

5th Annual Retreat



Saturday, April 3, 2010

Mississippi Room

Coffman Memorial Union

Retreat Schedule

8:30 – 9:05: Breakfast and Poster set up (Annex and Mississippi Room)

9:05 – 9:10: Introductory Remarks – Nathan Springer, Director, MPG

9:10 – 9:40: An essential role for *ushA* in processing of extracellular flavin electron shuttles by *Shewanella oneidensis*. Elizabeth Covington, Post Doctoral Associate, Biotechnology Institute

9:40 – 10:10: ARPA-E Project: Photosynthetic and Heterotrophic Microbes Make Fuel Hydrocarbons. Lawrence Wackett, Professor, Biotechnology Institute

10:10 – 10:30: Break (Annex)

10:30 – 11:00: Learning about the cell by breaking it: large-scale analysis of genetic interactions in yeast. Benjamin VanderSluis, Graduate Student, Computer Science and Engineering

11:00 – 11:30: Subspace Differential Coexpression Analysis for the Discovery of Disease-related Dysregulations. Gang Fang, Graduate Student, Computer Science and Engineering

11:30 – Noon: Population genetics on deep coverage sequencing of 30 *Medicago truncatula* inbred lines using Illumina Solexa. Antoine Branca, Post Doctoral Associate, Plant Pathology

Noon – 1:30: Lunch and Poster Session (Mississippi Room)

1:30 – 2:00: Sweet and sour: a scientific and legal look at Roundup Ready® sugar beet. Esther McGinnis, Graduate Student, Horticultural Sciences

2:00 – 2:30: Longitudinal comparison of multidrug resistance-encoding, *IncA/C* plasmids from *Escherichia coli* isolated from dairy cows in the United States. Claudia Fernandez, Graduate Student, Veterinary and Medical Biosciences

2:30 – 2:35: Closing Remarks – Nathan Springer, Director, MPG

An essential role for *ushA* in processing of extracellular flavin electron shuttles by *Shewanella oneidensis*.

Speaker: Elizabeth Covington

The facultative anaerobe *Shewanella oneidensis* can reduce a number of insoluble extracellular metals. Direct adsorption of cells to the metal surface is not necessary, and it has been shown that *S. oneidensis* secretes flavins, including riboflavin and flavin mononucleotide (FMN), into the surrounding medium to act as extracellular electron shuttles. However, the mechanism of flavin secretion by *Shewanella* remains unknown. We have conducted a transposon mutagenesis screen to identify mutants deficient in extracellular flavin production. Deletion of the 5'-nucleotidase gene *ushA* results in accumulation of flavin adenine dinucleotide (FAD) in culture supernatants, with a corresponding decrease in FMN and riboflavin. We find that like riboflavin and FMN, FAD is capable of enhancing iron oxide reduction by *S. oneidensis*. Cellular extracts of *S. oneidensis* convert FAD to FMN in an *ushA*-dependent manner, and cellular fractionation experiments show that UshA activity is enriched in the periplasmic space. UshA allows growth of *S. oneidensis* on adenosine monophosphate (AMP), a product of FAD cleavage, as carbon source. We hypothesize that *S. oneidensis* secretes FAD into the periplasmic space, where it is then hydrolyzed by UshA to liberate FMN that is used for electron shuttling and AMP that is recycled as a carbon source.

