

## **Intersectional Relationship between Eumusa and Rhodochlamys of the Genus *Musa* Using Morphotaxonomy and Microsatellite Markers**

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### **Abstract**

The genus *Musa* of the family Musaceae has been classified into four sections, i.e. Eumusa, Rhodochlamys, Callimusa and Australimusa. Eumusa members have contributed considerably to the evolution of present-day bananas. Rhodochlamys members, which are very close to the section Eumusa and more specifically to *Musa acuminata*, have a wide distribution in the Indian subcontinent. This paper deals with a detailed assessment of intersectional relationships between 24 accessions from Eumusa, Rhodochlamys and hybrids of Eumusa x Rhodochlamys, using morphotaxonomic and molecular characterisation. All the test accessions were morphotaxonomically characterised and documented. A total of 21 primer pairs were used to assess the microsatellite polymorphism, of which 81% amplified products, resulting in discrete, reproducible amplicons. A total of 145 alleles were identified with a mean of 8.05 alleles per primer pair. An average PIC of 0.55 was observed. The developed dendrogram failed to project a clear-cut distinction between Eumusa and Rhodochlamys members, indicating a close genetic make-up. Diversity analysis suggests that 'Matti', a Eumusa member, could be a parthenocarpic derivative of *M. acuminata* ssp. *burmannica*. Four *M. acuminata* wild forms identified from North Eastern India during recent explorations proved their uniqueness but exhibited higher genetic relatedness to Rhodochlamys. *Musa laterita* and its progenies grouped in the same cluster in both morphotaxonomic and molecular characterisation, indicating their close genetic make-up.

### **INTRODUCTION**

Banana belongs to the family of the Musaceae and is botanically referred to as *Musa*. The genus *Musa* has been classified into four sections, i.e. Eumusa, Rhodochlamys, Callimusa and Australimusa (Cheesman, 1947). Rhodochlamys species naturally occur together with *Musa acuminata* (Uma et al., 2002), which might have contributed to their close genetic make-up. But this has not been assessed either through morphotaxonomy or molecular markers, and further studies on the sectional relationship of Eumusa and Rhodochlamys are scarce. Hence the present study on elucidating the intersectional relationship between the two sections.

### **MATERIALS AND METHODS**

A total of 50 accessions, including wild relatives and parthenocarpic landraces, were collected from areas where *Musa* has originated and is cultivated. The morphotaxonomic data for 107 traits were recorded for 24 accessions. These scores were

subjected to Multivariate Hierarchical Cluster Analysis using NTSYS Pc version 2.01e (Rohlf, 1998). The isolation of genomic DNA was done with CTAB method. Twenty-three pairs of microsatellite primers were used to assess the polymorphism. Microsatellite bands were visualised by silver-nitrate staining according to Kaemmer et al. (1997) and Creste et al. (2003). The relationships among the tested accessions were calculated using Unweighted Pair Grouping Method with Arithmetic averages (UPGMA) and the Sequential Agglomerative Hierarchical and Nested (SAHN) clustering method (Sneath and Sokal, 1973).

## RESULTS AND DISCUSSION

In morphotaxonomic characterisation, *M. acuminata* ssp. *burmannica*, *M. acuminata* ssp. *burmannicoides*, ‘Matti’ (AA) and ‘Pisang Jajee’ were grouped in one cluster, but in molecular characterisation *M. acuminata* ssp. *burmannica* grouped with ‘Matti’. This suggests that *M. acuminata* ssp. *burmannica* might have contributed to the development of the parthenocarpic diploid landrace ‘Matti’. ‘Pagalapahad wild’, ‘Lairawk’ and ‘Chengdawt’ were grouped in one cluster in both morphotaxonomic and molecular characterisation, indicating their genetic proximity. They could be exploited for the development of synthetic improved diploids. *Musa acuminata* wild forms collected from Khasi hills and Meghalaya were identified as synonyms and had close genetic make-up with *Rhodochlamys* species. The present results suggest that these wilds forms can also be utilised for the development of intersectional hybrids. ‘Sanna Chenkadali’ (AA) and ‘Pisang Jari Buaya’ (AA), though morphologically very dissimilar, were genetically close. Similar results were also reported in diversity analysis using RAPD and AFLP techniques, suggesting that there is no strong correlation between genetic diversity and phenotypic characters (Crouch et al., 2000; Ude et al., 2003). Genetic closeness between *Musa laterita*, a *Rhodochlamys* species, and its progenies was shown. Results reiterated the fact that the sections *Eumusa* and *Rhodochlamys* of the genus *Musa* are genetically close (Simmonds and Shepherd, 1955; Wong et al., 2002) and could be successfully exploited in a gene pyramiding programme through intersectional hybrids.

