Biological Systems Science Division Update

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Update Outline

- ➢ *Personnel*
- ➢ *Completed Programmatic Activities*
- ➢ *KBase Status update*
- ➢ *Division Science Highlights*

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Personnel Update

➢ **New Permanent BSSD Division Director**
  - ▪ Start date March 12

➢ **New Program Manager**
  - ▪ Dr. Pablo Rabinowicz - *A new Fed as of Monday!*

Programmatic Activities

FY2012 Reviews of DOE National Laboratory SFA programs

➢ **Foundational Genomics**
  - Los Alamos National Laboratory (reverse site visit July 12-13)
  - Oak Ridge National Laboratory (reverse site visit July 12-13)
  - Argonne National Laboratory **(completed)**
➢ **Biofuels Research**
  - Lawrence Livermore National Laboratory (reverse site visit July 12-13)
  - National Renewable Energy Laboratory **(completed)**
  - Oak Ridge National Laboratory **(completed)**
➢ **Radiochemistry & Imaging**
  - Brookhaven National Laboratory **(completed)**
  - Jefferson Laboratory – (pending)

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Programmatic Activities Cont'd

FY2012 Panel Reviews

➢ *Plant Feedstock Genomics for Bioenergy: A Joint Research Funding Opportunity Announcement USDA, DOE (DE-FOA 0000598)*
- Estimated funding available – up to $6M
- Panel review - April 25-26
- 60 applications
- 9 total awards (2 funded by USDA) – *notifications pending*

➢ *Integrated Nuclear Medicine Research and Training Projects of Excellence (DE-FOA 000646)*
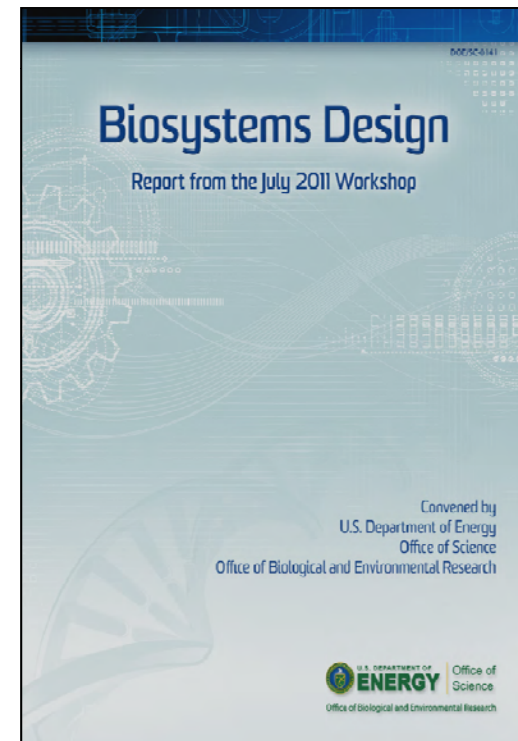- Estimated funding available – up to $10M
- Panel review - May 1
- 19 applications
- 5 awards – *notifications pending*

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Programmatic Activities Cont'd

FY2012 Panel Reviews

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

- Estimated funding available – up to $20M
- Panel review - May 21-23
- 88 applications (33 plants, 55 microbial)
- *Selections in progress*

Biosystems Design
Report from the July 2011 Workshop

Convened by
U.S. Department of Energy
Office of Science
Office of Biological and Environmental Research

ENERGY | Office of Science
Office of Biological and Environmental Research

http://genomicscience.energy.gov/biosystemsdesign

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Programmatic Activities Cont'd

Symposia/Conferences

➢PittCon 2012 "*Mass spectrometry advances conversion of biomass to biofuels*"
   (R. Hirsch and A. Katz organizers; Mar. 14, 2012)

➢ACS 2012 : "Glenn T. Seaborg Award for Nuclear Chemistry"
   (P. Srivastava, Chair, Mar. 27, 2012)

➢ 2012 NSLS/CFN Users Meeting – Applications of Synchrotron Techniques in Plant Biology.
   (C. Ronning, May, 23, 2012)

➢ Nuclear and Radiation Studies Board meeting at the NAS "*New Developments in Radiation Biology*"
   (N. Metting, May 30, 2012)

➢ASM 2012 *Microbial Powers to Tap Earth's Energy*
   (J. Graber, co-organizer; June 18, 2012)

Genomeweb: Bioinform Q&A: DOE's Susan Gregurick on Efforts to Develop a Systems Biology Resource for Microbes and Plants

http://www.genomeweb.com/newsletter/bioinform

Programmatic Activities Cont'd

FY2012 Workshops

> ### BER - Joint Genome Institute Strategic Planning Workshop
> - May 30-31 (last week!)
> - 38 participants
> - Draft report in progress

Addressing three main issues:

What new insights could be enabled by next generation sequencing? What vision can be identified for DOE-mission driven biology for the next 5-10 years?

