

**MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION  
OF *Musa* GERMPLASM, INCLUDING WILD SPECIES AND CULTIVARS,  
AND SELECTION OF SUPERIOR GENOTYPES**

**By**

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## ABSTRACT

Banana (*Musa* spp.) is the most important fruit crop in Sri Lanka and is identified as a species for genetic improvement. Genetic variability present in *Musa* spp. in the country is rich and needs characterization for its use in banana improvement. Genetic variability existing in commercial cultivars such as 'Ambon' and 'Kolikuttu' also needs to be assessed for their genetic improvement. Characterization or estimation of genetic diversity at molecular level, using Simple Sequence Repeats (SSR) is a rapid and accurate technique complementary to morphological characterization.

In this research, 27 *Musa* germplasm (*M. acuminata*, *M. balbisiana*, polyploids and interspecific hybrids), were characterized using SSRs and morphological characters. In addition, germplasms of 'Ambon' and 'Kolikuttu' were explored, collected and analyzed using SSR primers.

Morphological characterization of *Musa* generated useful information for clustering the germplasm. However, difficulties were faced in scoring morphological data as some character states were not discrete. Therefore, morphological characterization alone could lead to wrong conclusions.

Specific SSR regions of *Musa* were amplified by PCR, using SSR primers (AGMI and MaSSR primers). PCR products were separated by PAGE and the bands were detected by both autoradiography ( $P^{33}$  labeling) and silver staining. UPGMA grouping of *Musa* germplasm using SSR data showed a certain extent of similarity to morphological grouping. Characterization by both morphological and SSR gave a better picture of the

genetic relationship of *Musa* cultivars and wild species in Sri Lanka.

SSR primers MaSSR 20 a/b, MaSSR 18a /b, MaSSR 22a/b MaSSR 24 a/b, MaSSR 7a/b and AGMI 95/96 are useful for characterization of distantly related *Musa* spp. in Sri Lanka. *Musa* spp. used in analysis showed a great extent of SSR diversity, which reflects a rich genetic diversity among them. Therefore, the gemplasm used in this research is recommended for conservation in the field and *in-vitro*.

MaSSR 24ab can be used to differentiate inter-specific cultivars (AAB or ABB) from AA or AAA genotypes. SSR markers were used to identify 'Unel' (AA), 'Navari' (AA), 'Bahu' (ABB), 'Mondan' (ABB) and Etikesel (BB) which are useful in cultivar identification and breeding.

The wild spp. 'Unel' (*M. acuminata* colla, AA) is extremely diverse from the rest of the genotypes followed by 'Navari'. Therefore, the possibility of 'Unel' contributing genes into Sri Lankan cultivars is rather low in contrast to the other wild species 'Etikesel' (*M. balbisiana* colla). Fertile diploids viz. 'Unel', 'Etikesel' and 'Navari' are distinct genotypes useful for genetic mapping and breeding. 'Muwanethikesel' is a possible mutant of 'Walsuwandel'. 'Alukesel' and 'Etamuru' which produce seeds occasionally are also unique genotypes useful in banana improvement. 'Puwalu' and 'Seenikesel' are superior genotypes with respect to bunch, fruit and yield characters. These two genotypes were recommended for further evaluation and were morphologically characterized in detail. 'Kolambaseeni' is also a potential variety for commercial cultivation.

Genetic variation between 'Ambon' accessions observed was very little. Based on molecular and morphological data, two distinct genotypes: I. Typically long (> 20cm),

strait and shiny fruits with brown strips on mature fruits and II. Typically short (<20 cm), curved and dull fruits, pigmented with no brown strips were identified. Accessions collected from Alawwa and Wattedegama (in group I) were selected as superior 'Ambon' accessions in terms of bunch characteristics.

Morphological and molecular data suggest that considerable genetic variation exists within 'Kolikuttu' collected from different areas. In the germplasm collection, the genotypes 'Idal Puwalu' (Synonym 'Athdath Kolikuttu'), 'Kutti puwalu', Kotiyagala type in Siyambalanduwa and an ecotype in Samanthurai were identified. 'Kutti puwalu' and 'Idal Puwalu' were identified as superior genotypes with respect to bunch characteristics. Kotiyagala type seems to be superior for pest, diseases and drought tolerance/resistance while Samanthurai accession may be superior for salinity and drought resistance.

This information could be used in future exploration and collection of germplasm, characterization and evaluation of genetic resources of *Musa* in Sri Lanka.