Biological Systems Science Division Update

Todd Anderson, Ph.D.
Director, Biological Systems Science Division,
Department of Energy, Office of Biological &
Environmental Research

February 21, 2013

U.S. DEPARTMENT OF
ENERGY

Office
of Science

Office of Biological
and Environmental Research

Update Outline

- *Completed Programmatic Actions*
- *New Notices*
- *Significant Activities*
- *Division Science Highlights*

Programmatic Activities

FY2012 Reviews of DOE National Laboratory programs – Completed

- **Bioenergy Research Centers**
  - *BioEnergy Science Center* (Oak Ridge, TN) Oct. 31 – Nov. 1
  - *Great Lakes Bioenergy Research Center* (Madison, WI) Nov. 8-9
  - *Joint BioEnergy Institute* (Emeryville, CA) Dec. 11-12

Upcoming Science Focus Area (SFA) Triennial Reviews in FY2013

- ***Biofuels Research***
  - Pacific Northwest National Laboratory - Feb 27
- ***Radiochemistry & Imaging***
  - Lawrence Berkeley National Laboratory - TBD
  - Oak Ridge National Laboratory – TBD

2013 Genomic Science Program Annual PI Meeting

- ***Bethesda North Marriott Hotel (February 25-27) - Next week!***

New Notices

Plant Feedstocks Genomics for Bioenergy: A Joint Research Funding Opportunity Announcement USDA, DOE (DE-FOA-0000770)

- *Issued November 20, 2012*
- *Pre-apps due December 18, 2012*
- ***Full applications due February 25, 2013***

FINANCIAL ASSISTANCE
FUNDING OPPORTUNITY ANNOUNCEMENT

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

USDA

U. S. Department of Agriculture
National Institute of Food and Agriculture

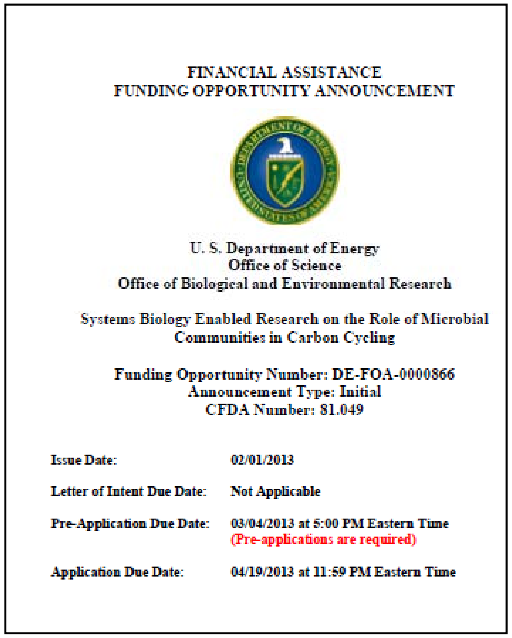
Plant Feedstock Genomics for Bioenergy: A Joint Research
Funding Opportunity Announcement USDA, DOE

Funding Opportunity Number: DE-FOA-0000770
Announcement Type: Initial
CFDA Number: 81.049 & 10.310

Issue Date: **November 20, 2012**
Pre-Application Due Date: **December 18, 2012, 4:30 p.m. Eastern Time**
(Pre-applications are Required)
Application Due Date: **February 25, 2013, 11:59 p.m. Eastern Time**

Systems Biology Enabled Research on the Role of Microbial Communities in Carbon Cycling (DE-FOA-0000866)

- *Issued February 1, 2013*
- ***Pre-apps due March 4, 2013***
- ***Full applications due April 19, 2013***



FINANCIAL ASSISTANCE
FUNDING OPPORTUNITY ANNOUNCEMENT

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

Systems Biology Enabled Research on the Role of Microbial
Communities in Carbon Cycling

Funding Opportunity Number: DE-FOA-0000866
Announcement Type: Initial
CFDA Number: 81.049

Issue Date: **02/01/2013**

Letter of Intent Due Date: **Not Applicable**

Pre-Application Due Date: **03/04/2013 at 5:00 PM Eastern Time**
(Pre-applications are required)

