



ABSTRACT

“The success strategies of transposable elements that diversify genomes”

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Despite the widespread prevalence of transposable elements (TEs) in the genomes of higher eukaryotes, what is virtually unknown is how they are able to amplify to high copy numbers without being silenced and without killing their host. In this seminar I will discuss our recent studies on MITEs (miniature inverted repeat transposable elements), a type of class 2 element that was discovered in my laboratory 20 years ago as the most prevalent TE associated with plant genes. To understand how MITEs can attain high copy numbers, we succeeded in identifying a MITE, *mPing*, in the midst of rapid amplification throughout the genomes of several related rice strains. Nextgen sequencing technologies are being employed to determine *mPing*'s strategies for success and to understand how *mPing* impacts host transcription and generates phenotypic diversity.