Genetic Improvement of Bananas for Resistance to Diseases and Pests: Plant-Related Constraints

A. CHARRIER*

This paper is taken from a synthesis presented by CHARRIER (1993) at the International Symposium on Genetic Improvement of Bananas for Resistance to Diseases and Pests, held at CIRAD in Montpellier, France, 7-9 September 1992. It is a review of the genetic structures of banana, with emphasis on organization of the species complex and fine genomic structures (genomic mapping, cytogenetics, etc.).

Biometric approach

PERRIER (1993), using a biometric approach, describes the challenging task for banana geneticists to reach a full understanding of this species group.

Indeed, it seems that intra- and interspecific crosses, vegetative multiplication and polyploidy have together created complex structures particularly characterized by wide allelic and structural diversity. The disappearance of a large number of intermediary genotypes does not facilitate the reconstitution of phylogenetic trees. Reliable results can, however, be obtained by combining different types of indicators of genetic diversity (morphological characters, biochemical and molecular markers).

The data can be processed by standard methods (principal component analysis, factor correspondence analysis) to reveal intraspecific diversity and interspecific affinity, and determine the relevant variables. Correspondence analysis of morphological criteria revealed wide dispersal of AAB genotypes, clearly differentiated from Plantains.

Cladistical analyses can also be used. However, they could lead to faulty interpretations for groups of species in which crosses and introgressions have been critical in their evolution.

Different approaches and diversity analysis tools have been developed for genetic evaluation of banana.

Evaluation based on morphological characters

A review of conventional taxonomy based on morphological characters (HORRY, 1993) revealed that 3 of the 13-15 *Eumusa* species are particularly significant:

- *M. balbisiana* shows no clear distinction of subspecies,
- *M. acuminata* presents high diversity and is divided into subspecies,
- *M. schizocarpa* includes two morphological types corresponding to two habitats.

M. acuminata and *M. balbisiana* are sympatric in some ranges and have produced large numbers of natural interspecific hybrids. The triploids are either AAB or ABB, depending on the predominance of *acuminata* or *balbisiana* characters as established from a set of 15 morphological variables. The overlap and interfertility of *M. schizocarpa* and *M. acuminata banksii* in Papua New Guinea have led to between-species introgressions.

Enzymatic polymorphism

Such hypotheses of genetic relationships between different banana groups are based on enzyme polymorphism studies. A compartment of AAB and diploid AA Plantains occurs within the distribution range of *M. acuminata banksii*. This seems to confirm the genetic resemblance between this group, *M. acuminata banksii* and the Plantain subgroup.

An important study on the classification of Pacific bananas (LEBOT *et al.*, 1993) analyzed 563 cultivars and 360 open-pollinated seedlings for three enzyme systems, thus revealing 52 electromorphs. This study confirmed the clear differentiation between *M. acuminata* and *M. balbisiana*. The geographic distribution of the three Pacific plantain subgroups (Popoulou, Maoli, Idena) was thus clarified. The close resemblance of their enzyme profiles indicates that their morphotypes occurred by somatic mutation.

Molecular markers

The development of RFLP and RAPD techniques along with greater and finer labelling potential offers further insight into the organization of the banana species complex. NOVAK's study (AFZA *et al.*, 1993) based on RFLPs revealed by oligonucleotide probes and RAPDs led to the identification of numerous markers specific to the A or B genome.

The study of CARREEL (CARREEL *et al.*, 1993) is along the same lines. However, here the RFLPs were revealed by single copy probes. This preliminary study confirmed the genetic

* ORSTOM, BP 5045, 34032 Montpellier Cedex 1, France.

resemblance between the species and cultivars of the Pacific zone. Novak's team used RAPD techniques to reveal polymorphisms between cultivars that were not identified by other molecular marking techniques. This was the case for the Cavendish subgroup whose morphotypes are known to be difficult to genetically classify. A Grande Naine mutant was thus distinguished from its parent. The University of Birmingham (UK) also used RAPDs to differentiate a cultivar from its dwarf mutant. The results show the clear research potential of the technique for controlling somaclonal variation, identifying induced mutants and legal protection of cultivars.

Structural diversity of genomes

The Novak team used flow cytometry to determine the difference in the size of the A (1.25 pg) and B (1.14 pg) genomes (AFZA *et al.*, 1993). The technique can also be used to evaluate ploidy levels and detect possible ploidy chimera.

The cytogenetic studies of BAKRY (FAURÉ *et al.*, 1993a) analyzed chromosome anomalies found in most diploid cultivars and counted translocations and inversions. All diploid cultivars were heterozygous for at least one translocation but no structural heterozygosity was observed in wild bananas. There seems to be no link between structural heterozygosity and sterility. Translocations do not exclude the formation of 11 bivalents and sterility could also be gene-induced. The high degree of structural heterozygosity observed in diploid cultivars suggests an intersubspecific origin. Chromosome rearrangements have already been observed within the same subspecies. A cytogenetic map of *M. acuminata* based on intra- and intersubspecific crosses would reveal clear and useful phylogenetic information.

The genome mapping of FAURÉ (FAURÉ *et al.*, 1993b) provides valuable information on structural rearrangements involved in the transmission and recombination of chromosomal segments. This work should provide a dynamic view of banana evolution and serve to develop better uses of rearrangements in breeding programmes based on wild x cultivated banana crosses. This mapping also indicates the heritability of some characters of agronomic interest, especially pest and disease resistance.

Conclusion

Banana offers interesting and unique biological characteristics, including:
- ploidy variation,
- gene flow and introgression between different genomes occurring in the same ecogeographic zone,
- somaclonal variation occurring by vegetative multiplication of cultivars, etc.

The reported studies are interrelated and highlight the expertise acquired in genetic marking and cytogenetics of banana. These new techniques provide fresh elements for analyzing allelic and structural diversity. The findings are useful for accurate genetic identification of cultivars, especially by the RAPD technique.

The use of cytogenetics and genome mapping for studying the organization and evolution of the species complex offers a wider scope for rational use of genetic resources and a choice of crosses with clearly identified genetic groups (intra- and intergroups).

Genetic molecular markers are highly effective means for selecting, screening and breeding plant material.

Recent innovative research on banana genetics (basic data) should be supported and developed. It would also be critical to adopt a multidisciplinary approach to enhance medium-term studies aimed at reaching specific objectives (banana type, disease resistance, adaptation to local conditions).

References

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Addendum: *Dr Novak, an active participant at the Symposium, has just passed away. On behalf of all participants at this Symposium, we would like to offer our deepest sympathy to his wife and family.*