

# MCB PLANT BIOLOGY SEMINAR SERIES F2009

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“Molecular determinants of MITE transposition and amplification”

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3:30 p.m.

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**ABSTRACT:** Transposable elements (TEs) are the most abundant component of probably all eukaryotic genomes, often >50%. Typical DNA transposons have low copy number and large size. Interestingly, novel transposon families collectively named miniature inverted repeat transposable elements (MITEs) are small (100-500 bp) and noncoding, yet can reach up to tens of thousands of copies and constitute a significant portion of a genome (e.g. 16% of yellow fever mosquito genome and ~10% of rice genome). They are closely associated with genes and can produce small RNAs, thus may play an important role in gene evolution. However, their origin(s) and amplification mechanism(s) are mysterious. To experimentally test a recent model that is based on *in silico* analyses, in depth experimental and computational analyses on members of two classical types of MITEs (namely Tourist and Stowaway) were performed. After setting up two assay systems in Arabidopsis and yeast, I dissected the mechanistic features of MITE transposition/amplification. Data obtained in these studies suggest that MITEs are internally special and cross-mobilization plays an important role in their amplification. Future investigation will be focused on MITEs in the genome of yellow fever mosquito genome.

Reference: Yang, G. et al, “Tuned for transposition: molecular determinants underlying a hyper active Stowaway MITE”, Science, 2009, Sept 11: 1391-1394.

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