THE MICROBIAL & PLANT GENOMICS INSTITUTE

5th Annual Fall Symposium

AUGUST 27TH, 2014
HOSTED BY NATHAN SPRINGER
CARGILL BUILDING ROOM 105

BEYOND GENOMES:
EPIGENETIC INHERITANCE

SYMPOSIUM SCHEDULE

8:00	Breakfast - Atrium
9:00	Opening Remarks
9:15	**Heather True-Krob, Ph.D.** Associate Professor, Dept.of Cell Biology & Physiology, Washington University School of Medicine
10:00	**Ellen Demerath** Associate Professor, Dept. of Epidemiology University of Minnesota
10:30	Break - Atrium
10:45	**Keith Slotkin, Ph.D.** Assistant Professor, Dept. of Molecular Genetics Ohio State University
11:15	**Dan Voytas** Professor, Dept. of Genetics, Cell Biology and Development University of Minnesota
12:00	Lunch - Atrium
1:00	**Scott Michaels, Ph.D.** Associate Professor, Dept. Biology & Molecular Biology Institute Indiana University
1:45	**Changbin Chen** Assistant Professor, Dept. of Horticultural Science University of Minnesota
2:15	Break, Atrium
2:30	**Jay Hollick** Associate Professor, Molecular Genetics Ohio State University
3:15	**Nathan Springer** Professor, Dept. of Plant Biology University of Minnesota
3:45	Reception - Atrium

POSTER SESSION

Gowtham Atluri, Graduate student, Computer Science
Discovering transient relationships between brain regions from fMRI time series data
Advisor: Vipin Kumar

Brittany Bennett, Graduate student, Microbiology & Biotechnology Institute
Discovery and Characterization of a Ferrous Iron Exporter in Shewanella oneidensis
Advisor: Jeff Gralnick

Jennifer Dale, Postdoctoral Associate, Microbiology
Enterococcus faecalis genetic determinants responsible for biofilm-induced antibiotic resistance and conjugal transfer of pCF10
Advisor: Gary Dunny

Kevin Dorn, Graduate student, Plant Biology
Genomics & domestication of the winter biofuel crop field pennycress (Ihlaspi arvense L.)
Advisor: David Marks

Dana Freund, Postdoctoral Associate, Horticulture
Direct Tissue Spray Ionization of Living Plants by Mass Spectrometry for Metabolomics
Advisor: Adrian Hegeman

Kevin Lang, Graduate student, Veterinary Biosciences
Dissecting the regulation of IncA/C plasmid conjugation
Advisor: Tim Johnson

Nicholas LeBlanc, Graduate student, Plant Pathology
Plant host identity and diversity influence community diversity and metabolic phenotypes of common eukaryotic soil microbes
Advisor: Corby Kistler

Baris Mutlu, Graduate student, Mechanical Engineering
Silica encapsulation of bacterial biocatalysts
Advisor: Larry Wackett

Christopher Staley, Postdoctoral Associate, Biotechnology Institute
Species Sorting Dynamics in the Bacterial Community of the Upper Mississippi River are Influenced by Land Use and Sediment Resuspension
Advisor: Mike Sadowsky

Peng Yu *(in absencia),* Recent Graduate, Horticulture
A facile means for the identification of indolic compounds
Advisor: Jerry Cohen

Heather True-Krob, Ph.D.
Associate Professor, Dept.of Cell Biology & Physiology,
Washington University School of Medicine

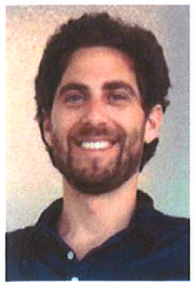
Prions: 31 Flavors of Infectious Protein

The True Lab is interested in the biological consequences of yeast prions- in both their capacity to function as novel epigenetic elements, as well as in their utility in modeling mechanisms of protein misfolding and aggregation that mimic important events in several neurodegenerative disorders. Additionally, we are interested in how prions in yeast impact survival and adaptation. We are also interested in understanding what other prions exist and how broadly prions affect cellular physiology. We are also using yeast prions to understand how the environment influences protein misfolding and aggregation, a question that has been difficult to address with current model systems of neurodegenerative disorders.

