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RESEARCH ARTICLE

WILD MANGO (*MANGIFERA INDICA* L) 'APPEMIDI' FROM WESTERN GHATS OF INDIA

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ABSTRACT

In India besides Indo-Burma (NE) region, the Western Ghats (WG) also happens to be one of the richest biodiversity hotspots in the world. However, in recent times this biodiversity is under threat due to degradation and fragmentation of prominently diverse tropical rainforest. This biodiversity of Western Ghats includes varieties of mango (*Mangifera indica*), which are mainly used for whole fruited immature fruits popularly known as 'Appemidi' in Karnataka. An exploratory study was carried out to review the morphological traits (fruit and leaf) and biochemical traits (total phenols and total flavonoids) in fifty Appemidi genotypes. The sap (latex) of the fruit is also a rich source of organic compounds (total volatiles) mainly, suggesting its potential to be used essentially in the food industry (pickling). Divergence observed in these traits, gives intimating advantage for multi-type cultivar advancement focusing on food and pharmacy. With several of the genotypes becoming extinct due to negligence and exploitation there is an urgent need to conserve *in situ* as well as *ex situ*. Not only some of them can be promoted for cultivation but also these could be used further in the breeding programs as a source for desirable traits for pickling. The outcome achieved in the study can be utilized as input for domestication and promote extensive use of the species, eventually helping to conserve wild fruit species.

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INTRODUCTION

India is habitat to remarkable population of extensive flora and fauna exhibiting some of the world's most diverse regions viz., Indo-Burma, Himalayas, Andamans and Western Ghats. Mango originated in the Indo-Myanmar region (De Candolle,1884; Mukherjee, 1951).The diversity with diverse bearing habits, fruit forms, flavours and tastes in mango has led to the identification of seven centers of diversity for *Mangifera indica* L.((Mukherjee,1951; Naik and Gangolly,1950 and Ganguly *et al.,*1957).The 'Peninsular Indian' region comprises of Western Ghats, which truly is magical 'global hottest hotspots' of biological diversity in India being one of the most highlighted areas for the conservation (Myers *et al.*, 2000).The indigenous tender mango type in this location is natively known as 'Appemidi' in Karnataka.

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These are unique to the moist, tropical rainforest and transmit by rainfall and proliferate via seeds, and get carried away by streams and rivers. These varieties having typical raw mango flavor, sharp latex flow and crunchy pulp with great storing choice are acquiring significance as export commodity due to their sustainability for pickling of the whole tender mango fruit named as 'midi' in native speech (Vasugi *et al.,*2012).There is enormous force on collection and conservation of Appemidi, due to rapid deforestation as no attempt is being made excepting for very limited initiatives. These seedling genotypes need to be located, evaluated and characterized so that the best ones can be commercialized and useful genes associated with desirable traits viz., disease and pest resistance, could be harnessed. The aim of the present study was to quantify the phenotypic and biochemical aspects in Appemidi prioritizing on morphological tree-to-tree variations and significance for recognition and establishing the advanced cultivar. The Appemidi field survey was carried out in the Western Ghats of Karnataka and more precisely addressing the variations among the genotypes, thereby initiating to locate and evaluate the

seedling mango genotypes of this region having desirable traits for pickling.

MATERIALS AND METHODS

Study Area

Mango (*Mangifera indica* L.) most commonly known as 'Appemidi' in Uttara Kannada and Shimoga districts of Karnataka. This species are being native to India and endemic mainly in tropical rainforest of Malnad region. For the present study samples were collected from Kumta, Ripponpet, Sagar, Siddapura, Sirsi and Thirthahalli (Figure 1.). The Sirsi region has the highest elevation compared to other sites. Such species generally grow in regions where average rainfall ranges from 4000 mm – 8000mm and high humidity (90%) with the optimum growing temperature being 18°C –20°C.

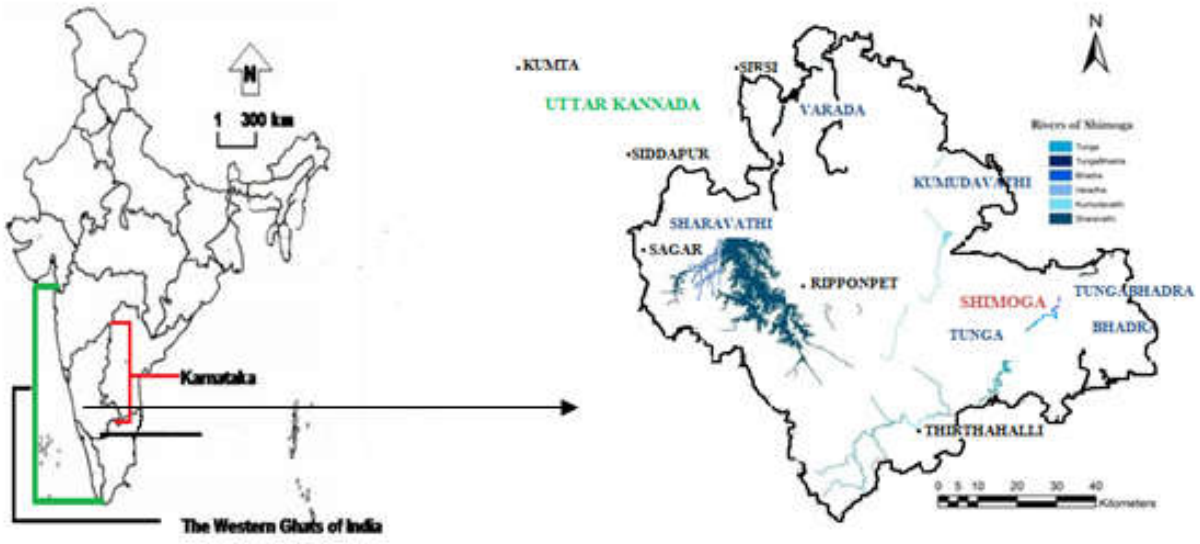

Figure 1. Study area map with sampling location of Appemidi from Western Ghats region of India

