Microbial and Plant Genomics Institute 7th Annual Retreat

Thursday, January 10th, 2013
Seminar Room 105 + Atrium
Cargill Building

RETREAT SCHEDULE

8:30 - 9:00	Breakfast and Poster Set up (Atrium)
9:00 - 9:10	Introductory Remarks - Nathan Springer, Director, MPGI
9:10 - 9:25	Statement: Anne-Francoise Lamblin Supercomputing Institute
9:25 - 9:40	Statement: Kenny Beckman - BMGC
9:40 - 10:00	Gerit Bethke - Glazebrook/Katagiri Lab
10:00 - 10:20	Mandy Waters - Springer Lab
10:20 - 10:40	Break (Atrium)
10:40 - 11:00	Brendan Epstein - Young Lab
11:00 - 11:20	Stephan Cameron - Wackett Lab
11:20 - 11:40	Aunica Kane - Gralnick Lab
11:40 - 12:00	Margaret Taylor - Ward Lab
12:00 - 1:30	Lunch and Poster Session (Atrium)
1:30 - 1:50	Yung-Tsi Bolon - Stupar Lab
1:50 - 2:10	Peng Yu - Cohen Lab
2:10 - 2:30	Jonathon Fankhauser - Travisano Lab
2:30- 2:40	Closing Remarks - Nathan Springer, Director

POSTER SESSION

Steve Eichten
Graduate Student
Springer Lab

Genetic and Epigenetic Control of DNA Methylation Variation in Maize

Zarath Summers
Postdoc
Gralnick Lab

Taking the Geo out of Geomicrobiology: Electrochemical Cultivation of Microbes from the Soudan Iron Mine

Carrie Eberle
Postdoc
Smith Lab

The Pistil-specific extensin-like protein is required for interspecific incompatibility in Nicotiana

David Chau
Graduate Student
Hu Lab

Elucidating the Mechanism behind Stem-Cell Derived Hepatocytes using Transcriptome Analysis

Benjamin Campbell
PhD Student
Stupar Lab

A natural nonsynonymous mutation in a magnesium chelatase subunit is a candidate for chlorophyll deficiency in 'Golden Gopher' soybean

Carles Pons
Postdoc
Meyers Lab

Evolution of Transcription Factor Networks in the Nematode C. elegans

Kathryn Turner
PhD Student
J. Anderson Lab

Comparing biparental and association mapping techniques to find new leaf rust resistance genes from 3,200 diverse wheat accessions

Pedro Pena
Postdoc
Srienc Lab

Genome-wide screen of gene over-expression for ethanol resistance in Saccharomyces cerevisiae

Yung-Chun Kim
Postdoc
Olszewski Lab

Identification of Arabidopsis proteins with single N-GlcNAc modification

POSTER SESSION

Yong Bao
Graduate Student
Young Lab

Genome-wide predictive modeling for agronomic traits in a diverse panel of soybean germplasm

Shaun Curtin
Postdoc
Voytas Lab

Genome Engineering of Soybean with Designer Nucleases

STATEMENTS

Anne Francoise Lamblin
Director, Supercomputing Institute

Update: UMII activities and what changes people might expect in the coming year
Hightlight: Introduction to the RISS staff

Kenny Beckman
Director, Biomedical Genomics Center

Update: BMGC activities and what changes people might expect in the 2013

PRESENTATION ABSTRACTS

Gerit Bethke
Postdoc, Glazebrook Lab, Plant Biology
Pectin Methylesterases contribute to plant disease resistance

Plant cell walls constitute an early line of defense against pathogen attack. To study if changes in plant cell wall composition influence disease resistance, we screened Arabidopsis thaliana T-DNA insertion lines known to have alterations in cell wall composition for changes in pathogen growth. Plants with mutations in genes encoding pectin methylesterases (PMEs) showed small but significant increases in growth of the bacterial pathogen Pseudomonas syringae pv. maculicola (strain ES4326). Infection with Pseudomonas or a fungal pathogen (Alternaria brassicicola) resulted in enhanced total PME activity and reduced pectin methylesterification. This enhanced PME activity is Jasmonate dependent and plant derived.

PRESENTATION ABSTRACTS

Mandy Waters
Research Assistant, Springer Lab, Plant Biology
High Levels of Conservation of Imprinting in Maize

Imprinting, the biased expression of alleles based on their parent of origin, is an epigenetic phenomena that likely plays an important role in seed development. The recent availability of RNA-seq provides an opportunity to study gene and allele specific expression rates. We collected allele specific expression data from 5 pairs of reciprocal hybrids. This allowed for a fairly complete catalogue of maize imprinted genes as well as an assessment of the variation/conservation of imprinting for different alleles. Slightly over 100 paternally expressed genes (PEGs) and nearly 70 maternally expressed genes (MEGs) were identified. There is evidence for functional and mechanistic differences between MEGs and PEGs. A comparison of allele-specific expression levels in multiple genes reveals that the majority of imprinted genes exhibit imprinting in all genotypes examined. However, a small number of imprinted genes exhibit allele-specific imprinting. Further experiments will study the allelic differences that contribute to variation in imprinting.