Ellen Demerath
Associate Professor, Dept. of Epidemiology
University of Minnesota

Epigenome-wide Association Study in African American Adults

Epigenetics is the study of mitotically heritable modifications in chromatin structure (i.e., modifications not involving the underlying DNA sequence), and their impact on the transcriptional control of genes and cellular function. Obesity is among the strongest modifiable risk factors for diabetes, atherosclerosis, and many cancers likely due, in part, to the increased systemic inflammation, immunological activation, and oxidative stress observed in obese individuals. Identifying the epigenetic signatures associated with obesity may therefore point to a common soil of genomic dysregulation involved in numerous common chronic diseases. As of 2014, only a small number of studies had been published showing obesity-related variation in CpG site methylation, the most widely studied and best understood form of epigenetic modification. Dr. Demerath will present a brief summary of the epigenetics of obesity and discuss recent findings from the Atherosclerosis Risk in Communities Study (ARIC) on the relationship of leukocyte DNA methylation to body mass index (BMI), waist circumference (WC), and BMI change in African American adults.



Keith Slotkin, Ph.D.
Assistant Professor, Dept. of Molecular Genetics
Ohio State University

Two independent mechanisms responsible for the recognition of transposable elements and the initiation of their epigenetic silencing

When a transposable element (TE) enters a genome via cross hybridization, horizontal transfer, or transgenesis, its default state is to actively transcribe and transpose. The mutagenic activity of new TEs is inhibited by host mechanisms that recognize the TE, methylate its DNA / modify its chromatin, and transcriptionally silence the TE. Our lab has characterized the molecular pathways responsible for TE recognition and silencing in the reference plant Arabidopsis. We have determined that there are at least two independent host mechanisms responsible for recognizing and silencing new TEs. The first pathway utilizes sequence homology mediated through 24 nucleotide (nt) small interfering RNAs (siRNAs) to recognize and silence new TEs. In this "homology sensor" pathway, previously silenced TEs are kept latent in the genome to produce the 24 nt siRNAs that act to target new TEs. The second pathway acts as a backup system for when the homology sensing mechanism fails due to the introduction of a TE with insufficient sequence homology to pre-existing TEs. This second pathway is RNA Polymerase II expression-dependent, and silencing is only triggered after the TE mRNA is digested in to 21-22 nt siRNAs via RNAi. The Slotkin lab has demonstrated that these TE 21-22 nt siRNAs can participate in RNA-directed DNA methylation and act to initiate TE epigenetic silencing. Our current research focuses on understanding the limits of the homology-sensing pathway, as well as elucidating the molecular mechanism responsible for the expression-dependent initiation of TE silencing.

Dan Voytas
Professor, Dept. of Genetics, Cell Biology and Development
University of Minnesota

The impact of chromatin on retrotransposon integration site choice

In most eukaryotes, retrotransposons constitute a large fraction of the genetic material, comprising, for example, up to half of the human genome. Retrotransposons attain such high copy numbers by reverse transcribing their mRNA into cDNA, which becomes inserted into new genomic sites through the action of the retrotransposon-encoded integrase (IN) protein. cDNA integration has genetic and epigenetic consequences for the host by creating mutations and altering gene expression. Recent work suggests that retrotransposons identify genomic integration sites through a conserved mechanism: IN interacts with a specific DNA-bound protein and this tethers the integration complex to specific genomic sites, resulting in target site biases. Work will be presented describing the molecular mechanism by which two retrotransposons of the yeast Saccharomyces cerevisiae select chromosomal integration sites, namely the Ty5 elements, which integrate preferentially into telomeric heterochromatin, and the Ty1 elements, which target sites of RNA polymerase III transcription.

