MPGI 9th Annual Retreat

Thursday, May 21st, 2015 | 9 AM - 3 PM

Seminar Rm 105, Cargill Building, St. Paul

About the Retreat

Gerit Bethke
Retreat Co-Host
Research Associate
Glazebrook Lab
Plant Biology

Anke Reinders
Retreat Co-Host
Sr. Research Associate
Ward Lab
Plant Biology

The mission of the Microbial and Plant Genomics Institute (MPGI) is to promote advances in microbial and plant genomics, genomics-enabled science, and molecular genetics for the benefit of society. The Institute will accomplish this through research, educational and outreach activities that foster a multi-disciplinary interchange of ideas and cutting-edge technologies and their applications. Activities of the Institute will contribute to basic science and the translation of genomics for applications to the environment, agriculture, and human health.

The function of the annual retreat is two-fold:

1. To recognize the annual scholarly achievements of MPGI member labs, and

2. To share research presentations delivered by travel grant recipients over the previous calendar year

Travel Grants

Graduate students and postdoctoral scientists who work in laboratories belonging to MPGI faculty members are eligible to apply for funds to help support travel to professional meetings, scientific laboratories, or workshops to learn new techniques, or for the collection of biological materials.

The next travel grant deadline is June 15th, 2015 for travel July 1st to December 31st, 2015.

Please visit the following for further information:
https://www.cbs.umn.edu/explore/departments/mpgi/opportunities/travel-grants

Retreat Schedule

9:00 - 9:30 Breakfast

9:30 - 9:40 Introductory Remarks

9:40 - 10:00 Emilie Snell-Rood
Assistant Professor
Variability in gene expression as a mechanism of developmental plasticity

10:00 - 10:20 Jonathan Clayton
DVM/PhD Dual Degree Candidate, Advisor: Timothy Johnson
MPGI Travel Grant Awardee
Similar trends in microbiome shift between captive primates and westernized humans

10:20 - 10:40 Justin Anderson
PhD Candidate, Advisor: Robert Stupar
MPGI Travel Grant Awardee
Comparison of genomic structural variation associated with cultivars, mutagenized, and transgenic soybean plants

10:40 - 11:10 Break

11:10 - 11:30 Suzanne McGaugh
Assistant Professor
The cavefish genome reveals candidate genes for eye loss

11:30 - 11:50 Maureen Quin
Research Associate, Advisor: Claudia Schmidt Dannert
Mapping sesquiterpenoid biosynthetic pathways in fungi

11:50 - 12:10 Tomas Cermak
Postdoctoral Associate, Advisor: Dan Voytas
MPGI Travel Grant Awardee
Targeting plant genes using geminiviruses: efficient and precise modification of the tomato genome

12:10 - 12:30 Scott Simpkins
Graduate Student, Advisor: Chad Myers
MPGI Travel Grant Awardee
Systematic functional annotation of compound libraries using high-throughput yeast chemical genomics

Retreat Schedule

12:30 - 1:45 Lunch

1:45 - 2:00 David Baumler - Musical Performance
Assistant Professor, Winner, Roche Life Sciences qPCR award

2:00 - 2:20 MSI

James Wilgenbusch
Associate Director, Minnesota Supercomputing Institute

Joshua Baller
Scientific and Operational Lead, RISS & Supercomputing Institute

MSI: Building communities of science surrounding cutting edge research areas

2:20 - 2:40 Vai Lor
Graduate Student, Advisor: Neil Olszewski
MPGI Travel Grant Awardee
Targeted mutagenesis of the tomato procera gene using TALENs

2:40 - 3:00 Shaun Curtin
Research Associate, Advisor: Nevin Young
MPGI Travel Grant Awardee
Genome engineering tools for legume functional genomics

3:00 - 3:10 Closing Remarks

Breakfast pastries by French Meadow; lunch buffet by Holy Land.