What large scale questions/challenges in DOE mission driven systems biology require a user facility for genome sequencing?

What new and/or high throughput capabilities/technologies are needed to advance systems biology to help meet DOE mission needs?

Systems Biology Knowledgebase

Kbase Status Update as of May 2012

- The **KBase Central Data Model (CDM)** focuses on genomes and includes annotation, expression, chemistry, and models.

- A reference implementation of the **KBase Unified API** has been released for Alpha testing.
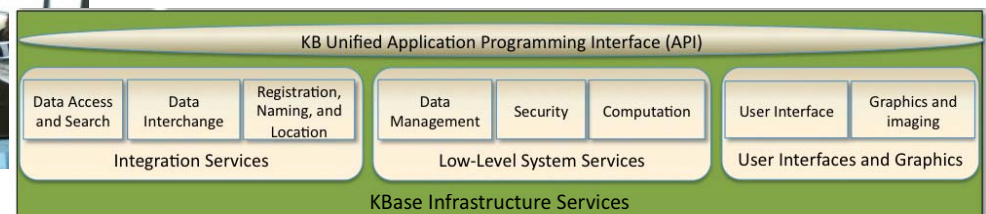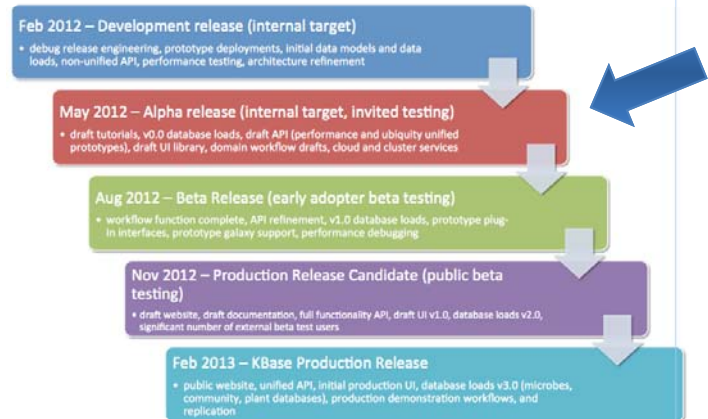

- A **100Gb ESnet Test** has been completed.

- The **KBase Cloud** has expanded to include hardware at ORNL. This is the first of several steps to build out the kbase.us network.