ARPA-E Project: Photosynthetic and Heterotrophic Microbes Make Fuel Hydrocarbons

Larry Wackett, Aditya Bhan, Jeffrey Gralnick, Lanny Schmidt, and Marc von Keitz

Speaker: Lawrence Wackett

ARPA-E is a new agency that uses a DARPA-like granting model to fund energy research. The research to be discussed is a collaboration of University of Minnesota Professors and the start-up company Bio-Cee. The research uses *Shewanella* bacteria to make hydrocarbon biofuels. Hydrocarbon biofuels are superior to ethanol, resemble current petroleum-based fuels, and thus can be produced with little change to public infrastructure. We have shown that native *Shewanella* species produce hydrocarbons, are tolerant to hydrocarbons, and can be engineered to produce higher levels of hydrocarbons. The Department of Energy (DOE) has invested heavily in sequencing more than twenty *Shewanella* genomes and carrying out systems biology on these bacteria. That investment is being leveraged. Research is also being conducted to use cyanobacteria to support hydrocarbon production, either singly or in combination with hydrocarbon-producing *Shewanella* species. With Bio-Cee, we are exploring an innovative bio-production methodology using microbes embedded in latex thin-films to allow continuous production and harvesting of hydrocarbon. The biohydrocarbons generated by these methods can be chemically cracked and reformulated using the knowledge obtained from a century of petroleum refining.

Learning about the cell by breaking it: large-scale analysis of genetic interactions in yeast

Speaker: Benjamin VanderSluis

Recent developments in high-throughput technology in model organisms have enabled the unprecedented construction and phenotyping of hundreds of thousands of combinatorial mutants. Such analyses have produced large collections of genetic interactions in yeast, which have proven to be a powerful means of defining gene function, identifying protein complexes, and even ordering linear pathways. However, due to the sheer number of possible mutant combinations, earlier genetic interactions studies were limited in their coverage as they typically measured less than 5% of even the pair-wise interaction network. Thus, we have so far been unable to assess the global structure of the network and several questions remain about the fundamental mechanisms governing genetic interactions.

Based on improvements in the throughput of Synthetic Genetic Array technology, we have compiled the largest genetic interaction network to date based on the construction of more than 5 million double mutant combinations. I will discuss technological obstacles overcome in constructing this network, including normalization and modeling techniques that allowed us to measure reliable, quantitative interactions. I will also describe several striking properties revealed by our mining of this global network, and demonstrate its utility for characterizing both specific pathway-level functions as well as its ability to provide a broader picture of cellular organization. Genome-scale studies of genetic interactions should enable us to understand fundamental properties underlying these relationships in yeast as well as higher organisms. I will discuss our progress in addressing these questions as well as a more specific effort in using genetic interactions to understand the evolution of duplicate genes.

Subspace Differential Coexpression Analysis for the Discovery of Disease-related Dysregulations

Gang Fang, Rui Kuang, Gaurav Pandey, Michael Steinbach, Chad L. Myers and Vipin Kumar. Proceedings of the 15th Pacific Symposium on Biocomputing, 15:145-156, Jan 2010.

Speaker: Gang Fang

In this paper, we study methods to identify differential coexpression patterns in case-control gene expression data. A differential coexpression pattern consists of a set of genes that have substantially different levels of coherence of their expression profiles across the two sample-classes, i.e., highly coherent in one class, but not in the other. Biologically, a differential coexpression patterns may indicate the disruption of a regulatory mechanism possibly caused by dysregulation of pathways or mutations of transcription factors. A common feature of all the existing approaches for differential coexpression analysis is that the coexpression of a set of genes is measured on all the samples in each of the two classes, i.e., over the full-space of samples. Hence, these approaches may miss patterns that only cover a subset of samples in each class, i.e., subspace patterns, due to the heterogeneity of the subject population and disease causes. In this paper, we extend differential coexpression analysis by defining a subspace differential coexpression pattern, i.e., a set of genes that are coexpressed in a relatively large percent of samples in one class, but in a much smaller percent of samples in the other class. We propose a general approach based upon association analysis framework that allows exhaustive yet efficient discovery of subspace differential coexpression patterns. This approach can be used to adapt a family of biclustering algorithms to obtain their corresponding differential versions that can directly discover differential coexpression patterns. Using a recently developed biclustering algorithm as illustration, we perform experiments on cancer datasets which demonstrates the existence of subspace differential coexpression patterns. Permutation tests demonstrate the statistical significance for a large number of discovered subspace patterns, many of which can not be discovered if they are measured over all the samples in each of the classes. Interestingly, in our experiments, some discovered subspace patterns have significant overlap with known cancer pathways, and some are enriched with the target gene sets of cancer-related microRNA and transcription factors. The source codes and datasets used in this paper are available at <http://vk.cs.umn.edu/SDC/>.

