GERMPLASM COLLECTION AND EVALUATION OF *MANGIFERA* L.

A.G. Yunus and M.S. Saad

Faculty of Agriculture
Universiti Putra Malaysia, 43400 UPM, Serdang, Selangor, Malaysia

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Introduction

There are 15 *Mangifera* L. species described as occurring in Malaysia (Mukherjee, 1985) and nine are cultivated. Three species, namely *M. indica* L. (mango), *M. odorata* Griff ('kuini') and *M. foetida* Lour ('bacang') are widely cultivated in the Peninsular Malaysia. The wild species of both *M. indica* and *M. foetida* can be found in Malaysia but the origin of M. *odorata* is unknown. The objective of the project was to sample the genetic resources of the three most commonly cultivated species in the Peninsular Malaysia for the purpose of conservation and utilisation. Before the germplasm can be utilised, the collection requires evaluation.

Materials and Methods

The genetic resources were sampled using the random and non-random methods as suggested by Hawkes (1980). Samples were collected in August and October 1997 from all the eleven states of the Peninsular Malaysia. Protocols for the molecular analysis of *Mangifera* using random amplified polymorphic DNA (RAPD) were developed at the Department of Biotechnology, UPM, Serdang.

Results and Discussion

The numbers of *Mangifera* accessions collected were 147, which include *M. indica* (58), *M. odorata* (44) and *M. foetida* (45) (Yunus and Saad, 1998). The three *Mangifera* species were found in all states but mostly in Trengganu (27), Kedah (21), Johore (20), Pahang (19), Kelantan (15) and Perak (13). For the other states, the number was less than ten. The plants are conserved as living collection at the Plant Genetic Resources Centre, UPM, Serdang. Collection data with location and botanical description of the accessions collected is with the first author at the Department of Crop Science, UPM, Serdang. The banding patterns after electrophoresis can be observed after the following treatments: Total genomic DNA was extracted using the sarkosyl method and the reaction mixture for polymerase chain reaction consisted of 10ng of DNA, 3mM MgCl2, 200μM of primer, 0.25 unit of Tag DNA polymerase, 200μM each of dCTP, dGTP, dATP and dTTP in a final volume of 10μl. Amplification was performed in the thermal cycler for 40 cycles after initial denaturation for 30 seconds at 94°C. Each cycle consisted of 1min. at 94°C, 1min at 34°C and 2min at 72°C. For electrophoresis 11μl of aliquot of amplified sample were run on a 1.4 % of agarose gel in TBE buffer (0.5x Tris Borate EDTA) at a constant 80 v for 2h. The gel was stained using ethidium bromide. The protocols were similar to that used for *Lilium* (Yamagishi, 1995) and taro (*Colocasia esculenta*) (Yunus et al. 1997) except for the extraction method. The present method used sarcosyl for genomic DNA extraction. The DNA extraction in *Lilium* and *Colocasia* used CTAB (Cetyltrimethyl ammoniumbromide) method, which is slower than the sarcosyl method. The protocols are being used in the analysis of the collected germplasm for the determination of genetic diversity.

Conclusions

The *Mangifera* accessions collected showed variability in the shape, size and taste of the fruits (Yunus and Saad, 1998), and most of the mango accessions have different vernacular names which indicated that the species can be identified morphologically. Molecular analysis will further reveal the diversity within each species and the presence of wild relatives of *M. indica* and *M. foetida* is a potential source of new genes.

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