- Developed a working prototype of an extensible MATLAB-like web application for accessing KBase data, running KBase tools, stringing tools together into workflows, and generating/viewing output.
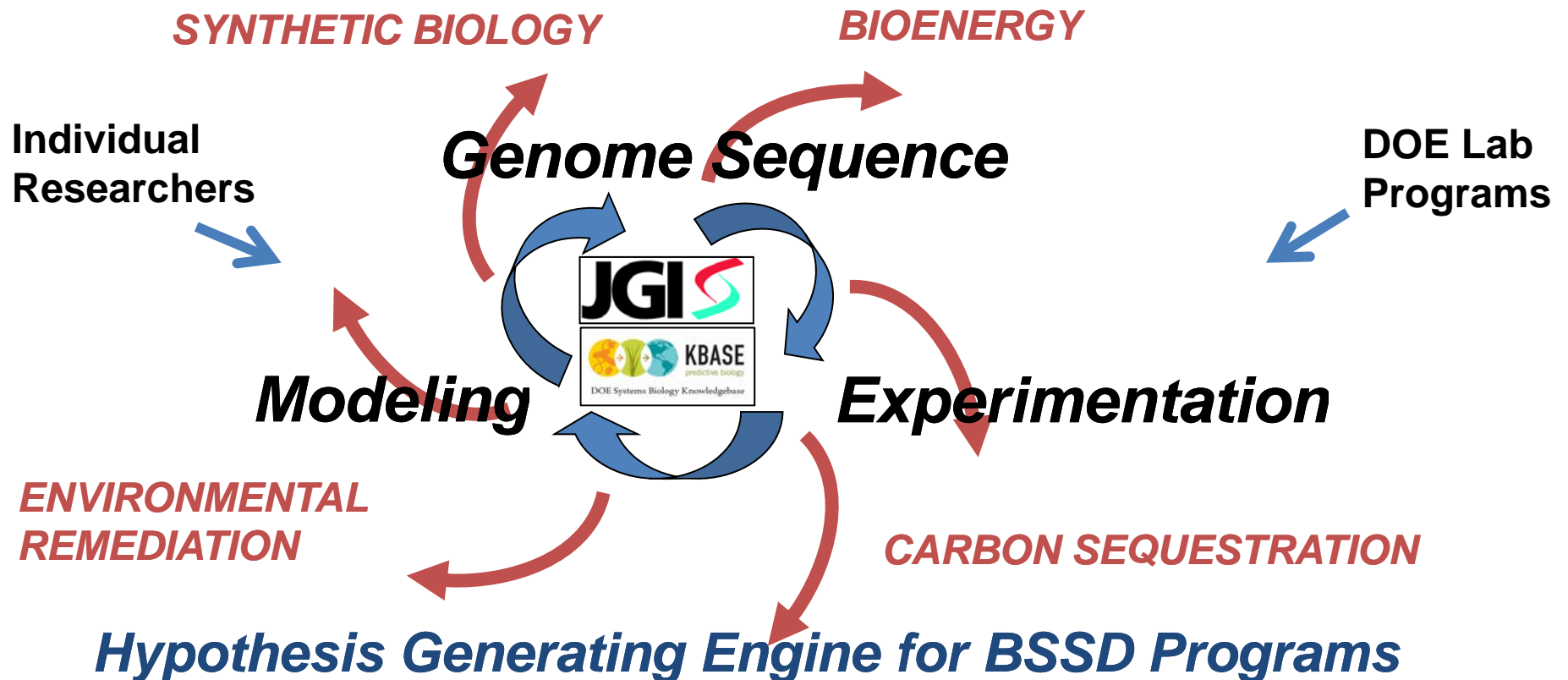

Kbase website: **http://kbase.science.energy.gov/**
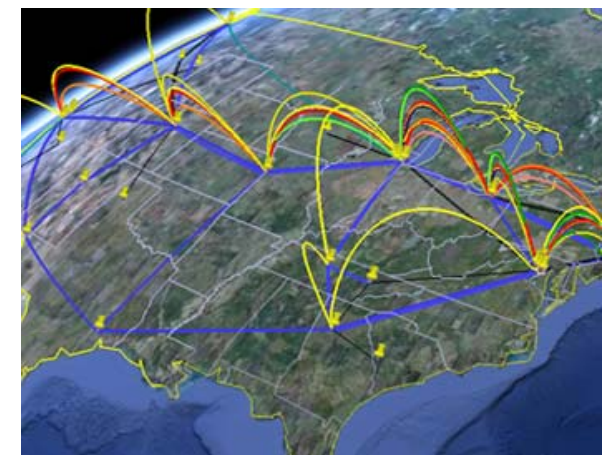
JGI-Kbase Connection
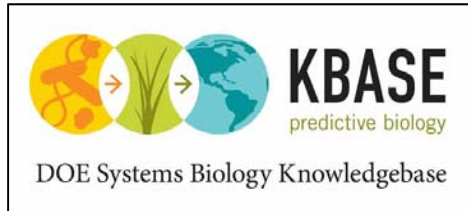
➤ **CRUCIAL**: **Advancing a new leadership role in fundamental Biology for DOE**
- centralized genome modeling and database portals
- open access and community centric
- enables broad scale integrative genomic science

SYNTHETIC BIOLOGY

BIOENERGY

Individual Researchers

Genome Sequence

DOE Lab Programs

Modeling

Experimentation

ENVIRONMENTAL REMEDIATION

CARBON SEQUESTRATION

Hypothesis Generating Engine for BSSD Programs

Complex Physiological Responses During Conversion of Biomass to Biofuels

GREAT LAKES
BIOENERGY
RESEARCH CENTER

Objective:

Improving the efficiency of biofuel production by understanding physiology of cells converting biomass hydrolysate to biofuel.

Approach:

▪ Meta-transcriptomic analyses identified gene expression patterns in an ethanologenic strain of *E. coli* (GLBRCE1) grown in AFEX-treated corn stover hydrolysates.

▪ Comparative expression patterns linked amino acid uptake and use to osmotic stress responses and cell energetics impacting growth during biofuel production.