Application Due Date: **04/19/2013 at 11:59 PM Eastern Time**

Subject to FY2013 Availability of Funds

Significant Activities

Joint Call for Exploratory Collaborations

- ***First-ever call between EMSL and DOE-JGI***
- ***Focused on plant, fungal, soil and microbial interactions and physiology related to***
  - *Biofuel production*
  - *Carbon cycling*
- ***Must require capabilities from both facilities***
- ***Schedule:***
  - *Letters of Intent due February 11 – April 8*
  - *Invited full proposals due May 27*
  - *Approved proposals start October 1, 2013*
  - *Details: http://www.emsl.pnnl.gov/access/calls/jgi/.*

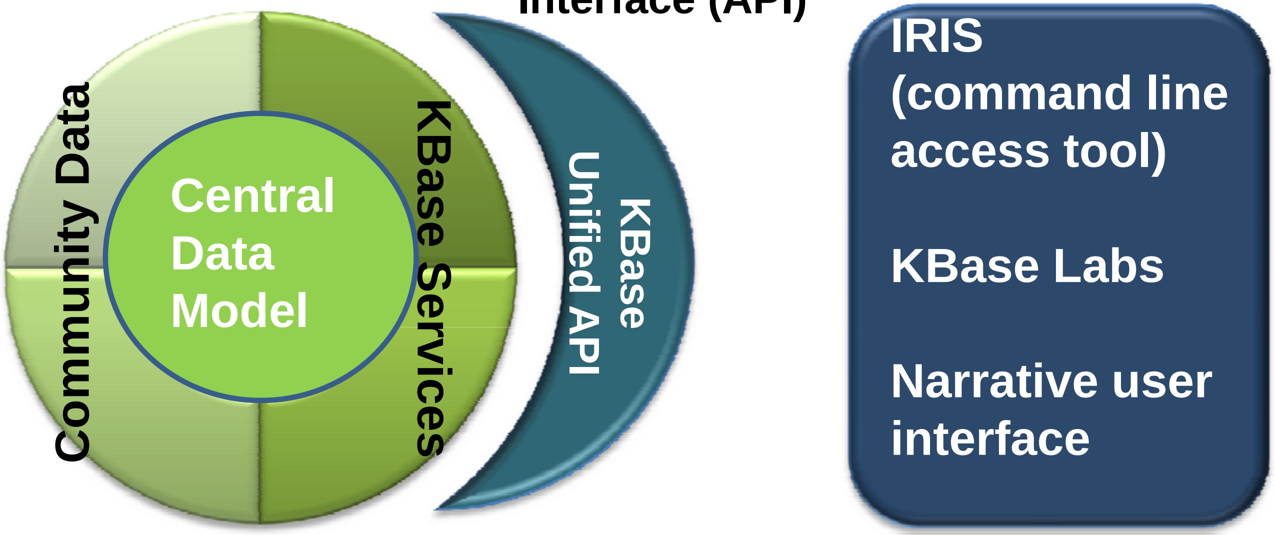
EMSL

JGI
DOE JOINT GENOME INSTITUTE
US DEPARTMENT OF ENERGY
OFFICE OF SCIENCE

KBASE predictive biology

DOE Systems Biology Knowledgebase

KBase Roll Out–February 2013



Data and services

Application programming Interface (API)

User interactions

Community Data

Central Data Model

KBase Services

KBase Unified API

IRIS (command line access tool)

KBase Labs

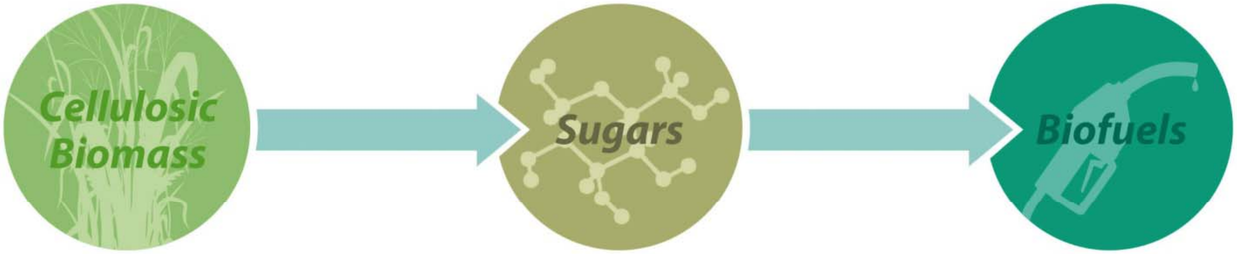
Narrative user interface

Through a series of Talks , Demonstration and Tutorials the KBase team will illustrate early functionality of KBase including:

