Poster Session

A poster session and open reception for the speakers will immediately follow the talks. Light refreshments will be served. Program participants who wish to present a research poster (4'X 4') are invited to do so. Graduate students and faculty associated with the Plant Breeding & Genetics and the Genetics program are particularly encouraged to participate. The poster session and reception will be held in the Conservatory in the Plant and Soil Sciences Bldg.

Participation

The Symposium is open to MSU faculty, staff, and students, as well as members of the East Lansing/Lansing community and researchers from neighboring institutions. There is no registration fee or requirement for preregistration.

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Symposium website:
http://www.hrt.msu.edu/pbgp/symposium.html

Plant Breeding & Genetics and the Genetics Graduate Programs

Symposium 2006

Transposable Elements and Genome Evolution

Friday, December 8, 2006
10:00 a.m. - 6:00 p.m.
A155 Plant and Soil Sciences Bldg

Dr. I. King Jordan
Georgia Institute of Technology

Dr. King Jordan is an associate professor in the Center for the Study of Systems Biology, Georgia Institute of Technology. His research program focuses on understanding the genome level determinants of the diversification between evolutionary lineages, including the contributions of transposable elements (TEs) to host gene regulatory and protein coding sequences. In a recent study, Dr. King Jordan's group analyzed the evolutionary and functional characteristics of TE-derived human genome regulatory sequences by the high throughput mapping of DNaseI-hypersensitive (HS) sites. Genes involved in immune response are over-represented among genes with TE-derived HS sites. A number of genes with both TE-derived HS sites and immune tissue related expression patterns were found to encode proteins involved in immune response such as T cell specific receptor antigens and secreted cytokines as well as proteins with clinical relevance to HIV and cancer. Genes with TE-derived HS sites have higher average levels of sequence and expression divergence between human and mouse orthologs compared to genes with non TE-derived HS sites. The results reported here support the notion that TEs provide a specific genome-wide mechanism for generating functionally relevant gene regulatory divergence between evolutionary lineages.

Kingdom Kwapata

Dr. Damon Lisch
University of California - Berkeley

Dr. Damon Lisch is a research professor in the department of Plant and Microbial Biology at University of California-Berkeley. His research focuses on the molecular and genetic analysis of the *Mutator* (*Mu*) transposons in maize and contributed significantly to our understanding about how the activity of transposons is regulated. The *Mu* family of DNA transposons is the most active and mutagenic transposon in plants. The *MuDR* elements contain two genes, *mudrA* encoding a 120 kDa transposase, and *mudrB* encoding the 23 kDa MURB protein, which is necessary for element insertion. Through a genetic screen followed by molecular characterization, Dr. Lisch and his group have identified the gene, *Mu killer* (*Muk*), which heritably silences the *Mu* transposon system. The *Muk* results from a duplication and inversion of a portion of the TIR and *mudrA* coding region. The silencing occurs through the formation of a hairpin transcript that is processed into small RNAs and targets the *Mu* transcripts. *Muk* is the first example of naturally occurring transposon derivative capable of initiating the heritable silencing of an active transpson. It also has profound implication in the origin of microRNA genes.

Ann Armenia

Symposium Schedule

10:00 a.m. **Opening Remarks**
Dr. Steven Pueppke
Director, Michigan Ag Exp Station

10:30 **Dr. I. King Jordan**
"Transposable Elements as Global Regulators"

11:30 **Lunch Break**

1:00 p.m. **Dr. Damon Lisch**
"Remembrance of Things Past: Heritable Silencing and Reactivation of Transposable Elements"

2:00 **Dr. Cedric Feschotte**
"Life After Death: Reincarnation of DNA Transposons into Genetic Networks. A Case Study in the Human Genome"

3:00 **Break**

3:30 **Dr. Daniel Voytas**
"Transposable Elements and Genome Organization: The Influence of Chromatin on Retrotransposon Target Specificity"

4:30 **Reception & Poster Session**
The poster session will be held in the Plant and Soil Sciences Conservatory. Refreshments will be served.

Dr. Cedric Feschotte
The University of Texas at Arlington

Dr. Cedric Feschotte is a faculty member in the department of Biology, University of Texas at Arlington. His research team uses a combination of computational and experimental tools to unravel the impact of TEs on eukaryotic genome evolution. Currently, Dr. Feschotte's lab is studying human transpsons and transposase-derived genes. In order to test this model, Feschotte's group conducted a detailed study of SETMAR, a human gene of unknown function that originates from the fusion of a SET domain with histone methyltransferase activity to a mariner transposase. SETMAR has emerged between 58 and 40 million years ago through an intricate stepwise process involving transposition, genomic deletion and the creation of a new intron. The DNA binding domain, but not the catalytic domain, of the transposase part in SETMAR has been subject to purifying selection in all the extant lineages of anthropoid primates, suggesting that the addition of a transposase domain to the pre-existing SET domain led to the advent of a beneficial new function in primates. Those data support a model whereby the specific DNA-binding activity of the ancestral transposase has been retained and now provides a means to target the SET domain to multiple sites within the human genome where it can act to modulate the structure of the surrounding chromatin.

Suneth Sithumini Sooriyapathirana

Dr. Daniel Voytas
Iowa State University

Dr. Daniel Voytas is a professor in Genetics, Development and Cell Biology Department at Iowa State University. Among many of his research interests, Dr. Voytas is the pioneer in studying the interaction between retrotranspsons and host proteins. Retrotranspsons are the largest component of plant genomes. In yeast, the Ty5 retrotranspson targets to heterochromatin through an interaction between the C-terminus of Ty5 intergrase and the heterochromatin protein Sir4p. This led to the hypothesis that retrotransposons become integral components of heterochromatin by actively targeting integration to heterochromatic domains. In plants, many retrotransposons have chromodomain-like motifs in their integrases and are exclusively located within centromeric heterochromatin. The chromodomains fall into three classes based on their homology to Heterochromatin Protein 1 (HP1). Chromodomain-YFP fusions appear as distinct foci within the nucleus that co-localize with the Arabidopsis HP1 homologue. Mutations in conserved residues in the chromodomain diminish the sub-nuclear localization. The chromodomain was also shown to interact with histone H3 that is dimethylated on Lys9. Collectively, these data support the notion that novel chromodomains mediate retrotranpson target specificity by recognizing specific chromatin features.

Matthew Christopher Berry