2nd Annual Fall Symposium

"Beyond the reference: Population genomics"

Thursday, September 1, 2011

Seminar Room 105

Cargill Building for Microbial and Plant Genomics

Symposium Schedule

8:00 – 8:50: Breakfast (Atrium)

8:50 – 9:00: Welcoming Remarks – Nathan Springer, Director, MPGI

9:00 – 9:45: "*The molecular diversity of adaptive convergence to high temperature in 115 Escherichia coli populations".* Brandon Gaut. University of California – Irvine. Ecology and Evolutionary Biology Department

9:45 – 10:15: "*A New Platform to Identify Utilized Coding Sequences".* Igor Libourel. University of Minnesota-Twin Cities. Plant Biology Department

10:15 – 10:45: Break (Atrium)

10:45– 11:30: "*Population genomics of yeast".* Justin Fay Washington University School of Medicine. Genetics Department

11:30 – Noon: "*High throughput SNP typing in a deeply sampled local mosquito population: An exploration of the variability in susceptibility to malaria infection".* Michelle Riehle. University of Minnesota-Twin Cities. Microbiology Department

Noon – 1:00: Lunch (Atrium)

1:00 – 1:30: "*Population-based approaches identify loci under selection for diverse phenotypes in the domestic horses"*. Molly McCue. University of Minnesota - Twin Cities. Veterinary Population Medicine Department

1:30 – 2:15: "*The role of genetic diversity, recombination, and genome structure in trait expression and heterosis in maize".* Michael McMullen. University of Missouri. Division of Plant Sciences

2:15 – 2:45: "*Genome content variation among maize individuals".* Nathan Springer. University of Minnesota - Twin Cities. Plant Biology Department

2:45 – 3:00: Break (Atrium)

3:00 – 3:45: "*Population-wide Epiallelic Variation in Arabidopsis thaliana".* Bob Schmitz. Salk Institute of Biological Sciences. Plant Molecular and Cellular Biology Laboratory

3:45 – 4:15: "*Genotype-phenotype mapping in the model legume Medicago truncatula"*. Peter Tiffin. University of Minnesota - Twin Cities. Plant Biology Department

4:15 – 4:30: Concluding Remarks – Nathan Springer, Director, MPGI

Bob Schmitz

Bob Schmitz earned his B.Sc. in Molecular & Cellular Biology from the University of Arizona and his Ph.D. in Genetics from the University of Wisconsin-Madison. During his graduate training he studied an environmentally-induced epigenetic switch known as vernalization in Dr. Richard Amasino's Laboratory. Bob joined Dr. Joseph Ecker's Laboratory in August of 2008 and is currently leading the Ecker lab's contribution to the Arabidopsis 1,001 (epi)genomes project which includes genome, DNA methylome and trancriptome sequencing of ~200 Arabidopsis thaliana strains isolated from diverse geographical locations throughout the Northern Hemisphere.

Nathan Springer

My research group studies genetic and epigenetic variation in maize. A combination of technologies are used to follow variation in genome structure, gene expression and chromatin modifications in different inbred lines of maize. We are interested in understanding how structural genomic variation (CNV/PAV) and epigenetic variation contributes to phenotypic variation. There is substantial interest in understanding epigenetics but we still have little knowledge of the overall importance of epigenetic variation. Our studies have also examined how domestication has shaped the maize genome and transcriptome.

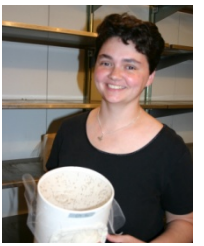
Peter Tiffin

Research in my lab is focused on understanding how biological interactions and environmental change affect plant evolution. We use a variety of organisms (including Zea , Clarkia , Arabidopsis , Medicago and Sinorhizobium) and a variety of molecular and organismal approaches (including molecular population genetics, greenhouse and field studies, and quantitative genetics). I am involved currently in a variety of projects investigating i) the molecular evolution of plant immune system genes, ii) evolutionary responses to elevated CO 2 concentrations and other environmental changes, and iii) the ecological and evolutionary limits to species range expansion. I also remain interested in understanding the ecology and evolution of plant resistance and tolerance to herbivores and pathogens.

