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.

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.

References

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