 transcription factor is a dominant negative of SND1 members and their regulation in *Populus trichocarpa*", *Proc Nat Acad Sci* 2012 109(36)14699-14704

The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes

Dimitrios Floudas *et al.* **Science** 336, 1715 (2012)

Defining the core Arabidopsis thaliana root microbiome

Derek Lundberg *et al.* **Nature** 448, 86-90 (2012)

Genomics of aerobic cellulose utilization systems in Actinobacteria

Iain Anderson *et al.*, **PLoS ONE** 7(6) 1-10 (2012)

The genome of the polar eukaryotic microalga Coccomyxa subellipsoidea reveals traits of cold adaptation

Guillaume Blanc, *et al.*, **Genome Biology** 13 (2012).

Metabolic potential of a single cell belonging to one of the most abundant lineages in freshwater bacterioplankton.

Garcia SL *et al.* **ISME J.** 2012 Jul 19.

Complete Genome Sequence of Paenibacillus strain Y4.12MC10, a Novel Paenibacillus lautus strain Isolated from Obsidian Hot Spring in Yellowstone National Park.

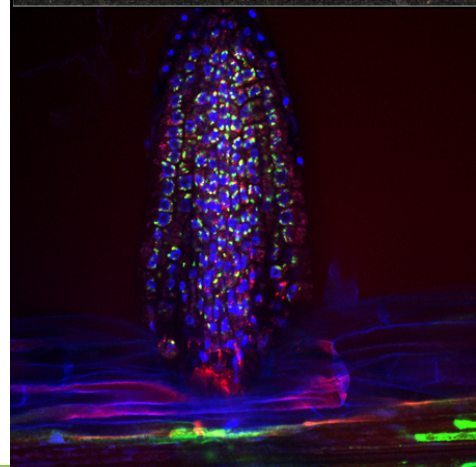
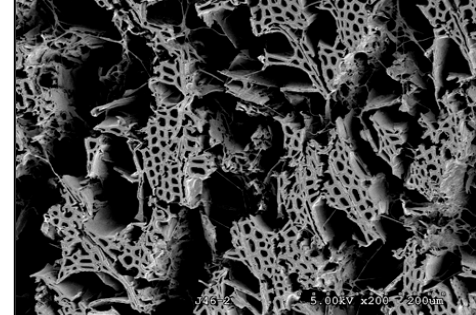
Brumm PJ *et al.* **Stand Genomic Sci.** 2012 July 27

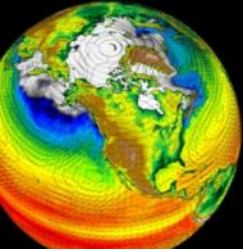
Complete genome sequence of Thauera aminoaromatica strain MZ1T.

Jiang K *et al.* **Stand Genomic Sci.** 2012 July 20

JGI Publication Highlights

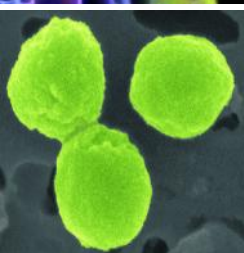
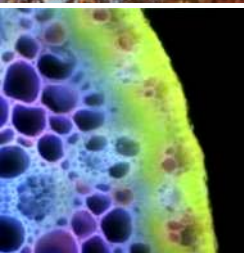
<http://www.jgi.doe.gov/News/pubs.html>





Systems science to meet DOE mission needs in bioenergy, climate and the environment.

<http://science.energy.gov/ber>



Thank you!

<http://genomicscience.energy.gov>