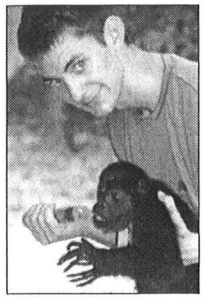
Speaker Abstracts

Dr. Emilie Snell-Rood
Assistant Professor
Ecology, Evolution and Behavior

Variability in gene expression as a mechanism of developmental plasticity

Variation in gene expression, followed by epigenetic reinforcement of particular expression patterns, is thought to underlie some forms of phenotypic plasticity. Such learning-like mechanisms of plasticity are quite costly. If such mechanisms indeed underlie plasticity, then plastic generalists that rely on variable gene expression should exhibit delays in trait function and increased investment in development relative to a specialist. Here we use gut gene expression in caterpillars to begin to test these ideas. Many caterpillars exhibit a form of physiological learning, where a species may be capable of feeding on a range of plants, but once an individual has experience feeding on a particular species, its performance suffers if it switches. We use RNAseq to compare gut gene expression at two developmental stages, on two host types, in a specialist and generalist population of cabbage white butterflies. We predict that patterns of gene expression in this context are analogous to learning curves, showing pronounced variation early in development and divergence over time in different environments, especially for the generalist population. To date, we have mostly been optimizing the analysis and sequencing runs for a non-model organism, but we hope to solicit advice for our upcoming analyses. Future experiments will tie such learning-like mechanisms at the level of gene expression to life history tradeoffs, in particular increased offspring investment.

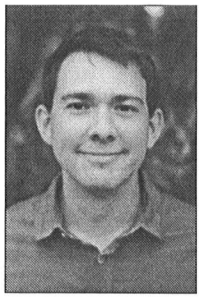
Speaker Abstracts



Jonathan Clayton
DVM/PhD Dual Degree Candidate
Advisor: Timothy Johnson
Veterinary & Biomedical Sciences

Similar trends in microbiome shift between captive primates and westernized humans

The primate gastrointestinal (GI) tract is home to trillions of bacteria that play major roles in digestion and metabolism, immune system development, and pathogen resistance, among other important aspects of host health and behavior. GI and autoimmune diseases such as obesity, diabetes, Crohn's disease, and ulcerative colitis, all correlated with shifts in microbiome composition, have been dramatically on the rise globally for at least the last 50 years. The Human Microbiome Project was established with the goal of better understanding the role microbial communities play in health and disease. While the research community has made substantial progress in understanding the role microbial communities play in human health and disease, much less attention has been given to host-associated microbiomes in nonhuman primates (NHPs). In an effort to bridge this gap, we have begun exploring host-associated microbiomes in NHPs, including red-shanked doucs (Pygathrix nemaeus). Red-shanked doucs possess a specialized GI system similar to ruminants. Maintenance of captive red-shanked doucs has been largely unsuccessful. Improving captive conditions is hindered by critical gaps in our understanding of their natural diet and the enteric microbial adaptations that facilitate the digestive process. We used the douc as a model system to study the relationships between dietary composition and microbial community activity within the GI tract. Fecal samples were collected from wild and captive red-shanked doucs between 2012-13. We measured gut microbiome composition using 16S rRNA sequencing. Statistical analyses were performed to identify correlations between diet, gut microbiome, and animal status (captive vs. wild). We identified microbial biomarkers of douc nutritional health. We hypothesize that captivity causes doucs to shift to severe gut dysbiosis, thereby resulting in GI issues, and we can use the douc as a model organism to study what is happening to the human gut microbiome in highly westernized countries like the USA, and also in humans over time.



Justin Anderson
PhD Candidate, Advisor: Robert Stupar
Agronomy & Plant Genetics

Comparison of genomic structural variation associated with cultivars, mutagenized, and transgenic soybean plants

Plant genetic transformation and tissue culture is an important component of modern plant breeding. Along with the introgression of a desired transgene, somaclonal variation is a well-established side effect of the plant tissue culture process. We used a comparative genome hybridization array to compare genic structural variation in three different classes of accessions: among cultivars, among fast neutron mutants, and among plants that have experienced a genetic transformation and tissue culture process. In the five transformed genotypes studied, a total of three deletions and one duplication were observed. None of these events were linked to a known transgene insertion site. The number of genes affected by these deletion and duplication events is on average one order of magnitude less than that observed following fast neutron mutagenesis and two orders of magnitude less than standing inter-varietal structural variation. This comparison provides a fresh perspective on the relative rates of genomic variation associated with these sources. The rarity of structural variants following genetic transformation and tissue culture and the common practice of backcrossing the transgene locus into elite genetic backgrounds indicates that this type of variation is essentially inconsequential to products developed from a trait introgression pipeline.