- Large Scale Integrated Gene Regulatory and Metabolic Capabilities in KBase
- Functional Characterization of Adaptive Variation in Plants
- Capabilities to integrate, search and visualize experimental data and existing models within the KBase environment
- Capabilities to integrate your own research methods into the KBase environment
- Vision, Progress and Longer term objective will also be discussed

Bioenergy Research Centers (BRCs)

2012 Annual Reviews



Feedstock Development
Develop crops with cell walls optimized for deconstruction and biofuel production.

Biomass Deconstruction
Improve enzymes and microbes that break down biomass into sugars.

Fuel Synthesis
Engineer metabolic pathways in microbes to produce diverse biofuels.

Significant progress towards understanding :

- Sustainability of bioenergy crop production
- Plant metabolism and techniques to decrease biomass recalcitrance
- Pretreatment methods to increase the efficiency of cellulose extraction
- Enhanced enzymatic methods to produce sugars from cellulose
- Modifications to microorganisms to combine conversion capabilities, tolerate biofuel production conditions and produce a range of biofuel compounds

As of the last review the BRCs have generated :

1100 journal articles,
286 Invention disclosures
146 patent applications

BRC Science Highlight

BESC
BioEnergy Science Center

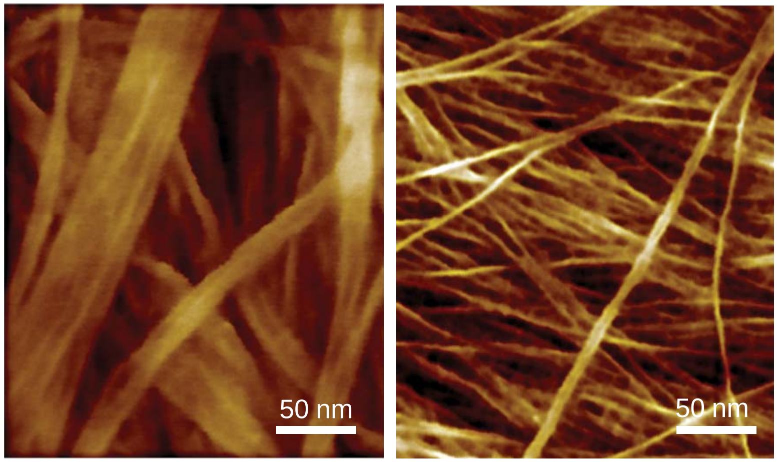
Nanoscale Architecture of Plant Cell Walls Determines Their Accessibility and Digestibility by Enzymes

Objective: Understand enzymatic digestion of biomass during pretreatment processes

Approach: Researchers at National Renewable Energy Laboratory conducted real-time in situ imaging of the action of two commercially-relevant enzyme systems (i.e., bacterial cellulosomes and fungal cellulases) on biomass under controlled digestion conditions across 10 nm to 10 um length-scales.

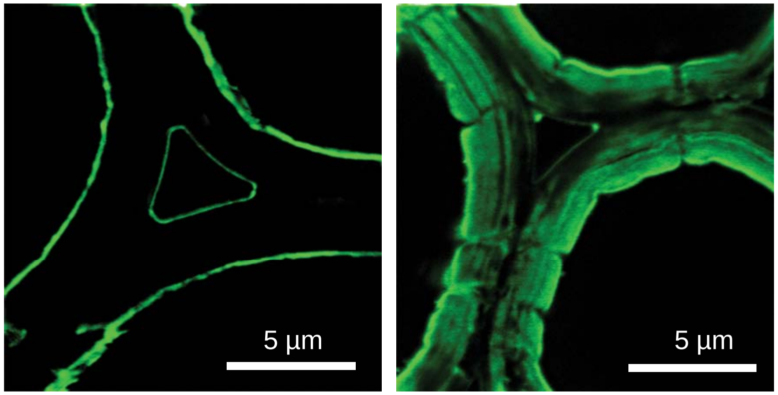
Results/Impact : Imaging reveals different mechanisms of enzymatic breakdown of biomass. Fungal enzymes penetrate into the cell wall, resulting in fast digestibility, large cellulosomes digest the cell wall from the surface. Lignin physically hinders the accessibility of polysaccharides in the cell wall to enzymes.

