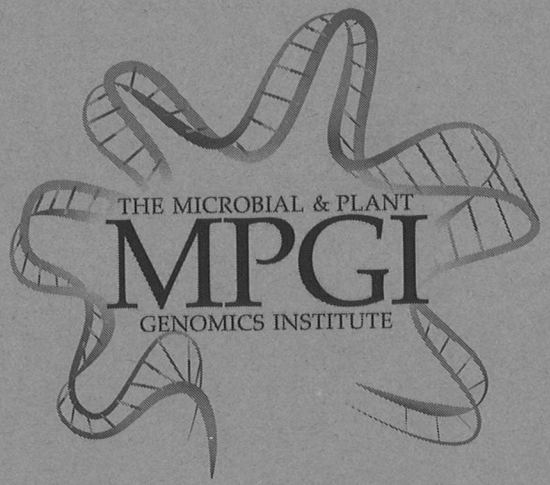


Annual Retreat

January 10th, 2018
Cargill Room 105

Schedule of Events

9:00 - 9:30	Light breakfast - Cargill Atrium
9:30 - 9:40	Opening Remarks
9:40 - 10:00	Carla Rosenfeld, Earth Sciences "Fungal community ecology of seleniferous reclaimed mine soils"
10:00 - 10:20	Jean-Michel Michno, Agronomy and Plant Genetics "Understanding the effects of transformation and CRISPR/Cas9 on the soybean genome"
10:20 - 10:40	Andres Gomez, Animal Science "Meta-OMIC reconstruction of the primate gut: understanding the human microbiome"
10:40 - 11:00	Nu Wang, Plant and Microbial Biology "High- and low-affinity ammonium transporters in *Marchantia polymorpha*"
11:00 - 11:20	Break
11:20 - 11:40	Allison Haaning, Plant and Microbial Biology "Branching out to gain a wider perspective of tiller development in barley"
11:40 - 12:00	Rodrigo Olarte, Plant and Microbial Biology "The impact of genome rearrangement on secondary metabolite diversity in the fungus *Tolypocladium inflatum*"
12:00 - 12:20	Maciej Maselko, Biochemistry, Molecular Biology and Biophysics "Engineering speciation: prospects for agricultural applications"
12:20 - 12:40	Fernanda Jimenez, Biochemistry, Molecular Biology and Biophysics "The omic landscape of respiring soluble vs. solid substrates"
12:40 - 1:50	Lunch, Cargill Atrium
1:50 - 2:10	Kathryn Fixen, Plant and Microbial Biology "'Fix'ing to make fuel: understanding electron transfer to nitrogenase"
2:10 - 2:30	Alex Brohammer, Agronomy and Plant Genetics "Harnessing genomics to exploit maize genetic diversity for crop improvement"
2:30 - 3:00	Kevin Smith, Agronomy and Plant Genetics "Genomes to growlers: the barley research feedback loop"
3:00 - 3:10	Closing Remarks
3:10	Reception - Cargill Atrium

Carla Rosenfeld
Research Associate, Santelli Lab
Earth Sciences, BioTechnology Institute
MPGI Travel Award recipient

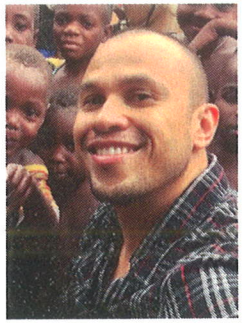
Fungal community ecology of seleniferous reclaimed mine soils

Worldwide, selenium (Se) is proving to be a significant environmental concern, with many anthropogenic activities releasing potentially hazardous concentrations into soil and natural water ecosystems. In southeastern Idaho, historic and on-going phosphate mining has resulted in Se-enriched soils throughout the region. Such metal(loid) contaminated environments have been shown to have altered soil microbial community structures, though few studies have explicitly included fungi. The goal of this study was to investigate the fungal community in Se-containing surface soils, and the potential role these communities play in mediating Se geochemistry in the area.