Michael McMullen

Michael McMullen is a research geneticist with the USDA-ARS. His research is focused on understanding the genetic, biological and molecular basis of agronomic traits in maize, particularly host plants response to pathogens and pests. The approach uses molecular markers to characterize the genetic basis of plant response. The eventual goal is to isolate genes controlling resistance to major maize pathogens/pests to allow direct manipulation of varietal response. Additional research projects involve development of molecular genetic resources (molecular probes, genetic maps, and mutants) for maize.

Michelle Riehle



We study the transmission of malaria by the mosquito vector. Malaria, caused by protozoan parasites of the genus Plasmodium, is one of the major global infectious diseases. More than 40% of the world population is at risk. Approximately 2 million children die from malaria per year and hundreds of millions of others are sickened by the disease. In addition to the human cost, the economic impact of malaria is also enormous. It is estimated that malaria alone reduces African economic productivity by at least 10%, and thus constitutes a major drag on economic development. Using new genomic research tools, it is now possible to directly query natural populations of mosquitoes and parasites in order to identify mechanisms of vector resistance and immunity against malaria parasites. Our research program bridges the field and laboratory by screening natural vector and parasite populations in Africa to identify genetic mechanisms that can be extracted to the laboratory for genomic, genetic and cellular studies aimed towards developing a new generation of malaria control approaches. Genetic approaches and technologies we use presently or hope to capitalize on in the near future include family based linkage studies, whole genome and targeted association studies, high density SNP arrays and whole genome sequencing.

Justin Fay

Identifying the molecular basis of complex traits is a major challenge to understanding phenotypic variation present in natural populations,

including adaptations and human diseases. A longstanding hypothesis is that changes in gene regulation contribute as much or even more than changes in protein structure. While both population genetics and quantitative genetics approaches have been developed, both have had been biased towards the analysis of protein coding sequences. Recently, comparative genomics studies have shown that there are just as many functionally conserved noncoding as coding sequences, implying that many functional changes in gene regulation have yet to be discovered. The overall goal of our research program is to combine genome technologies with computational methods to investigate changes in gene regulation and their contribution to adaptation and disease. Leveraging the power of yeast genetics, we hope to generate and refine both methods and models for use in humans and other organisms.

Brandon Gaut

We are ultimately interested in inferring the balance of forces that contribute to evolutionary change. Historically the lab has focused on the evolutionary genetics and comparative genomics of plant systems, including the genetics of domestication. Recently we have also been studying the evolution of transposable elements and experimental evolution of E. coli. We take a multifaceted approach to study these problems, using the tools of genetics, population genetics, molecular evolution and bioinformatics. With collaborators at UCI, we have evolved 120 lines of E. coli under high temperature (42 C). We are currently investigating the genetic and mechanistic underpinnings of adaptation to this stressful environment. A key feature of our experiment is its size; the number of evolved lines is an order of magnitude higher than previous experiments. As a result we can ask questions about parallel pathways to adaptation and the number of genetic solutions to the high temperature challenge.

Igor Libourel

Marine microalgae account for half of the earth's photosynthetic activity, and are exposed to environmental changes brought about by global warming. Climate change will affect the marine habitat and alter prevailing selective pressures. Consequently, algae will evolve to adapt to the new conditions. Evolved strains may interact with their surroundings differently, which is relevant to the global environment given their great abundance. Presumably, natural selection optimizes central metabolism to provide metabolic building blocks at the highest possible cost efficiency. Due to strong peer selection, this optimality assumption appears especially apt for organisms such as marine algae. Our research is focused on discovering the design principles of this core metabolism. The picoalgae Ostreococcus is a prevalent genus in the world's oceans and is used in our lab as a model system. We study the metabolic features of Ostreococcus, and investigate the relationship between metabolic adaptation and the environment.

Molly McCue

Our research group uses is to use the latest molecular genetics and genomics tools to study complex genetic disease, physiological variation and genetic diversity in equine populations. Our goals are to improve equine health through the understanding of complex genetic disease, allowing veterinarians to better predict, diagnose, and treat genetic disease, and to improve human health through the use of the horse as a biomedical model. We are working on a variety of diseases in horses including Equine Metabolic Syndrome, Polysaccharide Storage Myopathy, Recurrent Exertional Rhabdodyolysis, and melanoma susceptibility. We are also studying equine genetic diversity and the impact of selective breeding practices on equine health and disease susceptibility.