Nanoscale structure of plant cell walls by atomic force microscopy



Primary wall (PW) Secondary wall (SW)

Enzyme accessibility by Confocal laser scanning microscopy



Bacterial cellulosomes Fungal cellulases

Ideal pretreatments should maximize lignin removal and minimize polysaccharide modification thereby retaining the essentially native microfibrillar structure and improving accessibility.

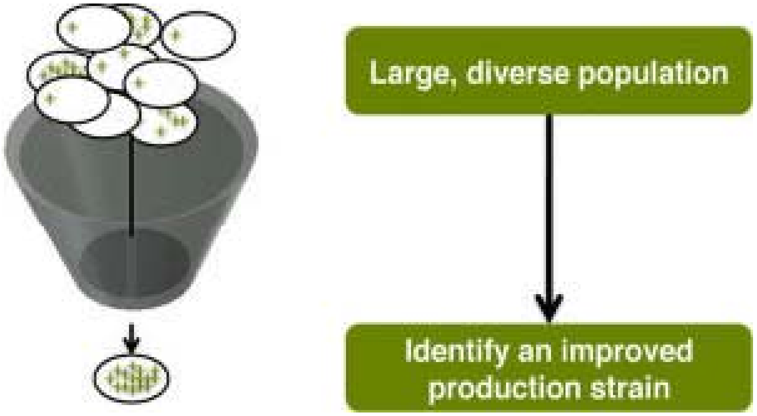
Ding, S.-Y.; Liu, Y.-S.; Zeng, Y.; Himmel, M.E.; Baker, J.O.; Bayer, E.A. (2012). “How does nanoscale architecture correlate with enzymatic digestibility?” ***Science*** *338, pp. 1055–1060.*

Joint BioEnergy Institute

Making the best biofuel-producing microbes identify themselves

Objective:

Develop a generalized approach to screen or select microbes with improved small-molecule biosynthesis capabilities involved in biofuel production.

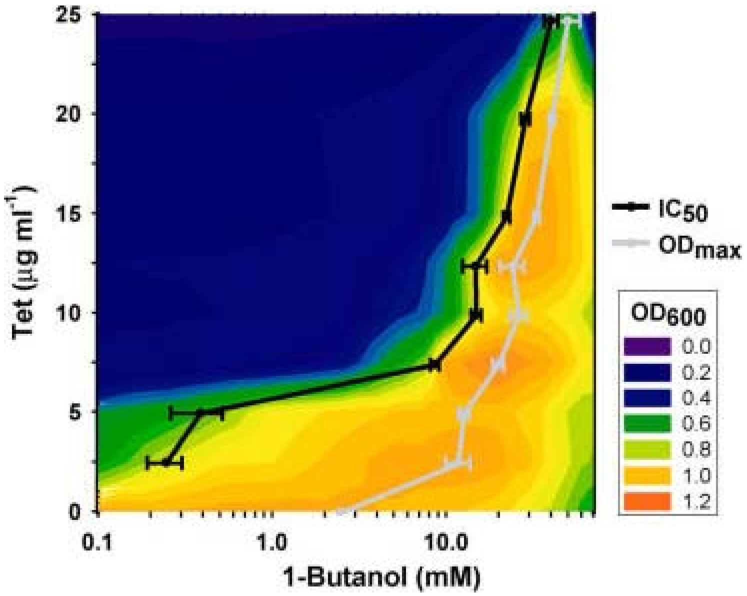


Large, diverse population

Identify an improved production strain

Approach:

- JBEI researchers developed transcription factor-based biosensors for desired small-molecules and coupled these sensors with the expression of a gene that confers a selection advantage to the microbe (e.g. resistance to the antibiotic tetracycline)
- Plasmids for the biosynthesis of a desired molecule, such as butanol, were then introduced and thus microbial growth rate was directly linked to the production of specific biofuel products.