▪ Expression patterns identified specific genes/responses indicating how cells adapt to changing conditions during biofuel production.

Results/Impact:

The identified genes/responses provide new targets for metabolic engineering to improve osmotic stress tolerances in biofuel-producing microorganisms and enhance production efficiency.
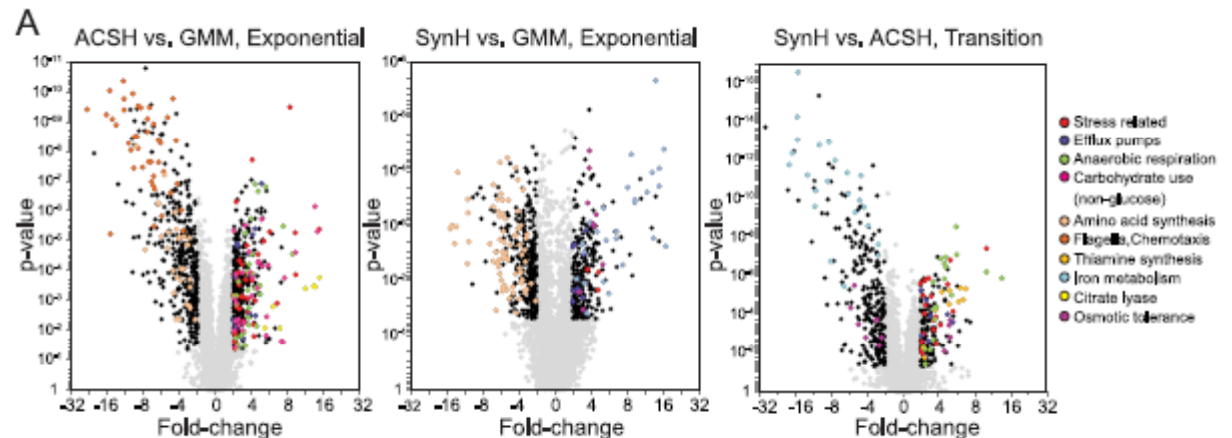
Swalbach, M.S. et al. 2012. *Appl. Environ. Microbiol.* 78: 3442-3457

Understanding Ionic Liquid Tolerance in Cellulose Degrading Microbes

jbei
Joint BioEnergy Institute

Expression log2 ratios
Histogram

Enterobacter lignolyticus SCF1 Cellular Overview
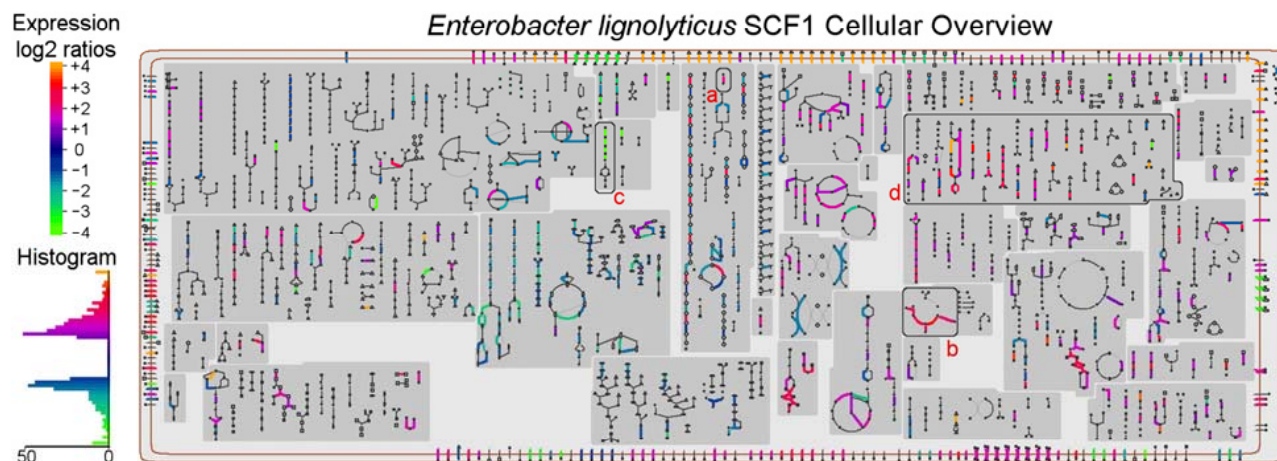
Objective:

Pretreatment of biomass with ionic liquids (ILs) effectively separates lignin and polysaccharides, but residual ILs are toxic to microbes involved in subsequent polysaccharide breakdown and fuel synthesis; how can we improve microbial tolerance to ILs?

