



Review

Morphological and molecular characterization and evaluation of mango germplasm: An overview



Ahmad Sattar Khan*, Sajid Ali, Iqrar Ahmad Khan

Institute of Horticultural Sciences, University of Agriculture, Faisalabad-38040, Pakistan

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ABSTRACT

Mango being famous as ‘King of Fruits’ is one of the excellent and admired fruit crops of tropical and subtropical areas around the globe. Characterization and evaluation of mango is an imperative step for germplasm conservation and utilization in the breeding programmes. Moreover, characterization of available germplasm is very crucial to identify desired traits or genes. For this purpose morphological and molecular markers are used. Morphological markers generally include those pivotal features that can be scored and distinguished by naked eye and easily be expressed in all environmental conditions. In contrast, molecular markers are used at molecular level and are more suitable for precise characterization, which in turn can successfully be utilized in the development of new cultivars with premium and desired fruit traits. Moreover, preservation of germplasm for future utilization in crop improvement needs accurate information. Consequently, there is an extreme need for integration of the precious available scattered information on various aspects of mango characterization. So, an attempt has been made to review all possible available literature comprehensively to provide essential details for identification of mango cultivars, characterization of desired traits or genes and evaluation of valuable germplasm with morphological as well as molecular markers. Consequently, the desired traits can be used successfully in future breeding programmes to boost quality mango production throughout the world.

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Contents

1. Introduction	354
2. Criteria for cultivar description	354
3. Morphological markers	355
3.1. Characterization and evaluation based on tree characteristics	355
3.2. Characterization and evaluation based on leaf characteristics	356
3.3. Characterization and evaluation based on inflorescence characteristics	356
3.4. Characterizations and evaluation based on fruit characteristics	357
3.5. Characterization and evaluation based on seed	357
4. Characterization and evaluation based on quality parameters	359
4.1. Fruit/pulp physical characteristics	359
4.2. Biochemical and sensory attributes	359
5. Biochemical markers	359
6. Molecular (DNA) markers	360
6.1. Restriction fragment length polymorphism (RFLP)	360
6.2. Variable number tandem repeat sequence (VNTRS)	360
6.3. Randomly amplified polymorphic DNA (RAPD)	360
6.4. Simple sequence repeats (SSR)	361
6.5. Expressed sequence tag-simple sequence repeat (EST-SSRs)	361

* Corresponding author. Fax: +92 41 9201086.

E-mail address: ahmad.khan157@yahoo.com (A.S. Khan).

6.6. Inter simple sequence repeats (ISSR).....	361
6.7. Amplified fragment length polymorphism (AFLP).....	362
7. Mango genomics and proteomics.....	362
8. Conclusion and future prospects.....	362
Acknowledgements.....	364
References.....	364

1. Introduction

Mango (*Mangifera indica* Linn.) is one of the choicest and admired fruit crops of the tropical and subtropical areas of the world. Its significance can easily be recognized by the fact that it is known as 'King of Fruits'. Utilization of germplasm with distinctive characteristics in breeding programmes desires precise information to develop new cultivars (Vasugi et al., 2012). Different mango cultivars in the world possess several handicaps such as alternate bearing, low yield, narrow ripening window and meagre fruit quality. Hence, it is very important to trace and exploit the genetic diversity in mango and ultimately preserve the vital germplasm of promising and threatened mango varieties/cultivars to broaden the genetic resource repository (Litz, 2004). Moreover, *Mangifera* species have originated in South-East Asia and this region has experienced enormous economic development. Natural and wild plantations of mango have been totally or partially destroyed due to the expansion of agriculture to feed the masses or for harvesting precious hardwood. Hence, this has resulted in irreversible genetic erosion of mango genetic resources (Kaur et al., 1980; Mukherjee and Litz, 2009; Sennhenn et al., 2014). Therefore, suitable efforts should be employed for the long term safeguard and conservation of precious mango genetic resources by utilizing both *ex-situ* and *in-situ* approaches (Bompard, 1993). However, conservation of mango genetic resources needs identification, characterization and evaluation of potential and unique germplasm for their utilization in various mango breeding programmes. Presently, it is extreme demand of time to identify, characterize, evaluate and conserve available precious genetic resources to improve yield and fruit quality of currently available mango germplasm (Rajwana et al., 2011). Therefore, several methodologies and procedures have been reported for the identification and detailed description of mango genotypes based on agronomic, morphological, biochemical and genetic traits (Krishna and Singh, 2007; Rajwana et al., 2011).

