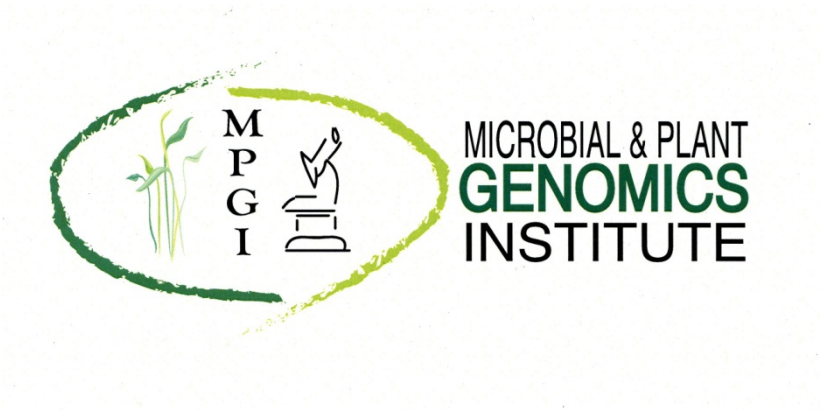
1st Annual Fall Symposium

"Biological Applications of Next-Generation Sequencing"



Thursday, September 2, 2010

Seminar Room 105

Cargill Building for Microbial and Plant Genomics

Symposium Schedule

8:00 – 8:45: Breakfast (Atrium)

8:45 – 9:00: Welcoming Remarks – Nathan Springer, Director, MPGI

9:00 – 9:45: *Exploration of the human microbiome using "omics" approaches.* Janet Jansson. University of California – Berkeley, Ecology Department.

9:45 – 10:30: *Genomic analysis of experimental evolution in yeasts.* Maitreya Dunham. University of Washington, Genome Sciences Department.

10:30 – 11:00: Break (Atrium)

11:00 – 11:20: *Metagenomic platforms for Human and Environmental Health .* Michael J Sadowsky. University of Minnesota, Biotechnology Institute.

11:20 – 11:40: *Co-evolution of symbiotic relationships in Medicago.* Nevin Young. University of Minnesota, Plant Pathology Department.

11:40 – Noon: *Unmasking induced and natural variation in soybean.* Robert Stupar. University of Minnesota, Agronomy and Plant Genetics Department.

Noon – 1:10: Lunch (Atrium)

1:10 – 1:30: *RISS: Developing informatics solutions for research communities*. Anne Françoise-Lamblin. University of Minnesota, Interdisciplinary Informatics.

1:30 – 2:15: *The power of comparative genomics for understanding genome evolution and fungal niche adaptation.* Li-Jun Ma. Broad Institute of Harvard and MIT, Genome Biology Program.

2:15 – 2:35: *High throughput sequencing for analysis of cancer insertional mutagenesis experiments.* David Largaespada. University of Minnesota, Genetics, Cell Biology and Development Department.

2:35 – 3:00: Break (Atrium)

3:00 – 3:45: *Evolution of eukaryotic DNA methylation.* Daniel Zilberman. University of California – Berkeley, Plant and Microbial Biology Department.

3:45 – 4:30: *Transposon evolution and genome scans in maize using next-gen sequence data*. Jeffrey Ross-Ibarra. University of California – Davis, Plant Sciences Department.

4:30 – 4:45: Concluding Remarks – Nathan Springer, Director, MPGI

Jeffrey Ross-Ibarra

Dr. Ross-Ibarra did his undergraduate degree in botany at UC Riverside, and then a M.S. in population genetics and ethonbotany with Norman Ellstrand and Arturo Gomez-Pompa at UC Riverside. He moved to Mexico for a year after that, where he taught botany at the Universidad Nacional Autonoma de Mexico. He moved back to the US to do a PhD with Jim Hamrick at the University of Georgia, where he focused on the genetics of domestication and worked some on tomatillo. He then did a postdoc with Brandon Gaut at UC Irvine, where he worked on population genetics of speciation and local adaptation, and finally moved to UC Davis in January 2009 where he has started a group working on maize domestication and the population genetics of maize and its wild relatives. He currently has funding from USDA to do selection mapping in maize, and from NSF to study centromere evolution in Zea. In addition, he is collaborating with the Maize Diversity Project to work on the population genomics of domestication.

Michael J Sadowsky

Research in my laboratory is directed at several areas of environmental microbiology. One of the major research efforts of my laboratory is directed toward the development of technologies to determine sources of fecal pollution in waterways. Specifically, we are using DNA fingerprinting and other genomic techniques to examine large populations of E. coli bacteria to determine which animal sources are contributing to the fecal loading of critical rural and urban streams, lakes, and rivers. Research efforts in my laboratory are also directed towards the identification and examination of bacterial genes involved in the early periods of legume-microbe symbioses. We are specifically interested in studying Rhizobium and Bradyrhizobium genes which play a prominent role in host/microbe communication and recognition and, those involved in competition among soil microbes in the root zone of soybean an clover plants. Lastly, researchers in my laboratory are involved in the identification and characterization of bacterial genes,- proteins, and metabolic pathways involved in the biodegradation of atrazine and related triazine herbicides. Moreover, we are investigating the use of purified enzymes, and transgenic bacteria and plants, to bioremediate herbicide-contaminated soils and water.

Robert Stupar

My research focuses on soybean molecular genetics. Specifically, my lab is interested in defining the transcriptional variation present in soybean and assessing the relationship

between this transcriptional variation and phenotypic variation. We are also interested in identifying the genetic and epigenetic causes of this variation. Additionally, I am responsible for course instruction in plant molecular biology and chromosome biology.

