3rd Annual Fall Symposium

"Systems Biology of Genetic Regulation"

Thursday, August 30, 2012
Seminar Room 105
Cargill Building for Microbial and Plant
Genomics

Symposium Schedule

8:30 – 8:50: Breakfast (Atrium)

8:50 – 9:00: Welcoming Remarks – Nathan Springer. Director, Microbial and Plant Genomics Institute

9:00 – 9:50: *"Gene Regulatory Networks"* Marian Walhout. Molecular Medicine Department. University of Massachusetts Medical School.

9:50 – 10:20: *"Improving Methodology for Plant Metabolomics"* Adrian Hegeman. Horticultural Sciences Department. University of Minnesota.

10:20 – 10:50: Break (Atrium)

10:50 – 11:20: "MicroRNAs: A Multifaceted Regulator in Cancer" Subbaya Subramanian. Surgery Department. University of Minnesota.

11:20 – 12:10: *"Using computer models to learn how cells talk to each other"* Vijay Chickarmane. Biology Department. California Institute of Technology.

12:10 – 1:00: Lunch (Atrium)

Symposium Schedule

1:00 – 1:50: *"The genetics of individuals: why do mutations kill some individuals but not others?"* Benjamin Lehner. Genetic Systems Division. Centre for Genomic Regulation.

1:50 – 2:20: *"Properties, structure, and dynamics of the plant immune signaling network"* Fumiaki Katagiri. Plant Biology Department. University of Minnesota.

2:20 – 2:40: Break (Atrium)

2:40 – 3:10: *"The Use of Microbial Transplantation and Metagenomics to Understand the Dynamics of Gut Microbiota In Disease and Health"* Mike Sadowsky. Soil, Water and Climate Department. University of Minnesota.

3:10 – 4:00: *"Systematic identification of gene function from genome-wide molecular networks in plants"* Sue Rhee. Biology Department. Carnegie Institute for Science.

4:00 – 4:05: Concluding Remarks – Fumiaki Katagiri and Chad Myers

Vijay Chickarmane

I am interested in applying quantitative methods to understanding biological processes in plants and animals. These methods use non-linear dynamics, stochastic processes, optimization and data analysis to model signaling and genetic networks, growth and proliferation of multicellular tissues. Some of the current topics I am pursuing are: 1) Computational approaches to studying plant development. Development of mathematical models and validation based on confocal microscopy and gene expression data to study: Perception of hormones (cytokinin) by plant two-component signaling networks, Homeostasis of stem cell numbers in the shoot apical meristem, Regeneration of shoots/roots due to relative hormonal levels (auxin/cytokinin), Patterning of giant cells in the sepal due to endo-reduplication (multiple copies of DNA). 2) Transcriptional dynamics of hematopoietic and embryonic stem cells. Development of mathematical models based upon ChIP-chip and microarray data to understand the transcriptional dynamics of stem cells, with a view to understanding stem cell commitment, and how differentiated cells are re-programmed to become stem cells. Understanding the role of stochastic fluctuations in stem cell lineage determination.

Adrian Hegeman

My laboratory uses high throughput chemical analysis to measure hundreds to thousands of compounds simultaneously in plant extracts. Conceptually, we attempt to make as many simultaneous unbiased measurements as is possible to allow analysis of metabolism in an entire biological system. This methodology, called metabolomics is related to other systems biology approaches such as genomics and proteomics, which also attempt to provide comprehensive descriptions of the molecular status of a biological system as an initial step prior to formulation of hypotheses and more traditional lines of scientific inquiry. The approach essentially looks at a biological system with new eyes provided by state of the art analytical technologies to create an image of a life processes that were not previously observable. We are interested in utilizing metabolomics to understand the means and regulation of production of secondary metabolites as a critical first step in finding out how an organism responds to its environment. We have started our analysis of secondary metabolism in Arabidopsis thaliana because, from a molecular perspective, it is the best characterized plant systems.