Suzanne McGaugh
Assistant Professor
Ecology, Evolution & Behavior

The cavefish genome reveals candidate genes for eye loss

Natural populations subjected to strong environmental selection pressures offer a window into the genetic underpinnings of evolutionary change. Cavefish populations, *Astyanax mexicanus* (Teleostei: Characiphysi), exhibit repeated, independent evolution for a variety of traits including eye degeneration, pigment loss, increased size and number of taste buds and mechanosensory organs, and shifts in many behavioural traits. Surface and cave forms are interfertile making this system amenable to genetic interrogation; however, lack of a reference genome has hampered efforts to identify genes responsible for changes in cave forms of *A. mexicanus*. Here I'll present the first de novo genome assembly for *A. mexicanus* cavefish, contrast repeat elements to other teleost genomes, identify candidate genes underlying quantitative trait loci (QTL), and assay these candidate genes for potential functional and expression differences. In addition, some preliminary population genomic analysis will be presented.

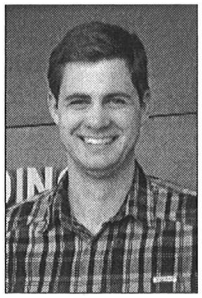
Speaker Abstracts

Maureen Quin
Research Associate, Advisor: Claudia Schmidt Dannert,
Biochemistry, Molecular Biology & Biophysics

Mapping sesquiterpenoid biosynthetic pathways in fungi

Basidiomycota produce an extensive array of secondary metabolites. Fungi are particularly prolific producers of sesquiterpenoids, the largest and most diverse class of natural products. Many sesquiterpenoids have antimicrobial and cytotoxic properties, making them pharmaceutically relevant and therefore key targets for natural product discovery and biocatalysis. Previously, fungal terpene synthase identification was a challenging process, limiting the number of studies in this area. We have addressed this problem and opened new paths to fungal sesquiterpenoid discovery by building a predictive framework for genome mining and directed enzyme discovery across all Basidiomycota. Using our framework to search fungal terpene synthase diversity, we have selectively identified several novel terpene synthases that produce the precursors to a class of anticancer compounds. In-depth characterization of these terpene synthases has shed light upon a previously unexplored mechanistic diversity. These studies have resulted in the creation of an enzyme toolbox, a valuable resource for enzyme evolution and engineering approaches to the tailor design of robust biocatalysts.

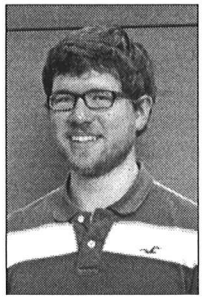
Speaker Abstracts



Tomas Cermak
Postdoctoral Associate, Advisor: Dan Voytas
Genetics, Cell Biology & Development

Targeting plant genes using geminiviruses: efficient and precise modification of the tomato genome

Making precise modifications to plant genomes has been challenging, due to the lack of efficient methods for delivery of DNA repair templates to plant cells. Here, we create heritable modifications to tomato genome by homologous recombination, using geminivirus replicons. We targeted insertion of a strong promoter upstream of a gene controlling anthocyanin biosynthesis, resulting in its overexpression and accumulation of purple pigment in tomato tissues. Both TALENs and CRISPR/Cas9 were used as DNA breaking agents with similar efficiencies. This is a first example of endogenous gene regulation by targeted promoter insertion in plants and to the best of our knowledge also the first example of gene targeting in tomato. Our work provides a foundation for efficient and precise modification of crop genomes.



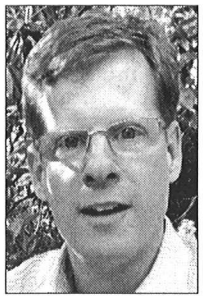
Scott Simpkins
Graduate Student, Advisor: Chad Myers
Computer Science & Engineering

Systematic functional annotation of compound libraries using high-throughput yeast chemical genomics

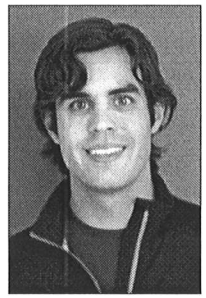
The current paradigm of "target-centric" compound bioactivity screening allows for the screening of 100,000's of compounds, but only against a small number of predetermined biological targets. This limited target space inhibits progress in fields such as therapeutic development, toxicology screening, and biological probe discovery. To complement target-centric screens, we have developed a high-throughput yeast assay for mapping chemical-genetic interactions that enables the prediction of a compound's gene and biological process targets across the entire genome. We performed chemical genomic screens for more than 13,000 compounds from the RIKEN NPDepo and several NIH/NCI collections, including natural products and derivatives, combinatorially-synthesized compounds, and several hundred approved drugs. We interpret a compound's chemical genetic interaction profile using the well-characterized yeast genetic interaction network as a reference and use this information to predict both the genes and biological processes perturbed by the compound. Our large-scale chemical genomic screen has revealed insights into the biological function of compounds, at both the individual compound and compound collection levels.