Population genetics on deep coverage sequencing of 30 *Medicago truncatula* inbred lines using Illumina Solexa

Antoine Branca, Tim Paape, Roman Briskine, Peng Zhou, Shelley Wang, Roxanne Denny, Joann Mudge, Gregory D. May, Arvind Bharti, Andrew Farmer, Peter L. Tiffin, Nevin D. Young

Speaker: Antoine Branca

Medicago truncatula is a model legume that is also central to the study of mutualist interactions with *Sinorhizobium* bacteria and the process of biological nitrogen fixation. To explore the genetic basis of this interaction, the *Medicago* HapMap Project initially consists of sequencing the whole-genomes of 30 inbred lines (eventually 384 lines) with deep coverage through an Illuminaâ Solexa sequencing pipeline. In parallel, multiple phenotypes revealing symbiotic success are being measured in greenhouse experiments on the *Medicago* lines. The goal of this study is to discover associations between phenotypic and genotypic variation. Whole-genome resequencing of the 30 lines has been achieved when greenhouse phenotyping is still ongoing. Here we present preliminary results of analysis on whole genome diversity in *M. truncatula* including linkage disequilibrium, heterozygosity and genetic structure.

Sweet and sour: a scientific and legal look at Roundup Ready® sugar beet

Esther E. McGinnis, Mary H. Meyer, and Alan G. Smith

Speaker: Esther McGinnis

The U.S. District Court in San Francisco will soon determine whether Roundup Ready® sugar beet (“RR sugar beet”) may be planted in the United States. In 2005, after preparing a concise Environmental Assessment (“EA”) under the National Environmental Policy Act (“NEPA”), the USDA Animal and Plant Health Inspection Service (“APHIS”) unconditionally approved RR sugar beet for commercial production. In reliance on this decision, U.S. farmers embraced RR sugar beet for its superior weed control and cultivated 95% of U.S. acreage in RR sugar beet by 2009. Center for Food Safety sued APHIS and alleged that it violated NEPA by failing to prepare an Environmental Impact Statement (“EIS”) instead of an EA. In September, 2009, the District Court ruled in the first phase of *Center for Food Safety v. Vilsack* that APHIS violated NEPA, because it failed to evaluate the crop’s impact on the human environment and that it should have prepared a detailed EIS assessing gene flow to related cultivated species like table beet and Swiss chard. In the second phase of this bifurcated decision, the District Court will determine what, if any, restrictions will be placed on the cultivation of RR sugar beet pending APHIS’s preparation of an EIS. A decision on continued use of this technology hinges on several factors, including sugar beet reproductive biology and the Supreme Court. We propose that the District Court should consider the scientific as well as the legal factors of this case and impose sensible geographic restrictions that will preserve coexistence between farming industries.

Longitudinal comparison of multidrug resistance-encoding, IncA/C plasmids from *Escherichia coli* isolated from dairy cows in the United States

C. Fernández-Alarcón¹, T. Johnson¹, J. Anderson¹ and R. Singer^{1, 2} Department of Veterinary and Biomedical Sciences¹, College of Veterinary Medicine, University of Minnesota, St. Paul, Minnesota 55108, ²Instituto de Medicina Preventiva Veterinaria, Facultad de Ciencias Veterinarias, Universidad Austral de Chile, Valdivia, Chile².

Speaker: Claudia Fernandez

IncA/C plasmids have received recent attention for their broad host range and ability to confer resistance to multiple antimicrobial agents. We recently completed the sequences of two animal-source IncA/C plasmids. One of these plasmids was from an *E. coli* isolate from a Chilean cow and the second plasmid was from an *E. coli* isolate from an Illinois cow. These two plasmids, each approximately 150 kb in size, were initially selected because they contained the *floR* and *tetA* genes encoding for florfenicol and tetracycline resistance, because they came from different geographical locations, and because the plasmid from Illinois contained the *cmx-2* gene encoding for extended-spectrum beta-lactam resistance while the Chilean plasmid lacked this gene. Analysis of the completed sequences of these plasmids revealed that, with the exception of the integration “hotspots” on these plasmids, they were virtually identical to one another. We thus expanded the scope of this sequencing effort to test the hypothesis that environmental selection pressures influence the persistence and genetic stability of the IncA/C plasmids within the same Illinois farm system.