Jean-Michel Michno
Graduate Student, Stupar Lab, Myers Lab
Agronomy and Plant Genetics

Understanding the effects of transformation and CRISPR/Cas9 on the soybean genome

Recent advances in CRISPR/Cas9 technologies have drawn considerable interest in altering DNA sequences for crop improvement. However, the mutations that can result from these technologies, including the relative frequency of on-target sequence alterations compared to off-target sequence alterations, have not been well characterized. To address this question, we performed genome-wide resequencing of CRISPR/Cas9 soybean lines to identify SNPs, insertion-deletions, and structural variants unique to each respective line. This talk will highlight recent findings from this work, including the mutation rates of CRISPR/Cas9 plants compared to various control treatments, and the developmental timing of editing events. We will also highlight possible sources that could contribute to the appearance of off-target mutations, including natural de novo mutation processes, tissue culture, transformation, and the activity of the CRISPR/Cas9.



Andres Gomez
Assistant Professor
Animal Science

Meta-OMIC reconstruction of the primate gut: understanding the human microbiome

Gut microbiome composition patterns across members of the primate order have been shown to be largely species-specific, which has lead us to hypothesize that host phylogenetic background is the main driving force of the primate gut microbiome. However, evidence also shows that the gut microbiome of primates, including humans, is extremely plastic in response to environmental and dietary change, suggesting that host phylogeny may only exert partial control. Here, I show that the species-specific patterns characterizing the gut microbiome of primates significantly correspond with their gut metabolomic profiles, and hence with particular dietary behaviors characterizing each host species. Further, following evolutionary trends and concordant with a diet-driven speciation hypothesis, humans in industrialized and agricultural societies seem to have lost specific microbe-metabolite features present in wild primates and contemporary hunter-gatherers, in favor of a gut micro-ecology likely capable of increased energy harvest. Meta-genomic reconstruction of these lost microbe features, along with meta-transcriptomic analyses of the host gut regulation landscape further showed how diet, host genes, and gut microbes converge to shape primate phenotypes, including current configurations of the human microbiome.

Nu Wang
Graduate Student, Ward Lab
Plant and Microbial Biology
MPGI Travel Award recipient

High- and low-affinity ammonium transporters in *Marchantia polymorpha*

Nitrogen (N) is a plant macronutrient and N deficiency often limits growth in natural and agricultural environments. In plants, ammonium transporters (AMTs) play an essential role in taking up ammonium from the soil. There are two families of AMTs in plants, AMT1 transporters are electrogenic, they transport a charge across the membrane, while AMT2 transporters are electroneutral.

To date, most of what we know about ammonium transporters in plants comes from the study of AMTs in angiosperms.
The liverwort *Marchantia polymorpha* has been used as a model organism that represents the earliest land plants. *M. polymorpha* has 19 ammonium transporter genes, nine AMT1 and ten AMT2 genes. The AMT1 and AMT2 transporters form distinct clades. Detailed characterization of ammonium transporters from *M. polymorpha* provides more information for structure/function analysis in this family and studying the evolution of ammonium transporters in plants.

Our initial studies focused on MpAMT1;2 and MpAMT1;5 from *M. polymorpha*, we analyzed transport activity using electrophysiology (Two Electrode Voltage Clamping), studied gene expression with different N sources and determined sub-cellular membrane localization of the transporter proteins. We are now investigating potential regulation of AMTs mediated by CIPKs and CBLs in *M. polymorpha*.