Fumiaki Katagiri

A major type of plant defense against pathogen is inducible defense: i.e., defense mechanisms are turned on upon recognition of pathogen attack. Research in my group is directed towards understanding (1) how plants recognize pathogen attack and (2) how this recognition leads to induction of coordinated responses in plants. We use Arabidopsis thaliana and its bacterial pathogen Pseudomonas syringae as a model to study these problems. We are interested in a network of molecules that enables inducible defense: how are the components and connections of the network organized?; how is the behavior of the network controlled? Pattern-triggered immunity (PTI) and effector-triggered immunity (ETI) are two well defined modes of inducible defense. PTI is initiated by recognition of molecular patterns common among related microbes (microbe-associated molecular patterns, MAMPs) by pattern recognition receptors (PRRs). It is necessary for a potential pathogen to negate PTI sufficiently to be a real pathogen. For this purpose, real pathogens deliver effectors into the plant cell that interfere with PTI signaling. Plants may have receptors, resistance (R) proteins, which recognize some of the pathogen effectors and trigger ETI. The plant immune signaling network that controls inducible defense is different from other plant signaling networks because pathogens not only initiate signaling events but also interfere with plant signaling. Microbial pathogens also evolve much faster than plants. Therefore, the plant immune signaling network must have properties that allow it to withstand perturbations from a wide variety of pathogens without heavily relying on evolutionary adaptation. Unnecessary immune responses carry negative impacts on plant fitness, further constraining possible network properties.

Benjamin Lehner

We use experiments and computational analysis to understand the principles and evolution of genetic systems, with a particular focus on the biology of individuals. Our recent work has focussed on understanding and globally predicting how mutations map to phenotypic changes, how mutations combine to cause disease, the evolution and importance of genetic redundancy, the evolution of regulatory networks and tissue-specific biology, and the interplay between noise, plasticity and evolutionary potential.

Sue Rhee

Our group is interested in how plants respond and adapt to environmental challenges such as drought. We are tackling this problem by building biological networks from large-scale data and computational modeling and testing the models using molecular genetic approaches at the bench. Current research in my group focuses on characterizing novel regulators of drought sensing and root architecture, analyzing genome-wide gene-association networks and building metabolic and membrane protein-protein interaction networks. We focus on the model plant Arabidopsis thaliana for most of our work, though we are expanding our efforts to building metabolic network of other plants.

Mike Sadowsky

One of the major research efforts of my laboratory is directed towards the identification and characterization of bacterial genes and metabolic pathways involved in the biodegradation of chlorinated herbicides. My laboratory (in collaboration with Dr. Larry Wackett, Department of Biochemistry Biophysics, and Molecular Biology) is using recombinant DNA methodologies to examine the genes and enzymes involved in the mineralization of the broadleaf herbicide atrazine by a Pseudomonas sp. strain. We have cloned and sequenced the first three genes in the atrazine biodegradation pathway; and isolated, purified, and characterized the first two proteins involved in the dechlorination of atrazine. Using PCR, combinatorial DNA methodologies, and other recombinant DNA techniques, we are examining the ecology of atrazine-degrading microorganisms in soil, examining the evolution of the atrazine chlorohydrolase gene, and investigating the role that plasmid gene transfer and catabolic transposons play in the dissemination of atrazine degradation genes in soil microbial communities. Moreover, we are investigating the use of purified enzymes, and transgenic bacteria and plants, to bioremediate atrazine-contaminated soils and water.

Subbaya Subramanian

Our laboratory is basically interested in understanding the microRNA (miRNA) mediated gene regulatory networks in sarcoma and other cancer types. We explore miRNA-mRNA associations that have potential role in tumor onset, progression, and aggressiveness through miRNA and mRNA profiling as well as functional characterization of candidate miRNAs using in vitro and in vivo approaches. This will aid in the identification and development of novel miRNA-based biomarkers and targets for therapy. Our laboratory also is interested in engineering miRNA dysregulation in vivo and developing assays for screening small molecule inhibitors that can potentially modulate miRNA expression.

Marian Walhout

We use a variety of experimental and computational systems biology approaches to map and characterize gene regulatory networks and to understand how regulatory circuitry controls animal development, function, and homeostasis. Ultimately, we aim to understand how dysfunctional networks affect or cause diseases like diabetes, obesity and cancer.