Poster Session

Aneuploidy associated with exposure to echinocandin antifungal. Darren Abbey, Graduate Student, Genetics, Cell Biology and Development. PI: Judith Berman.

The role of DNA damage and repair in the UV-B response of etiolated *Arabidopsis thaliana*. Jessica Biever, Graduate Student, Horticultural Sciences. PI: Gary Gardner.

Genetic structure and virulence of the *Cochliobolus miyabeanus* population infection wild rice (*Zizania palustris* L.) in Minnesota. Claudia Castell Miller, Post Doctoral Associate, Plant Pathology. PI: Deborah Samac.

Application of comparative genomics for the identification and monitoring of the highly virulent wheat stem rust fungus *Puccinia graminis*. Jo Anne Crouch, Post Doctoral Associate, Plant Pathology. PI: Les Szabo.

Soybean Dicer-like homoeologous and tandem duplicates exhibit transcriptional subfunctionalisation in response to biotic and abiotic stress. Shaun Curtin, Post Doctoral Associate, Agronomy and Plant Genetics. PI: Robert Stupar.

A scalable algorithm for discovering conserved active subnetworks across species. Raamesh Deshpande, Graduate Student, Computer Science and Engineering. PI: Chad Myers.

A novel biochemical approach to identification of interspecific incompatibility factors in *Nicotiana*. Carrie Eberle, Graduate Student, Horticultural Science. PI: Alan Smith.

Manipulating the intracellular bacterium, *Wolbachia pipientis*, in mosquito cell lines. Ann Fallon, Professor, Entomology.

Microbial hydrocarbon synthesis in the pursuit of potential biofuels. Janice Frias, Graduate Student, Biochemistry, Molecular Biology and Biophysics. PI: Lawrence Wackett.

Improving Biodegradation Pathway Prediction. Junfeng Gao, Graduate Student, Health Informatics. PI: Lynda Ellis/Lawrence Wackett.

Poster Session

Elucidating relationship between genetic interactions and the regulatory networks in yeast. Yungil Kim, Graduate Student, Computer Science and Engineering. PI: Chad Myers

Environmental Regulation of Auxin Metabolism. Xing Liu, Graduate Student, Horticultural Science. PI: Jerry Cohen/Gary Gardner

Transcriptome analysis of a breeding program pedigree reveals target genes for the improvement of malting quality. Maria Muñoz Amatriain, Post Doctoral Associate, Agronomy and Plant Genetics. PI: Gary Muehlbauer

Potential for renewable energy in *Chlamydomonas reinhardtii*. David Nelson, Graduate Student, Plant Biology. PI: Pete Lefebvre

Toward mutagenesis of tandemly repeated genes in *Arabidopsis* using zinc finger nucleases (ZFN's). Yiping Qi, Post Doctoral Associate, Genetics, Cell Biology and Development. PI: Daniel Voytas

In vitro fungal interactions: changes on secondary metabolites and biomass. Alma Rodriguez, Post Doctoral Associate, Ecology Evolution and Behavior. PI: Georgiana May

Microbial Consortia Associated with Long-lived Perennial Plant Species *Andropogon gerardii* and *Lespedeza capitata*: OUT Analysis of Richness, Diversity and Community Structure. Noah Rosenzweig, Post Doctoral Associate, Plant Pathology. PI: James Bradeen

Functional Role of *Bradyrhizobium japonicum* Trehalose Biosynthetic and Metabolic Genes during Physiological Stress and Nodulation. Masayuki Sugawara, Post Doctoral Associate, Soil Water and Climate. PI: Michael J Sadowsky.