Speaker Abstracts

For example, we have characterized entire compound collections by the general cellular functions their members tend to disrupt. Interestingly, the larger and least biased collections were depleted for compounds affecting nuclear processes, suggesting these targets tend to be relatively less accessible. Additionally, we have discovered molecular substructures that are enriched in sets of compounds with similar biological effects, which shows this method's ability to relate chemical structure to function. We can screen 10,000 compounds and generate genome-wide mechanism-of-action predictions within a few months' time, demonstrating that we have developed an efficient, high-throughput method for rapid genome-wide annotation of bioactivities present in large compound collections.



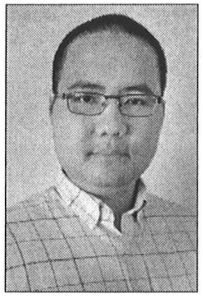
James Wilgenbusch
Associate Director
Minnesota Supercomputing Institute



Joshua Baller
Scientific & Operational Lead, RISS & Minnesota Supercomputing Institute

MSI: building communities of science surrounding cutting edge research areas

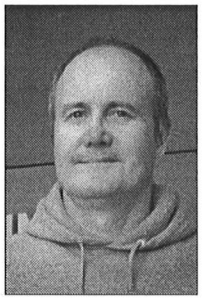
The Minnesota Supercomputing Institute (MSI) manages and operates advanced computing, storage, networking, and user services in order to advance leading-edge research and accelerate technology transfer through the interchange of ideas. We are committed to expanding and developing resources and services that will accelerate research across the growing spectrum of scientific fields and will help to facilitate public private collaborations and partnerships. MSI is actively promoting cutting edge research tools accessible to every biologist, promoting outreach and training to broaden our impact, and actively building communities that bridge the gaps across colleges in such burgeoning new fields as metagenomics, single-cell biology, 3rd generation sequencing, data analytics and more. A staff of about 50 skilled individuals supports 600 user groups, comprising approximately 3,500 unique users. Our HPC resources provide well over seven hundred million corehours a year, and 5 PB of specialized data storage provide the capacity and capability for big data and data intensive research. The institute also operates four disciplinary laboratories on campus that feature specialized support for structural biology, advanced visualization, imaging, and drug design.



Vai Lor
Graduate Student, Advisor: Neil Olszewski
Plant Biology

Targeted mutagenesis of the tomato procera gene using TALENs

Transcription activator-like effector nucleases (TALENs) are efficient custom tools increasingly used for genome engineering. We successfully used TALENs under the control of an estrogen-inducible promoter for targeted mutagenesis in tomato (Solanum lycopersicum). Stable transgenic lines with TALENs targeting the negative regulator of gibberellin signaling PROCERA (PRO) were produced. Plants were regenerated bearing pro mutations following induction of TALEN expression in somatic cells of cotyledons. Six mono-allelic and one bi-allelic plants with deletions ranging in sizes from 1bp to 88bp at the TALEN target site. Progeny from two independent heterozygous plants were examined, and the mutant alleles were heritable. Homozygous mutant pro plants exhibited phenotypes consistent with increased gibberellin response. Our work demonstrates that TALENs can be used for targeted mutagenesis in tomato.



Shaun Curtin
Research Associate, Advisor: Nevin Young
Plant Pathology

Genome engineering tools for legume functional genomics

Advances in legume research have been frustrated by a lack of mutants and mutagenesis methodologies. This is especially relevant as scientists seek to explore the biological functions of gene candidates discovered through methods such as RNA-seq or genome-wide association studies (GWAS). Here we demonstrate a suite of mutagenesis platforms including; Tnt1 retro-transposons, hairpins constructs, zinc-finger (ZFNs), TAL-effector (TALEN) and CRISPR/Cas9 (RNA-guided) nucleases to engineer Dicer-like and nodulation mutants in soybean and Medicago truncatula respectively. We have used the genetic transformation of Tnt1, hairpin, ZFNs, TALENs and CRISPRs to knock-out/down single copy and duplicated legume genes, both in hairy root and whole plant systems. These developments demonstrate the utility of these mutagenesis platforms for functional genomic studies and for potential trait improvement strategies in legumes.

Notes

Notes

Thank you for attending.

If you have further questions regarding
the retreat or MPGI please contact
Kit Leffler at mleffler@umn.edu