Branden Epstein
Graduate Student, Advisors: Tiffin and Sadowsky, Plant Biology
Population genomics of the legume symbionts Sinorhizobium meliloti and S. medicae

The facultative mutualism between rhizobial bacteria and legume plants contributes approximately half of all biologically fixed nitrogen, an essential plant nutrient, and is an important source of nitrogen to both natural and agricultural ecosystems. We resequenced the genomes of 44 strains of two closely related species of the genus Sinorhizobium that form facultative mutualisms with the model legme Medicago truncatula. These data provide one of the most complete examinations of genomic diversity segregating within microbial species that are not causative agents of human illness. Our analyses reveal that horizontal gene transfer, a common source of new genes in microbial species, disproportionately affects genes with direct roles in the rhizobia-plant symbiosis. Analyses of nucleotide diversity segregating within each species suggests that strong selection, along with genetic hitchhiking has sharply reduced diversity along an entire chromosome half in S. meliloti. Despite the two species' ecological similarity, we did not find evidence for selection acting on the same genetic targets. In addition to providing insight into the evolutionary history of rhizobial, this study shows the feasibility and potential power of applying population genomic analyses to microbial species.

Stephan Cameron
Graduate Student, Wackett Lab, BTI

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Aunica Kane
Graduate Student, Gralnick Lab, BTI
Getting By With a Little Help From Your Friends: Using Synthetic Ecology to Engineer Bacterial Cooperation

For centuries, microbiologists have primarily studied organisms in pure culture, yet it is becoming increasingly apparent that the majority of biological processes rely on multi-species cooperation and interaction. While little is known about how such interactions permit cooperation, even less is known about how cooperation arises. The goal of my research is to use synthetic ecology to connect metabolic pathways and enable previously non-interacting species to work together. I have engineered co-culture communities ranging from commensalism to obligate mutualism between the Gram-negative bacteria Shewanella oneidensis and Geobacter sulfurreducens. These bacteria were chosen due to their unique electron transfer pathways, which enable them to use insoluble metals and electrodes as terminal electron acceptors—a process with many important applications in biotechnology. Using microbial fuel cells, the ability of Shewanella and Geobacter to pass electrons to their outer surface can be harnessed for electricity production. We are also finding that we can run these reactors in reverse, push electrons back into cells, and power cellular reactions. While both Shewanella and Geobacter have been cultured alone for these applications, we have yet to be able to grow them together. An engineered community enabling cooperative growth allows us to harness the metabolic capabilities of each species while also providing information on pathways required for electron transport.

PRESENTATION ABSTRACTS

Margaret Taylor
Graduate Student, Ward Lab, Plant Biology
Functional Characterization of Amino Acid Permeases in Rice

In plants, the repartitioning of organic nitrogen from mature tissues to developing leaves and seeds is essential for development. The amino acid permeases (AAPs) are a family of integral membrane transport proteins that have been implicated in the long-distance transport of amino acids. First discovered in Arabidopsis, the AAPs are believed to be involved in loading of amino acids into the companion cells of the phloem and to transport amino acids across the apoplasmic barrier that separates developing seeds from the rest of the plant. Monocots have more than twice as many AAPs as Arabidopsis, however, little is known about AAP function in this clade. Using a heterologous expression system, I have evidence of transport function for five AAPs from Oryza sativa. The AAPs have a broad specificity for the proteinogenic amino acids with a moderate affinity.

Yung-Tsi Bolon
Postdoc, Stupar Lab, Agronomy and Plant Genetics
"How resilient is the soybean genome? Insights from fast neutron mutagenesis"

Previously, we described the development of a fast neutron mutant population resource in soybean and identified mutations of interest through phenotypic screening. Here, we consider the resiliency of the soybean genome by examining structural variation in over 150 fast neutron soybean mutants. We seek to map genomic regions with differential susceptibility to structural changes, provide insight to gene essentiality, and contribute to the demarcation of a minimum soybean genome.

Peng Yu
Graduate Student, Cohen Lab, Horticultural Science
"Development of a mass spectrometry based method for identifying novel indole-3-acetic acid conjugates in Arabidopsis"

Auxin has been indicated to be mostly conjugated to other biomolecules in plants. The bulk of the conjugates remain unknown in most species due to lack of proper analytical techniques to characterize them. We report here a mass spectrometry based method for detecting and identifying these unknown IAA conjugates. This work will have implications in understanding auxin biology.

Jonathon Fankhauser
Graduate Student, Travisano Lab, Plant Biology

"Decoding genetic changes in experimentally evolved Saccharomyces cerevisiae"

The transition from unicellular to multicellular life is one of the most important evolutionary innovations in the history of life on earth. Starting with unicellular Saccharomyces cerevisiae, we experimentally evolved simple multicellular strains with specialized cellular behavior and gene regulation. Using RNA-seq and genome sequencing we are able to dissect the genetic mechanism of this evolutionary transition. We have identified alternative evolutionary directions in ten independently evolving lines ranging from large-scale transcriptional changes to convergent genomic variations conferring a selective advantage. The multiple genetic routes to multicellularity suggest that this transition may not be as constrained as previously expected. We also explore constraints on genomic stability, dispensability, and mutation rates in different genetic functional groups. We investigate the molecular evolution of regulatory sequences, identifying the complex phenotypic consequences of differential gene expression and the influence of transcriptional regulation on adaptability. Investigating regulatory dynamics were essential to understanding the rapid adaption to multicellular life. An exciting observation from whole transcriptome analysis is we find that cellular adhesion in our multicellular yeast is not due to flocculation. Indeed, loci associated with flocculation are down-regulated in multiple lines, potentially reducing exploitation by adhesive unicellular competitors. The importance of reduced flocculation is illustrated by evidence of evolution in multiple gene types from cell surface glycoproteins to transcription factors.

Thank you for attending the
7th Annual Microbial and Plant
Genomics Institute Retreat

If you have any further questions regarding
the retreat or MPGI please contact:

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