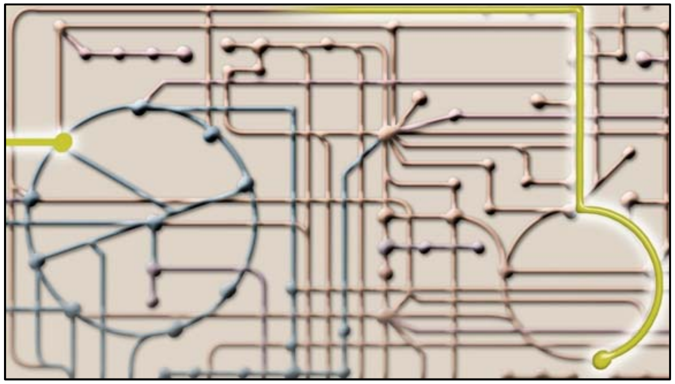


Results/Impact:

This approach facilitates the selection of microbial strains that produce large quantities of any small molecule, an important step toward the development of renewable biofuels.

Dietrich et al. 2012. **ACS Synthetic Biology**. DOI: 10.1021/sb300091d.

Innovative computational approach accurately maps biochemical reactions at the atomic level



Objective:

In the design and bioengineering of metabolic pathways it is important to understand and eventually manipulate the movement of atoms in these biochemical reactions.

Approach:

- A new computational system (Minimum Weighted Edit-Distance or MWED) allows researchers to map the flow of atoms in biochemical reactions.
- MWED relies on predicting the propensity of forming or breaking chemical bonds during a biochemical reaction and optimizes all possible solutions to the reactions of interest.

Results/Impact:

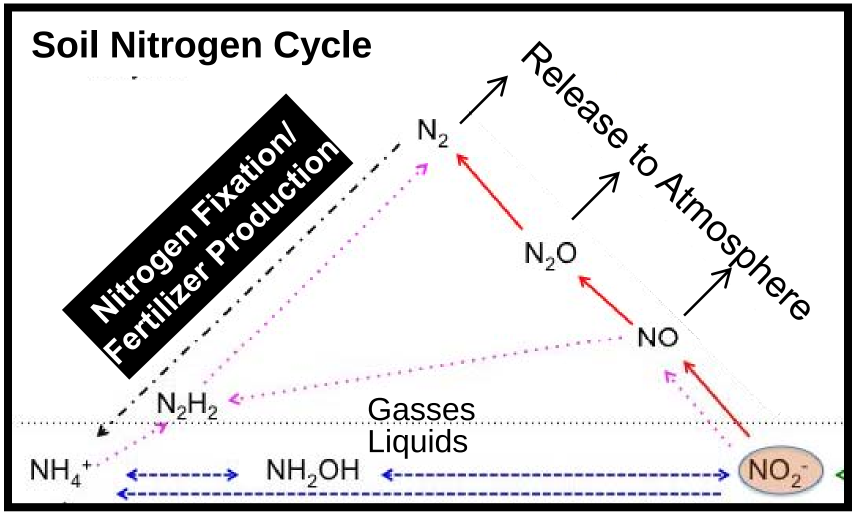
2,446 manually curated biochemical reactions from the KEGG database were fully mapped with an error rate of 0.9, offering scientists an extremely fast and highly accurate method to model the movement all atoms in biochemical reactions.

Mario Latendresse, Jeremiah P. Malerich, Mike Travers and Peter D. Karp, “Accurate Atom-Mapping Computation for Biochemical Reactions”, ***Journal of Chemical Information and Modeling***, 2012 10.1021/ci3002217

Discovery of New Types of Nitrous Oxide (N_2O) Consuming Bacteria

Objective:

Models of the soil nitrogen cycle predict that more of the greenhouse gas N_2O should be produced than is actually observed. Why is this?

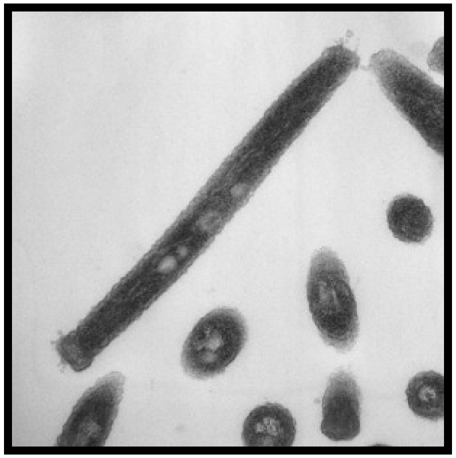


Approach:

Use comparative genomics to identify new types N_2O-consuming bacteria and search for them in soil environments.

