Genotyping of Composite Germplasm Set, Tier 1, *Musa* (SP1)

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Genetic resources sampling

Leaves of 549 genotypes were collected in the following three major *Musa* collections (and breeding programs):

- CIRAD (Neufchateau, Guadeloupe): 237 accessions
- IITA (Onne, Nigeria): 192 accessions
- CARBAP (Njombe, Cameroon): 120 accessions

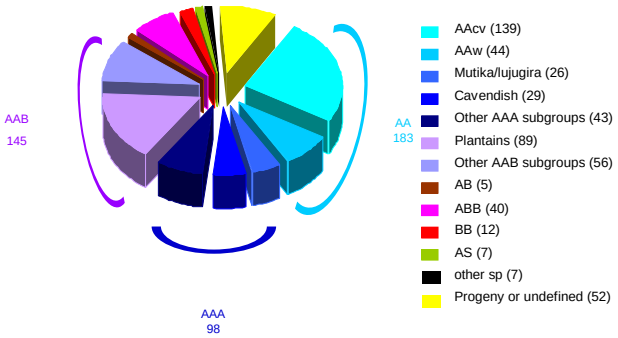


Fig. 1: Genome constitution of the 549 genotyped accessions

Genotyping using SSR markers

Genotyping of the 549 accessions using microsatellite markers was undertaken by CIRAD (22 SSRs) and IITA (27 SSRs).

Difficulties encountered:

1) Competitive amplification does not allow definition of the correct dose for multiallelic complexes (polyploids).

2) Preferential amplification of certain alleles makes the scoring decision difficult.

3) Due to a broad range of allele sizes, comparability among experiments was difficult to assess.

To overcome these difficulties, multiple controls were used at IITA and CIRAD which, in addition, are working with two different sequencers (ABI and LICOR respectively).

- Migration ladder
- 1st internal standard (mixture of 3 accessions: Popoulou (AAB), Kunnan (AB) and Paka (AA))
- 2nd internal standard (mixture of 3 subgroups: African plantains, Cavendish and East African Highland bananas)

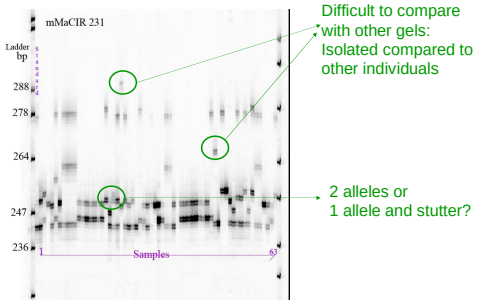
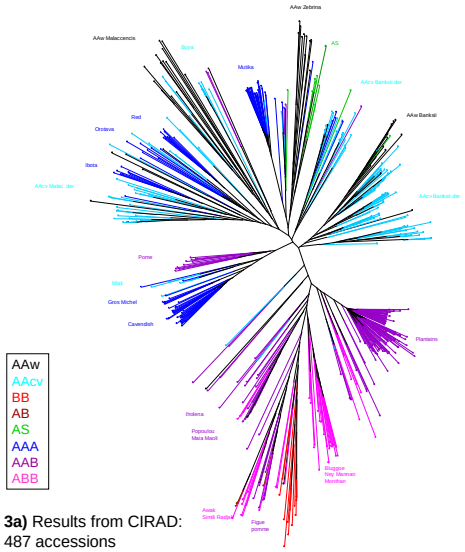
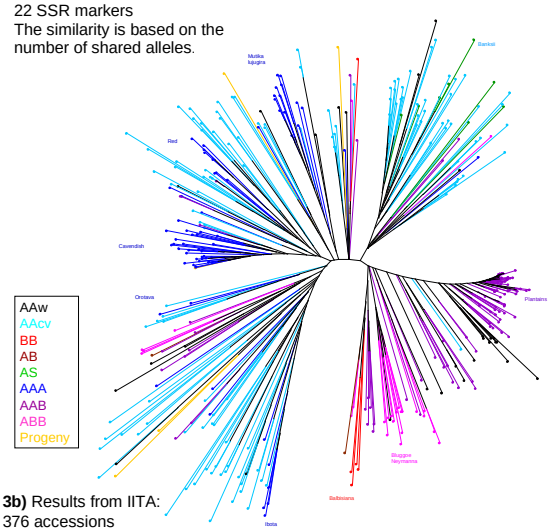


Fig.2: Acrylamide gel migration of SSR amplicons on LICOR Sequencer

Diversity analysis



3a) Results from CIRAD:
487 accessions
22 SSR markers
The similarity is based on the number of shared alleles.



3b) Results from IITA:
376 accessions
20 SSR markers
The similarity is based on Dice index

Fig. 3 a) and b): Phylogenetic trees based on The Neighbor-Joining method (developed by Saitou, N., Nei, M., 1987). The software used is Darwin5: http://darwin.cirad.fr/darwin

Conclusions

The study allows clear definition between different genome constitutions and subspecies/subgroups.

Analyses performed at CIRAD with 22 SSR markers and at IITA with 20 SSR markers were found to correlate, although there are some discrepancies which still require further analysis.

For the first time it is possible to distinguish among accessions originating from Papua New Guinea.

Better fine tuning now allows tracing diploid ancestors of triploids.

Breeding programmes performing affiliation studies will gain from this study, enabling cross predictions.

It is possible to see the evolution of *Musa acuminata*, but not *Musa balbisiana* for which there is a need to include a wider range of representatives.