Allison Haaning
Graduate Student, Muehlbauer Lab
Plant and Microbial Biology
MPGI Travel Award recipient

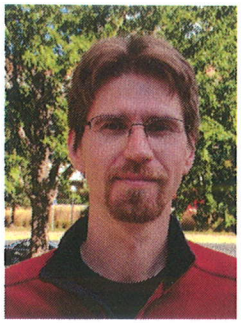
Branching out to gain a wider perspective of tiller development in barley

Tillers are modified lateral branches that develop near the base of the plant in barley. Shoot architecture of barley is largely defined by the number and vigor of tillers, and the majority of grain harvested comes from tillers. The main goal of this work was to identify primary sources of variation that impact tiller number and rate of development, which are not well characterized, especially under field conditions. Genetically diverse lines, split equally between two- and six-row spike morphology, were genotyped by GBS and 50K SNP array and grown in the field in 2014, 2015, and 2016; and data for the following traits was collected: tiller number from two to seven weeks past-emergence, productive tiller number, plant height, days to heading, seeds per spike, fifty seed weight, stem diameter, and leaf width. Tiller number and rate of development were highly variable between years and lines, and phenotypic modeling and correlations suggest that these differences are primarily influenced by environment, flowering time, and spike morphology. Results of association mapping suggest the same, as very few QTL associated with tiller number or rate of development were detected in both years while nearly half were also associated with flowering time or spike morphology.

Rodrigo Olarte
Postdoctoral Associate, Bushley Lab
Plant and Microbial Biology
MPGI Travel Award recipient

The impact of genome rearrangement on secondary metabolite diversity in the fungus *Tolypocladium inflatum*

Secondary metabolites in fungi are among the most rapidly evolving gene families in fungi and contribute to important intraspecific phenotypic differences. While genetic mechanisms such as recombination, transposition, gene-conversion, and horizontal gene transfer are often discussed as forces generating diversity in secondary metabolism, few studies have examined these mechanisms in detail at the population scale. We sequenced six isolates of the cyclosporin producing fungus *Tolypocladium inflatum* using PacBio next generation sequencing technology to generate near chromosomal level assemblies of all strains in order to address the role of genome rearrangement in generating intraspecific diversity of secondary metabolite genes and clusters. We discover that genetic processes involved in chromosomal rearrangement such as translocations, recombination in subtelomeric regions, inversions, and microdeletions all contribute to the evolution of secondary metabolite biosynthetic clusters in *Tolypocladium*. Our results support previous claims that higher rates of rearrangement and transposition in clusters located in subtelomeric regions on the ends of chromosomes contributes substantially to their rapid evolution and intraspecific diversification. In particular, we find evidence for a cryptic aflatoxin-like cluster closely related to the aflatoxin cluster in *Aspergillus* species that is present in only a few isolates. This research illuminates fine-scale evolutionary genetic mechanisms that contribute to diversification of fungal secondary metabolite clusters.



Maciej Maselko
Research Associate, Smanski Lab
Biochemistry, Molecular Biology and Biophysics

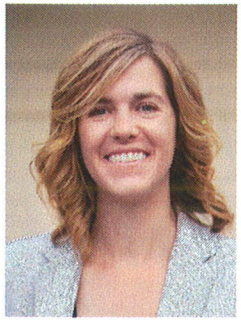
Engineering speciation: prospects for agricultural applications

We present data that demonstrate the feasibility of Synthetic Incompatibility (SI); a method of engineering species-like barriers in sexually reproducing organisms. SI utilizes genome editing to introduce a silent mutation in a conserved region of a promoter followed by the expression of programmable transcriptional activator targeted to the non-edited sequence. Hybridization between an edited organism expressing the programmable transcriptional activator and an organism with a non-edited promoter results in lethal overexpression caused by transcriptional activation of the non-edited promoter. Agricultural applications include preventing transgene flow from engineered crops which may enable the use of herbicide resistant traits in plants with closely related weeds, large scale production of crops engineered to make high-value compounds, and the genetic biocontrol of insect pests. Results from proof of principle experiments in *Saccharomyces cerevisiae* and *Drosophila melanogaster* will be presented.