Results/Impact:

A novel metabolic pathway for N_2O consumption was identified in the soil bacterium *Anaeromyxobacter dehalogens.* Genes of this pathway were detected in soil samples and appear to be associated with other common soil microbes as well. These organisms may represent the missing "sink" for N_2O in soil ecosystems.



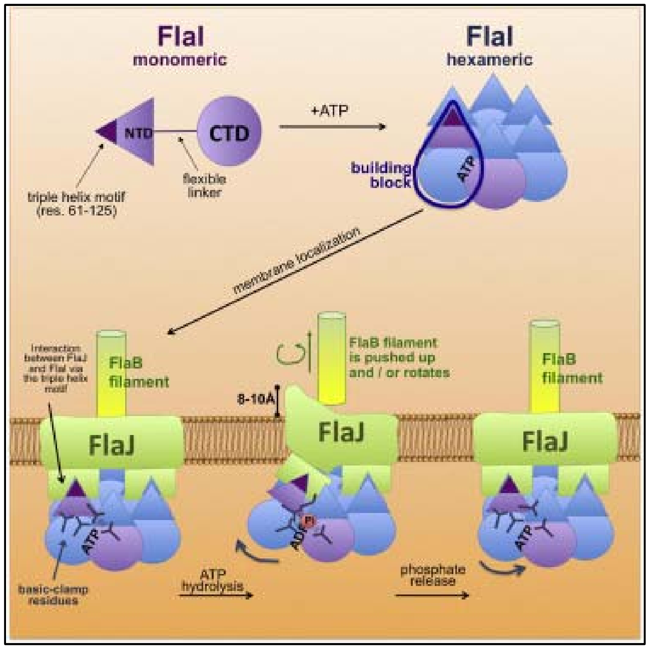
Sanford et al. 2012. **PNAS** www.pnas.org/cgi/doi/10.1073/pnas.1211238109

Structural Biology Science Highlight

SAXS Study of Motor Assembly and Motility in Archaea

Objective

Understand how archaeal flagella (archaella) assemble and cause movement by identifying essential components and modeling how they come together.



Approach

Study the ATPase enzyme FlaI in *Sulfolobus acidocaldarius.* Obtain its structure in solution using Small Angle X-ray Scattering (SAXS) and build models using crystal structures of the enzyme interacting with other key elements of the archaella. Determine which portions of FlaI are involved in assembly and which are involved in motion.

Results/Impacts

“Overall, collective results reveal detailed and global FlaI activities in transducing nucleotide binding and hydrolysis into translational and rotatory motions suitable for assembly and motility without destabilizing the integrity of the hexameric crown assembly”

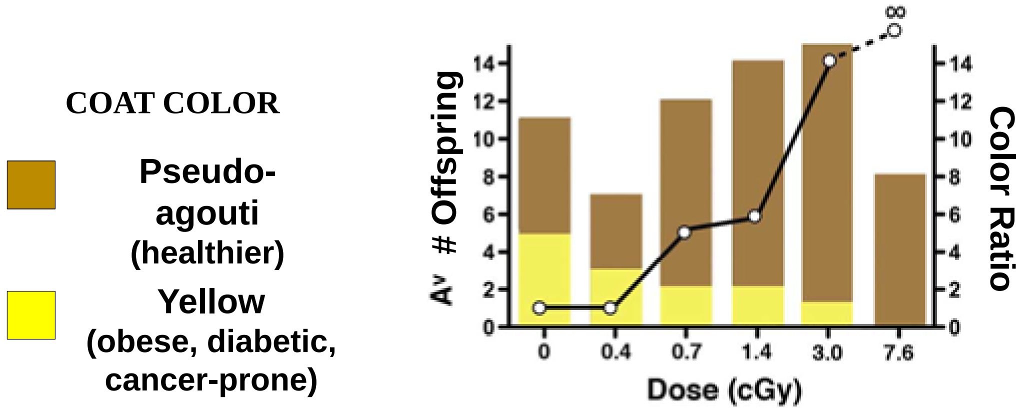
Sophia Reindl, Abhrajyoti Ghosh, Gareth J. Williams, Kerstin Lassak, Tomasz Neiner, Anna-Lena Henche, Sonja-Verena Albers, John A. Tainer (2013) “Insights into FlaI Functions in Archaeal Motor Assembly and Motility from Structures, Conformations, and Genetics” **Molecular Cell** February 14, 2013. http://dx.doi.org/10.1016/j.molcel.2013.01.014