Approach:

Used transcriptomics to examine IL induced shifts in gene expression by *Enterobacter lignolyticus,* a halotolerant biomass degrading bacterium isolated from rainforest soil.

Results/Impact:

E. lignolyticus was shown to activate a complex set of IL exposure specific genes involved in activation of membrane pumps, alteration of cell membrane composition, and overall balance of osmotic pressure. These provide new targets for potential modification of microbes for IL tolerance.

Genome Scale Models Advance Understanding of Methanogen Physiology
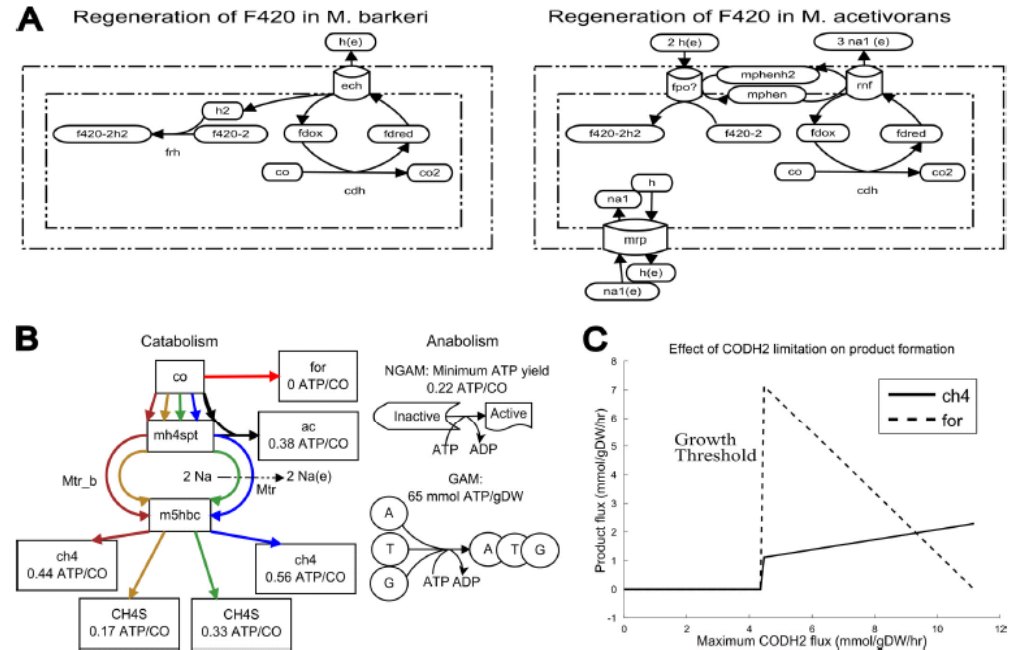
Objective:

Resolve key differences in methanogen physiology by iteratively coupling genome scale model results into experimental designs.

Approach:

▪ A genome scale model of *Methanosarcina acetivorans* C2A was constructed to help identify key gaps in central and peripheral metabolism between among three methanogenic species.

▪ Pathway predictions using experimental data from the literature and the laboratory in a FBA-model environment enabled a series of testable hypotheses on the previously unknown energetics and pathways of CO reduction and F420 regeneration by C2A.

Results/Impact:

Genome scale model (FBA) proved to be a useful iterative research tool for incorporating the latest results from the literature and the laboratory to assemble, guide and converge testable hypotheses towards validated understanding.

Benedict et. al., 2012 J. Bacteriology, 194(4):855-865

The TCTP Protein has a Protective Role in DNA Damage Sensing and Repair

Objective: To determine the role of the *translationally controlled tumor protein* (**TCTP**) after low dose irradiation.

Approach:

- Normal human cells irradiated with low doses of gamma rays were assayed for DNA damage and protein endpoints

Results:

- **TCTP** is up-regulated in the cytoplasm and nuclei of irradiated normal human cells following low dose gamma-ray exposure.