Fernanda Jimenez
Graduate Student, Bond Lab
Biochemistry, Molecular Biology and Biophysics

The omic landscape of respiring soluble vs. solid substrates

A large portion of soil and aquatic microbiomes contains organisms that use sulfur, nitrogen, or metals as respiratory substrates with slower growth rate and specialized metabolic strategies compared to heterotrophs. Transcriptomic analyses are commonly used to determine pathways that these hard to culture microbes use to grow in their environment. While being valuable sets of data, the conclusions drawn from such transcriptional analyses are based on characteristics of metabolically versatile, fast-growing bacteria. For example, highly expressed loci are assumed to be important for growth, and large changes in expression are assumed to result from changes in conditions. Here, we present the case of a soil -proteobacterium specialized for growth using extracellular metals as electron acceptors with a remarkably stable transcriptome. Pathways discovered through saturated transposon mutagenesis and genetic deletions to be required for growth using different extracellular electron acceptors did not show differential expression or protein abundance when their respective substrates were present/absent. In addition, these pathways demonstrated relatively low expression levels across different conditions. We propose these are characteristics of the fast response time required to respire highly variable substrates such as metal oxides for which a response within a transcriptional time frame may not be competitive, and a continuous expression level adapted to avoid additional burden. Our results indicate conclusions about microbial activity from environmental transcriptomic analyses might miss pathways with important roles due to low and unchanging expression.



Kathryn Fixen
Assistant Professor
Plant and Microbial Biology

"Fix"ing to make fuel: understanding electron transfer to nitrogenase

Nitrogenase is a highly conserved enzyme that catalyzes the reduction of nitrogen gas to ammonia and the reduction of protons to hydrogen. This requires a large input of energy in the form of ATP and a source of low potential electrons. Nitrogenase has been studied in detail in vitro, where it is usually supplied with an artificial source of low potential electrons. This begs the question of what the natural source of reductant is inside a cell. Although it is known that reduced ferredoxins and flavodoxins can serve this function, nitrogen-fixing bacteria generally encode multiple homologs of these proteins and it is unclear if there is specificity to their role in supplying reductant to nitrogenase. I will present evidence that a conserved electron transfer pathway to nitrogenase involves a specific ferredoxin as the preferred electron donor to nitrogenase in the purple nonsulfur bacterium, Rhodopseudomonas palustris. I will also show that this bacterium can also uses a flavodoxin as an alternative electron donor when it is iron-limited. This suggests that there is specificity for which ferredoxin and flavodoxin are involved in donating electrons to nitrogenase. Understanding this specificity would allow for rational engineering of electron transfer pathways used in synthetic biology and may open the door to re-routing metabolism to direct electron flow to nitrogenase for maximal activity of this enzyme.

Alex Brohammer
Graduate Student, Hirsch Lab
Agronomy and Plant Genetics

Harnessing genomics to exploit maize genetic diversity for crop improvement

The question of how natural variation can best be utilized for crop improvement is a central interest of scientists and plant breeders. Exploring the mechanisms that create variation in a genome to better understand how different sources of variation contribute to phenotypic diversity is one way in which such variation can be harnessed. A strategy that utilizes multiple reference genome assemblies together with extensive genotypic data in both inter- and intraspecific comparisons of maize and ancestral species to uncover the role of differential fractionation in maize gene content variation will be presented.

Kevin Smith
Professor
Agronomy and Plant Genetics

Genomes to growlers: the barley research feedback loop

For decades, the barley research community has been nourished by malted beverages produced from barley. Barley researchers were some of the early pioneers in genetic linkage mapping, QTL discovery, and marker-assisted breeding. Genetics and breeding research was aimed at agronomic traits, disease resistance, and malting quality. With the recent rise in the craft brewing industry, new research aims to understand the role of barley varieties in the flavor of beer. One direction that our lab has taken is to explore the development of winter barley (planted in the fall) for Minnesota and the Upper Midwest. As one of the "Forever Green" crops, winter barley deployed as a cash cover crop could deliver ecosystem services that reduce water use and preserve water quality. Craft brewers are widely distributed across the U.S. and are interested in locally produced barley as ingredients for their beer. The barley research community has proposed a national project that links genetics and breeding to develop winter barley varieties that can be deployed in regions with local demand from brewers, preserve and protect water in critical watersheds, diversify cropping systems, and support farming communities.

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