Nevin Young

My colleagues and I use genomics to understand the genetic organization of legumes, the plant family that includes crops like soybean, pea, and alfalfa. A key starting point toward our goal is sequencing the complete genome of a simple model legume known as Medicago truncatula. With this information, we are working to understand the molecular evolution that has taken place over millions of years and resulted in the modern crops. Of special interest to us are the genes responsible for defending against disease pathogens. These so-called disease resistance genes are an especially interesting and important gene family in plants. Understanding the molecular evolution and genomic organization of plant resistance genes is essential for sustainable use of genetic resistance in agriculture.

Daniel Zilberman

The genetic material of virtually all eukaryotes exists as chromatin. The basic unit of chromatin is a nucleosome, an octameric complex of histones H2A, H2B, H3 and H4, around which about 150 base pairs of DNA are wrapped. Chromatin is a complex and highly dynamic environment. Nucleosomes are differentiated by variants of histones H2A and H3 and by many histone post-translational modifications, chromatin-associated proteins and linker histones. Nucleosomes are positioned both by the underlying DNA sequence and by remodeling enzymes and histone chaperones that can mobilize, disassemble or replace histone subunits. In most eukaryotes, chromatin is also modified by methylation of cytosine bases in DNA. Our goal is to understand how chromatin components interrelate and integrate to regulate transcriptional activity. We combine genetics and biochemistry with genomics and computational analysis to study DNA methylation, deposition of histone variants, chromatin associated proteins and nucleosome remodeling. Our primary model organism is Arabidopsis, which has a compact, gene-rich genome with extensive DNA methylation and numerous viable mutants in key chromatin-related proteins. These features provide an exciting opportunity to analyze chromatin on a genome-wide scale.

Maitreya Dunham

The Dunham Lab combines experimental evolution with genomic analysis to study the structure and function of genetic networks in yeast. Cultures of S. cerevisiae can be maintained for hundreds of generations of nutrient-limited, steady-state growth in chemostats. During this time, more fit mutants appear and sweep through the culture. By comparing the "evolved" strains to the ancestral founders, we can study the adaptations selected in the chemostat. Growth phenotypes, cell morphology, global gene expression, and other parameters all change during the course of chemostat evolution. Genetic dissection of the small number of mutations responsible for these many changes should allow us to recognize the rate limiting steps and control points governing the cells' response to long-term, narrow selection.

Janet Jansson

Professor Jansson received her Ph.D. in Microbial Ecology from Michigan State University. She spent 20 years in J Janssen lab in blue shirts Sweden, starting with her postdoctoral research at Stockholm University. She was a Professor of Microbiology at Södertörn University College and then Professor (Chair) of Environmental Microbiology at the Swedish University of Agricultural Sciences (SLU). She was also Vice Dean of the Faculty for Natural Resources and Agricultural Sciences at SLU. She is currently a Senior Staff Scientist in the Earth Sciences Division and a Chief Editor of The ISME Journal. Her expertise is in the area of molecular microbial ecology and “omics” approaches with a focus on soil, marine sediment and the human gut environments.

Anne-Françoise Lamblin

Dr. Lamblin is formally trained biochemist and molecular biologist with a long interest in the regulation of gene expression and systems approach to biological problems. In 2001 she moved into the field of bioinformatics where she became liaison between the biology and the software engineering and computational biology communities she was working with. In 2004 she became Informatics Lead for the U of MN Cancer Center Bioinformatics Shared Resources and in 2006 joined the National Science Foundation as Program Director in the Division of Biological Infrastructure with affiliation to interdisciplinary informatics programs PGRP, ABI, CDI. In 2009 she returned to the University and joined the Office of the Vice President for Research as Coordinator of the newly established program for Interdisciplinary Informatics (UMII) whose goal is to promote the use of informatics approaches and methodologies. Working with the communities and using her experience, she is developing the Research Informatics Support Systems (RISS) infrastructure program which goal is to provide informatics support to the university research communities. As part of this program and focusing on the life sciences she leads the implementation of the Galaxy analytical framework, an integrated discovery environment to support analysis of high throughput molecular data (genomics, proteomics).

David Largaespada

Dr. Largaespada's laboratory is working to exploit insertional mutagenesis for cancer gene discovery and functional genomics in the mouse. The Largaespada lab is using a vertebrate-active transposon system, called *Sleeping Beauty* (SB), for insertional mutagenesis in mouse somatic and germline cells, and for gene therapy. Using SB they have developed a powerful method to find new cancer genes using transgenic mouse models. This approach can be used to understand the genetic basis of many types of cancer, including brain tumors, carcinomas of the liver and gastrointestinal tract, leukemias, sarcomas, and many more (Collier, Carslon et al., *Nature*, 2005; Dupuy et al., *Nature*, 2005, Keng et al., *Nature Biotechnology*, 2009; Starr et al., *Science*, 2009). Insertional mutagenesis is also being used to identify genes and genetic pathways underlying acute myeloid leukemia (AML) development. Ongoing work includes genetic studies of myeloid leukemia chemotherapy resistance and RAS pathway oncogene addiction.

Li-Jun Ma

Li-Jun Ma is a principle research scientist for the Fungal Genome Initiative (FGI) at the Broad Institute. She is interested in using the rich fungal genomic resources within the scientific community to explore the mechanisms that guide eukaryotic genome evolution. Specifically, Li-Jun is leading several comparative genomics projects to study the genetic determinants of fungal pathogenicity and host specificity, and participating in functional studies to test the hypotheses generated through genomic analyses. Li-Jun earned her Ph.D. in fungal genetics from the College of Environmental Science and Forestry at the State University of New York. After receiving her degree, she completed a postdoctoral fellowship to study protein evolution in Walter Gilbert's laboratory at Harvard University before joining the Broad Institute (then part of the Whitehead Institute/MIT Center for Genome Research).