

WNRF Technical Bulletin : 10

Collection, Conservation, Characterization and Identification of Superior Clones of *Morinda citrifolia* L. in Bay Islands

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Published by	Edited by	Author	Year of Publication
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Citation :

Singh, D. R. 2012. Collection, Conservation, Characterization and Identification of Superior Clones of *Morinda citrifolia* L. in Bay Islands. WNRF Technical Bulletin 09, Central Agricultural Research Institute (CARI), Port Blair, Andaman & Nicobar Islands and World Noni Research Foundation, Chennai, India, p.43.

Summary and Conclusion

We have mapped and identified DNA markers linked to morphology, yield and yield components. Morphological characters in plants may be affected by environmental conditions, and a species grown in different environmental conditions may be different and thus the use of morphologically characters for classification may result in some mistakes. But it might be support the identification of superior clones.

The genetic similarity analysis demonstrates an extensive genetic variability between the tested clones and the dendrogram depicts the genetic relationships among the clones, suggesting a geographic relationship. The results indicate that the RAPD and ISSR markers permitted the identification of the assayed accessions, although they are derived from the same geographic origin. Efficiency of a molecular marker technique depends upon the amount of polymorphism it can detect among the set of accessions under investigation.

Genotype distribution on the consensus tree based on the combined banding patterns of RAPD and ISSR significantly differed may be due to the possibility that each technique amplified different parts of the genome. RAPD and ISSR has been extensively used in many crops concluded that ISSR would be a better tool than RAPD for phylogenetic studies (Ravi *et al.*, 2003; Galvan *et al.*, 2003). RAPD showed the BBD and MAA-1 as most divergent ones and the BMN, MEM and BGL-2 accessions were most diverse as per the ISSR results. Combined RAPD-ISSR results showed that BMN with BGL-2 accessions were found most divergent. A close genetic similarity was found in some of the cultivars analyzed as shown by high values of similarity index. Based on similarity matrix using simple matching coefficient, the similarity values between all the *Morinda spp.* were from 38 - 94% for RAPD, 25-94% for ISSR and 33-95% for combined RAPD-ISSR analysis. Although, the similarities detected with ISSRs (0.944) between MTC and JGH were nearly same as similarity observed with RAPDs (0.943) between AHD and SHE-1. Also for combined RAPD-ISSR it was found 0.948 between SEH-1 and AHD-1 similar to RAPD and ISSR result. This may be due to either seed dispersal through sea or the seedlings transported from one place to another by migrating people for its medicinal uses. Genetic variations observed in some of the accessions are very narrow like BMN and MEM and between BMN and BGL-2, it might be because less distance between accessions. This study provides evidence that RAPD and ISSR polymorphisms could be used as efficient tools for the detection of similarities and phylogenetic relationships of the studied genotypes. The same conclusion was obtained by several authors (Seehalak *et al.*, 2006; Heikal *et al.*, 2007).

We conclude that RAPD variation is useful in establishing genetic relationships between *M. citrifolia* accessions. In the future, the inclusion of more clones in the analysis with other molecular markers (*viz.* SSR, etc) and the complementing of molecular data with other techniques will improve the

resolution of genetic relationships and the potential use in *M. citrifolia* plantations in Bay Islands. The techniques used in the present study seem to be useful for organization and conservation of *M. citrifolia* accessions collections. PCR-RAPD and ISSR technique may provide useful information on the level of polymorphism and diversity in *M. citrifolia*, showing their utility in the characterization of germplasm accessions. The establishment of genetic relatedness and molecular characterization of clone collection in Chile is fundamental as an informational basis for breeding and plantations programs. The results obtained from this study would be useful for better management and identification of clones and also for avoiding mislabeling of the genotypes studied.

Comparison for morphological, molecular and biochemical components has provided a valuable set of markers having potential for breeders to use in the selection of improved *M. citrifolia* genotypes. The studied markers might be used to selection of potentially superior accessions and the elimination of undesirable ones in early stages of a *M. citrifolia* breeding program aimed at developing improved synthetics.

These experimental findings shared in this bulletin are only a preliminary observation. Consequent and consistent visits in the future can provide more information about the identified clones on *Morinda citrifolia*, which helps us to draw some more conclusions. With advancement of scientific research in the arena of plant molecular biology a number of molecular techniques have been developed in recent years. Most of these have been efficiently employed for characterization of genetic diversity of *M. citrifolia* L. to produce similar notion of low level of genetic diversity in the species despite wide phenotypic variability and significant differences in biochemical properties, due to different geographical regions. *M. citrifolia*, an undomesticated plant species uniquely exhibits naturally widespread genetic monomorphism as revealed in most of the molecular studies.

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