Transposable element evolution and mobility in *Musa* genomes

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Transposable elements can be identified

- by studying their mobility and insertions/deletions in comparisons of homologous or homeoeologous chromosome sequences
- by characteristic sequence properties such as repeats and short duplications
- by homology to known elements
Alignment of two homologous Musa BACs shows in-dels in B genome *M. balbisiana* and A genome *M. acuminata*

DNA transposons hAT are particularly frequent

8-bp TSD, and short TIRs of 5-27 bp
transposase (sometimes degenerate) including a DDE site.
Non-autonomous (MITE) derivatives of hAT with deletion coding sequence

TIR
Terminal Inverted Repeat
Repeat conservation in Musa hATs
HMM identifies three abundant Musa hAT families

Insertional polymorphisms of three Musa hATs in 48 Musa/banana accessions by PCR of flanking primers

Hidden Markov Model: 274 transposase sequences, 114 (shown) span the five conserved hAT-specific amino acid blocks in the assembly (D’Hont et al. 2012) 61 + 47 = 6 Complete and autonomous: 70 MuhAT (I); no autonomous MuhAT III

MuhAT I: autonomous and derived MITES
Retroelements

Sequences which amplify through an RNA intermediate

- 50% of all the DNA!

Homologous BAC sequences from Calcutta 4
- Homologous over the full length
- except for a 5kb insert
- a Ty1-copia retroelement

A-genome specific MuhATI on ABB Musa
hAT transposons and derived MITEs evolution in Musa
– Three major families
– Hundreds of copies of hATs
– Thousands of copies of MITEs
• Subtelomeric, gene-rich regions
• Species (A and B genome) - specific mobility of MuhMITEs
• MuhMITE II showing transduplications of genomic sequences
  – active MuhAT transposons
  – MuhMITEs as modulators of genome evolution

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Some Musa / banana papers from Pat Hosel-Harrison and www.molcyt.com

http://pag.confex.com/pag/xxiii/webprogram/Paper14993.html

hAT transposons and derived MITEs evolution in Musa

http://dx.doi.org/10.1038/nature11241

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How do genomes evolve?
- Gene mutation very rarely (human: $10^{-8}$/site/generation)
- Chromosome evolution
- Polyploidy and genome duplication (ancient and modern)
- Repetitive sequences: mobility & copy number ($10^{-4}$/gen.in µsat)
- Recombination
- Epigenetic aspects – centromeres & expression

How can we exploit knowledge of genome evolution?
- Biodiversity
- Chromosome and genome engineering
- Breeding
- Markers