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## Genomic scale sorting and characterization of MITEs in the entangled mobilome

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Miniature inverted repeat transposable elements (MITEs) are interesting transposable elements (TEs) because of their high copy numbers and mysterious identifies. Despite their low DNA content percentage in a genome, their numerous copies can disturb genomic stability and cause important genetic variations. Historically, MITE families were often discovered individually, a practice cannot keep pace with the large scale genome sequencing. Automated genome wide discovery of MITE families and their characterization are desirable. We developed a whole pipeline from MITE discovery to detailed analyses of MITEs at genomic scales. Using the pipeline, we performed in depth analyses of the MITE families in multiple recently release crop genomes. These analyses revealed the diversity of MITE families and their evolution in the host genome. We have also predicted the transposases that may be responsible for the mobilization of some MITE families. These MITE families can potentially be used as genetic markers for the improvement of these crop species.

## Biography

Guojun Yang holds a Ph.D. from the Department of Biology, Texas A&M University (1998-2003). He did his postdoctoral research from the Department of Plant Sciences, University of Georgia (2004-2008). He started his current position as an assistant professor in Department of Biology, University of Toronto Mississauga in 2008. His research interest is in the mobile genetic elements of eukaryotic genomes. He teaches Biotechnology at undergraduate and graduate levels.

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