- **Low doses protected against endogenous as well as high-dose-induced DNA damage, as measured by micronuclei formation. TCTP knockdown abrogated this protection.**

- **TCTP** interacts with elements of DNA damage sensing and repair systems, and modulates radiation-induced cell-cycle checkpoints.
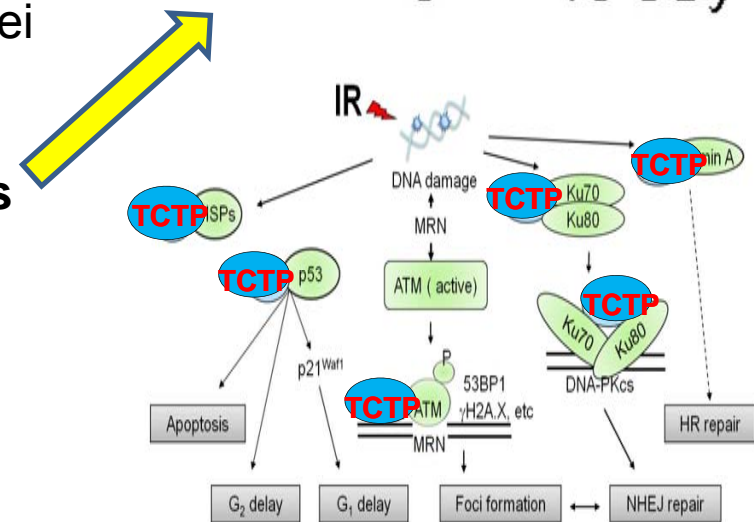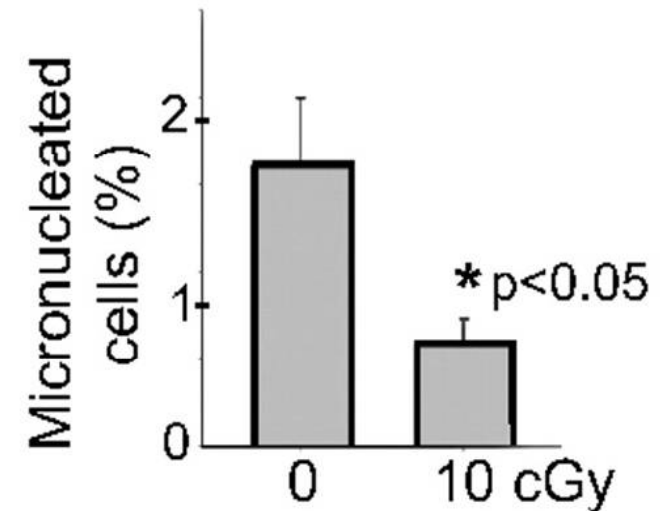

J Zhang, *et al.* **El Azzam, PNAS 2012;109:E926-E933**

Selected JGI High Impact Publications

- *Genome Sequence of the model plant Setaria.* Bennetzen J et al. **Nat Biotech** 2012 May 13.

- Comparative genomics of *Ceriporiopsis subvermispora* and *Phanerochaete chrysosporium* provide insight into selective ligninolysis. Fernandez-Fueyo E et al. **Proc Natl Acad Sci** 2012 Mar 20.

- The genome of *Tetranychus urticae* reveals herbivorous pest adaptations. Grbić M et al. **Nature** 2011 Nov 23.

-Deep metagenome sequencing illuminates permafrost response to thaw. Mackelprang R et al. **Nature** 2011 Nov 6.

- Comparative genomics screen identifies a Sinorrhizobium meliloti 1021 sodM-like gene strongly expressed within host plant nodules. Queiroux et. al. **BMC Microbiology** 12:74 (May 15)
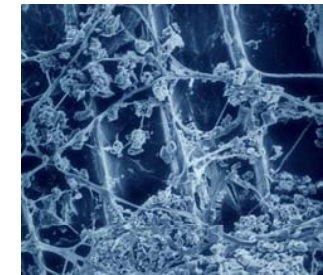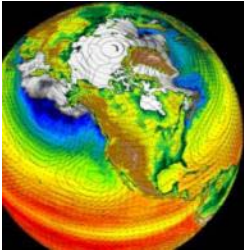
JGI Publication Highlights
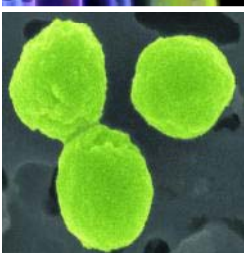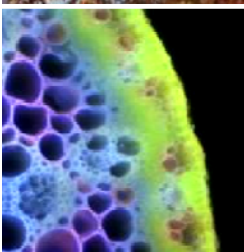http://www.jgi.doe.gov/News/pubs.html

JGI User Meeting: March 20 - 22, 2012
www.jgi.doe.gov/meetings/usermeeting/

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

http://science.energy.gov/ber

Thank you!

http://genomicscience.energy.gov