Low Dose Science Highlight

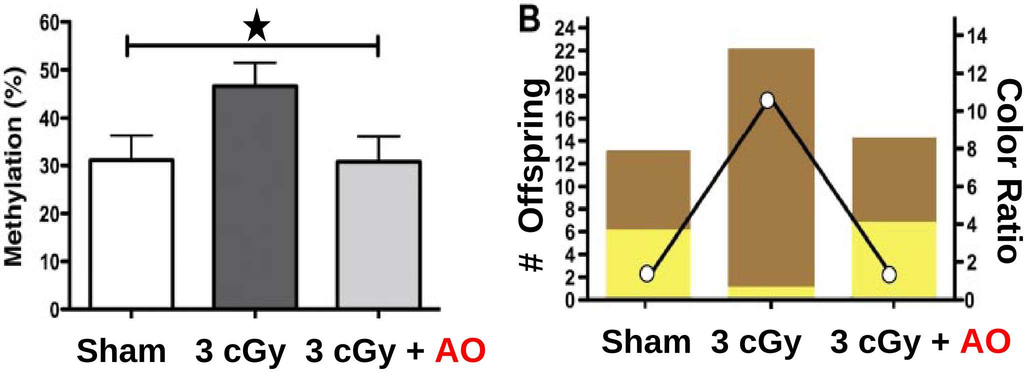
Low dose radiation-induced epigenetic alterations in the A^{vy} yellow agouti mouse model

- Irradiation of pregnant mouse mothers in gestational day 4 increased methylation of agouti gene in the offspring
- DNA sequence of the A^{vy} gene locus was not altered
- Larger numbers of offspring were darker brown as a function of dose, with concomitant better health
- Anti-oxidant supplementation of mouse mothers reduced locus methylation, and the ratio of brown /yellow mice to near control levels
- Conclusion: In this isogenic mouse model, low dose-induced epigenetic changes play a role in radiation hormesis

Very low doses of radiation induce epigenetic alterations



Adaptive radiation-induced epigenetic alterations are mitigated by antioxidants (AO)



Bernal, A. J., Dolinoy, D. C., Huang, D., Skaar, D. A., Weinhouse, C., Jirtle, R. J. *Adaptive radiation-induced epigenetic alterations mitigated by antioxidants*. ***FASEB J.*** **27; 665-671 (2013). www.fasebj.org**

Selected JGI Publications – Feb. 2013

Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. Curtis BA et al. ***Nature* 2012** 492(7427): 59-65

Anoxic carbon flux in photosynthetic microbial mats as revealed by metatranscriptomics. Burrow, L, et. al**. *ISME J*. 2012** 6(11): 1-13

A 34K SNP genotyping array for Populus trichocarpa: Design, application to the study of natural populations and transferability to other Populus species. Geraldes, A., et. al. ***Mol Ecol Resour*. 2013** Jan 11.

The fast changing landscape of sequencing technologies and their impact on microbial genome assemblies and annotation. Mavromatis K et al ***PLoS One.* 2012**;7(12):e48837.

Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Paterson AH et al ***Nature*. 2012** 492(7429):423-7..

Comparative Analysis of 126 Cyanobacterial Genomes Reveals Evidence of Functional Diversity Among Homologs of the Redox-Regulated CP12 Protein. Stanley DN et al ***Plant Physiol*. 2013** Feb;161(2):824-35

Complete Genome Sequence of Desulfurococcus fermentans, a Hyperthermophilic Cellulolytic Crenarchaeon Isolated from a Freshwater Hot Spring in Kamchatka, Russia. Susanti D et al ***J. Bacteriol*. 2012**;194(20):5703-4.

JGI Publication Highlights: http://www.jgi.doe.gov/News/pubs.html

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