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## Tables

Table 1. Clustering patterns among *Rhodochlamys* and *Musa acuminata* wild forms and landraces.

Cluster	Grouping of the accessions	
	Morphotaxonomic analysis	Microsatellite analysis
Ia	Matti, Anaikomban, <i>M. acuminata</i> ssp. <i>burmannica</i> , <i>M. acuminata</i> ssp. <i>burmannicoides</i> , P. Jajee	Matti, <i>M. acuminata</i> ssp. <i>burmannica</i>
Ib	Pagalapahad wild, Lairaw, Chengdawt	Pagalapahad wild, Lairaw, Chengdawt
Ic	Khasi wild, Meghalaya wild, <i>M. aurantiaca</i> , H-3, H-2, <i>M. ornata</i> , <i>M. rosacea</i> , <i>M. laterita</i> , H-1, NISH	Khasi wild, Meghalaya wild, <i>M. ornata</i> , <i>M. velutina</i>
Id	<i>M. velutina</i> , <i>M. velutina</i> hybrid	Sanna Chenkadali, P. Jari Buaya
Ie	Sanna Chenkadali, Cv. Rose, P. Lilin	<i>M. rosacea</i> , <i>M. aurantiaca</i> , NISH, <i>M. velutina</i> hybrid
If	-	<i>M. laterita</i> , H-3, H-1, H-2
Ig	-	<i>M. acuminata</i> ssp. <i>burmannicoides</i> , P. Jajee
Ih	-	Cv. Rose
II	P. Jari Buaya	Anaikomban, P. Lilin

## Figures

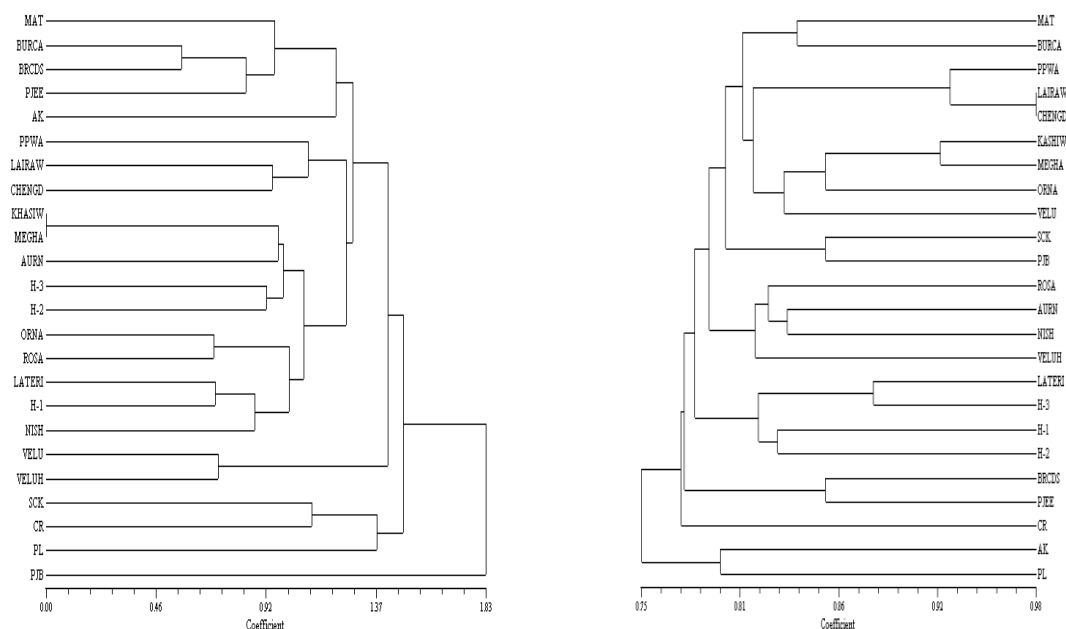


Fig. 1. Dendrogram showing the genetic affinities among test accessions, analysed by morphotaxonomic (left) and molecular (right) characterisation.