Scott Michaels
Associate Professor, Dept. Biology & Molecular Biology Institute
Indiana University

Large-scale heterochromatin remodeling linked to re-replication-associated DNA damage

Chromatin is the term used to describe DNA and its associated packaging proteins (e.g. histones). DNA methylation and posttranslational modifications of histones, such as methylation and deacetylation at specific positions can cause the DNA to be packaged more tightly and become less transcriptionally active (heterochromatin), whereas other histone modifications can increase transcriptional activity by opening the chromatin structure (euchromatin). These modifications are sometimes referred to as the "histone code" and play an important role in the regulation of gene expression in all eukaryotes. In the model plant Arabidopsis, histone H3 lysine 27 mono-methylation (H3K27me1) is associated with heterochromatic structures called chromocenters. Our work has shown that two functionally redundant enzymes Arabidopsis Trithoras-Related Protein 5 (ATXR5) and ATXR6 are responsible for H3K27me1 at chromocenters. The importance of this epigenetic mark is shown by the phenotypes of atxr5 atxr6 double mutants, which show partial decondensation of chromocenters, loss of gene silencing, and, surprisingly, an over-replication of heterochromatic DNA. Over-replication results from the repeated firing of origins of replication during a single S-phase. This "re-replication" results in genome instability and is associated with diseases such as cancer. Interestingly, chromocenters are extensively remodeled in atxr5 atxr6 mutants and contain compartments that facilitate DNA repair, suggesting a novel mechanism for heterochromatic DNA-damage repair that involves large-scale chromatin remodeling. Taken together, these results demonstrate that H3K27me1 is a highly important epigenetic mark and that Arabidopsis is a powerful system in which to study the many roles of H3K27 methylation.

Changbin Chen
Assistant Professor, Dept. of Horticultural Science
University of Minnesota

Epigenetic features of maize meiosis

My lab focuses on plant meiosis and meiotic recombination. We aim to explore the mechanisms that regulate gene expression and homologous recombination during meiosis. Applying the high throughput sequencing techniques (ChIP-seq, Bisuilfite-Seq, smallRNA-seq), we used isolated male meiocytes (the cells undergoing meiosis) from Zea mays to generate deep sequencing data on histone modification, DNA methylation and small RNAs. We will present their distribution, correlations and specific findings relevant for the process of meiosis.

Jay Hollick
Associate Professor, Molecular Genetics, Center for RNA Biology
Ohio State University

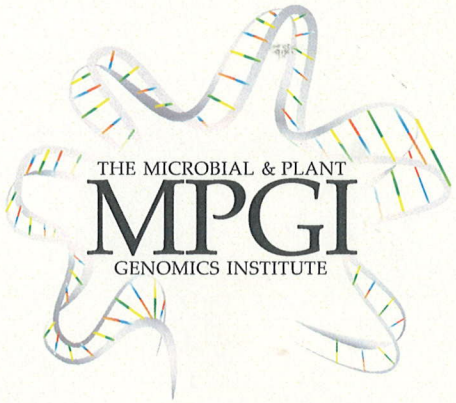
Non-Mendelian inheritance of epigenetic variation in maize

In both plants and animals, meiotically-heritable regulatory states of specific alleles can be altered through trans-homologue interactions known as paramutations. This behavior presents exceptions to the laws of Mendelian genetics and challenges basic tenets of evolutionary theory. We used forward genetics and mutational analyses to discover that paramutations occurring in maize involve components of a small RNA-directed DNA methylation pathway. Our findings establish a plant-specific RNA polymerase (Pol IV) as an important determinant of trans-generational inheritance. Pol IV appears to interfere with Pol II access to LTR retrotransposons (RT) and this has led to models in which expression of specific alleles is regulated by Pol IV through competitions with Pol II. Global run-on sequencing identifies more than 200 such haplotypes subject to transcriptional control by Pol IV. These studies indicate that much of the epigenetic variation defined by Pol IV is due to specific juxtapositions of genic regions and transposons. Our goal is to understand how such a nuclear system creates and maintains epigenetic variation to enable novel strategies for plant improvement.

Nathan Springer
Professor, Dept. of Plant Biology
University of Minnesota

Genetic and epigenetic control of chromatin modifications

Variation in chromatin modifications, such as DNA or histone methylation, are often considered to be epigenetic. However, this variation may depend upon changes in DNA sequence (genetic changes) or might not be heritable. A variety of approaches have been used to study the genetic and epigenetic influences on DNA methylation variation in maize. While some changes in DNA methylation may be purely epigenetic there are also a number of examples of DNA methylation variation that can be attributed to polymorphic transposon insertions. We have found examples in which polymorphic transposon insertions can influence epigenetic regulation such as imprinting. These studies point to an important role for genetic variation and suggest that DNA methylation contributes to the mechanism by which these genetic changes influence gene expression.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