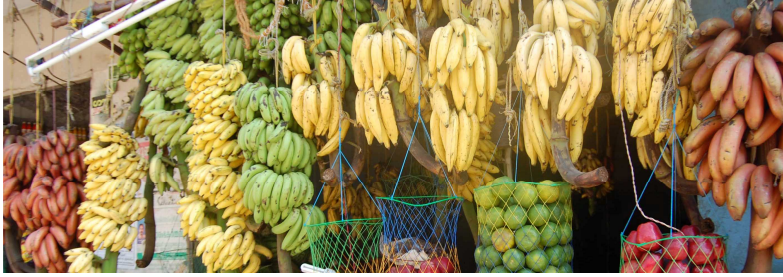


DNA and Genome Diversity in Bananas and Plantains (*Musa*)

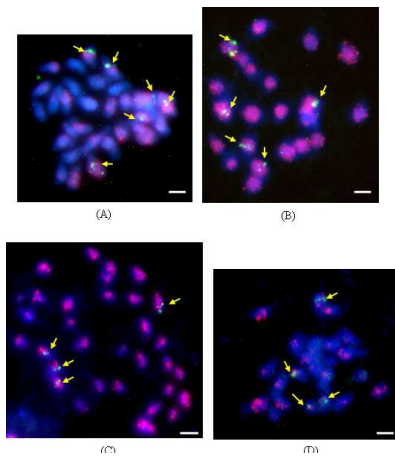
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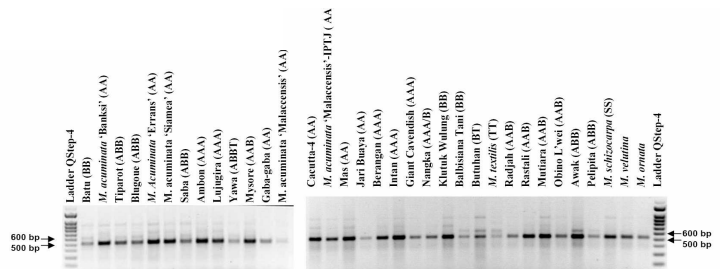


Bananas, genus *Musa*, are giant perennial herbs with a small genome of 600 Mbp. Cultivars and their relatives in section Eumusa, including the A (*Musa acuminata*), B (*M. balbisiana*) and S (*M. schizocarpa*) genomes have a basic chromosome number, n, of 11 and occur as diploid (2n=2x=22), triploid (2n=3x=33) and tetraploid (2n=4x=44) plants throughout the tropics with a centre of diversity in South-East Asia. Other species (Rhodochlamys, Callimusa) have a basic chromosome number of n=10.

Abiotic and biotic stresses are major factors affecting banana production, and it is important to measure and characterize genetic diversity within the gene-pool at the molecular level for future improvement of the crop. Genes which are repeated many times in the genome include the rDNA, those related to retroelements, and signalling genes that are related directly to the plant stress responses and resistances.



Metaphases showing diversity in ploidy and 5S rDNA number from banana cultivars (A) Obino L'Ewai (2n=3x=33), (B) Mas (2n=2x=22), (C) Giant Cavendish (2n=3x=33) and (D) Butuhan (2n=2x=22). Blue chromosomes counterstained with DAPI show distribution 5S rDNA (labelled green) and a retroelement from a BAC clone related to pseudoviridae (magenta) on mitotic metaphase chromosome by fluorescent *in situ* hybridization. Bar represents 5µm.

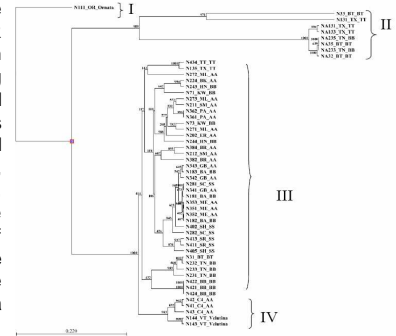


Primers designed from genomic and EST databases were exploited to characterize sequences containing Nucleotide Binding Sites (NBS) and Leucine-Rich Repeat (LRR) motifs associated with disease resistance. In Arabidopsis, there are 400 of these genes and the number is similar in banana. PCR products were cloned and sequenced and used to generate the tree (below) based on deduced protein sequences.



Specific LRR primers designed to isolate motifs from *Musa* accessions gave conserved sequence motifs (above left), which formed four significant clusters (right) corresponding to intra- and extra- cytoplasmic groups of the gene identified in other species. Within the clusters, the sequences did not correspond to *Musa* genomic constitutions. The conserved LRR motifs are present in many copies, with independent sizes and/or specific structures.

Four significant clusters were identified. Neither NBS nor LRR sequences are conserved with respect to genome, indicating that R-genes are specific and exist independently. BAC libraries allow tagging of conserved domains of NBS, LRR, retroelement and SSR motifs, giving understanding of the genomic context and control of R-genes. Reliable characterization of these domains in *Musa* is possible via PCR-based screening.



Conclusions

Repetitive DNA sequences are extremely diverse in the genomes of *Musa* species. While sub-families of repetitive genes could be identified, most families were not specific to particular diploid species (or genomes), indicating that the divergence had occurred in the common ancestor. Study of diversity of DNA sequences of repeated genes gives a broad insight into genome organisation, evolution and the diversity of banana, enabling progress towards gene discovery and exploitation for plant breeding.

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