Characterization of various fruit plants can be carried out with the help of different markers. Markers are those particular plant features which can be documented with confidence, comparative affluence and ease (Beckman and Soller, 1986). However, two basic types of markers have been reported *i.e.* non-morphological markers (molecular markers) and naked eye polymorphism or morphological markers (Bhat et al., 2010). A basic informative descriptor list is developed by "International Plant Genetic Resources Institute" (IPGRI) to assist the identification of mango germplasm (IPGRI, 2006). This descriptor list comprises of passport data essential for the classification of various concerned accessions or cultivars/varieties and information perceived by the collectors. Characterization of data includes parameters as highly heritable traits, which can be recorded in the field and can easily be expressed in all environments and assessment data to help the evaluation of biotic and abiotic stress liability (IPGRI, 2006).

Nonetheless, it has been reported that extensive differences exist among mango genotypes of the similar clones in any particular orchard specifically with respect to fruit shape, size, colour, aroma, flavour, eating quality and texture which is usually endorsed either by outcrossing or natural mutations (Singh, 1960; Mukherjee and Litz, 2009). Moreover, with the passage of time, mutations accrued in various mango genotypes, which may have resulted in polymor-

phism amongst the current commercially grown mango varieties in various mango growing pockets of the world. Consequently, it becomes essential to identify the phylogenetic associations and explore possible variations at morphological as well as molecular level in all available germplasm. At the same time, it further helps to evaluate the possible range of differences regarding morphological traits conferring to ecological variability (Manchekar, 2008). Various mango cultivars/varieties have also faced prodigious confusion about nomenclature as numerous synonyms are present for the same cultivars/varieties. Plant breeders and geneticists are mainly more concerned with germplasm diversity at molecular level for crop improvement programmes (Hawkes, 1991). However, farmers are generally interested in morphological parameters as it is simplest and easy to execute. But they usually face challenges for the identification of cultivars which are more productive in their native agro-climatic areas as they are generally unfamiliar with various traits of mango cultivars that are growing in their respective countries, resulting in low productivity. Hence, characterization is the standardized, simple as well as repeatable method for identification, evaluation and conservation of mango germplasm diversity (Griesbach, 2003; Wahdan et al., 2011).

Different markers have been used increasingly for screening of vital germplasm to study heritable diversity, identification of redundancies in the germplasm collections, assessment of the varietal stability and therefore, help to resolve the taxonomic relationships among various cultivars or species (Bally, 2011). However, there is still an extreme need for integration of the precious available scattered information on various aspects of mango characterization. So, we have endeavoured to review some of the important and recent progress in application of various markers in the identification, characterization and evaluation of genetic diversity in mango and this review enables reader to effectively utilize morphological and molecular markers in breeding programmes for sustainable mango fruit crop improvement around the globe.

2. Criteria for cultivar description

In past, some efforts had been made to accumulate the available mango descriptors but due to narrowness, those descriptors had not been properly employed for mango germplasm description (Mukherjee, 1953; IBPGR, 1989). The comprehensive descriptor list (IPGRI, 2006) prepared by IPGRI consists of valuable passport data for the identification of various accessions/cultivars, characterization of recorded traits (considered to be inherited that can easily be noted in the field and generally are express-able in all environmental conditions) and initial evaluation at morphological level, has further enhanced the cultivar/varietal description and evaluation process. Morphological data are imperative in preliminary germplasm evaluation as it consist of tree (growth habit and height of the concerned mature tree), leaf (shape, margins, length, width and colour of young as well as mature leaf) and inflorescence (growth habit, position, flowering density, flowering pattern, shape, length, width, colour, pubescence, absence or presence of leafy bracts in inflorescence) characteristics which can be recorded easily in the field (Mukherjee and Litz, 2009; Knight et al., 2009). Moreover, additional data used in initial eval-

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