Sample collection, preparation and analysis

Collection and preparation

Samples of fresh and ripe fruits were collected from six geographic locations (Kumta, Ripponpet, Sagar, Siddapura, Sirsi and Thirthahalli) in Karnataka from January 2012 to May 2014.A total of fifty genotypes from six sites were selected (Table 1.). Five fruits per tree were collected randomly throughout the canopy. The traits fruit weight, fruit length, fruit width, fruit thickness, firmness and leaf area were assessed. For the biochemical analyses, fruits were collected and refrigerated (at -4^{o}C) soon after collection. All fruits were then transferred to ICAR-IIHR, Bengaluru for further analysis, washed, cleaned and separated into peel, pulp and kernel. The frozen pulp samples were free dried and stored in air tight bags and kept in the freezer at -20°C before further analysis. These samples were used for biochemical analysis total phenols, total flavonoids and Sap test (Vasudeva and Rajeshwari, 2014; AOAC, 2000).

Statistical Analysis

Descriptive statistics were derived by assessing the diversity using Mahalanobis D^2 statistics (Mahalanobis, 1936); clustering pattern of genotypes as described by Rao (1952) was followed. For phenotypic variation, the extent of trait variation between sites was determined from average of fruit weight (gm), fruit length (cm), fruit width (cm), fruit thickness (cm), pulp firmness (cm), total phenols (mg/100ml), total flavonoids(mg/100ml), sap test (sec) and leaf area (sq cm).

RESULTS AND DISCUSSION

Genetic Parameters

The fundamental pre-requisite for productive breeding program is genetic diversity. Collection and assessment of genotypes of any crop is a requirement for any breeding programme ensuring a major scope for utilizing genetic diversity. Morphological studies can be utilized to get selective data on variance within species. This constant variation in fruit character has essential significance for domestication, suggesting the potentiality for development of cultivar along with identification of elite genotypes (Leakey and Page, 2006). Additionally, domestication of wild fruit species relies on the development of the industry requirement as food products (Leakey, 1999). Therefore it is suggested that selecting genotypes must not be on the basis of morphology traits alone, but also biochemical traits should be given importance. Numerous studies is been certified variation in fruit traits in fruit tree species (Abasse *et al.,* 2011; Assogbadjo *et al.,* 2011; Fandohan *et al.,* 2011; Gouwakinnou *et al.,* 2011).The multivariate analysis (D^2) is a potent tool to measure genetic divergence across the genotypes (Murthy and Arunachalam,1966). Study was proposed to analyse the curve of genetic discrepancy in 50 Appemidi genotypes. The assessment of variability indicates extremely huge considerable difference among genotypes for all the characters under

Table 1. List of Genotypes and place of collection from Western Ghats of Karnataka

Genotypes	Species	Place of Collection
Aruna Gowda Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Balekoppa Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Chansi Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Dannalli Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Gedalahalli Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Gidagana mane	*Mangifera indica*	Sirsi, Uttara Kannada
Gidaganamavu	*Mangifera indica*	Sirsi, Uttara Kannada
Gorana Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Haldota Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Jeerige	*Mangifera indica*	Sirsi, Uttara Kannada
Jeerigeneermavu	*Mangifera indica*	Sirsi, Uttara Kannada
Kadikai	*Mangifera indica*	Sirsi, Uttara Kannada
Kalakai	*Mangifera indica*	Sirsi, Uttara Kannada
Kalgundikoppa Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Kalkuni	*Mangifera indica*	Sirsi, Uttara Kannada
Kalwa Gudda	*Mangifera indica*	Sirsi, Uttara Kannada
Kangaramatha	*Mangifera indica*	Sirsi, Uttara Kannada
Karigal Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Kashimidi	*Mangifera indica*	Sirsi, Uttara Kannada
Kovesara	*Mangifera indica*	Sirsi, Uttara Kannada
Kutumba Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Mahabalagiri Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Malanji Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Manadoorkatta Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Mandmane Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Manibhatta Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Modur Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Murgeer	*Mangifera indica*	Sirsi, Uttara Kannada
Nandgar Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Shidadakke Appe	*Mangifera indica*	Sirsi, Uttara Kannada
Thumbebeedu	*Mangifera indica*	Sirsi, Uttara Kannada
Adderi Jeerige	*Mangifera indica*	Sagar, Uttara Kannada
Hitalahalli Appe	*Mangifera indica*	Siddapura, Uttara Kannada
Holekoppada Appe	*Mangifera indica*	Siddapura, Uttara Kannada
Huliappekai	*Mangifera indica*	Siddapura, Uttara Kannada
Gurumurthy Appe	*Mangifera indica*	Kumta, Uttara Kannada
Isgoor Appe	*Mangifera indica*	Kumta, Uttara Kannada
Admundga	*Mangifera indica*	Thirthahalli, Shimoga
Athigadde Appe	*Mangifera indica*	Thirthahalli, Shimoga
Honasgadde Appe	*Mangifera indica*	Thirthahalli, Shimoga
Kuntehole Appe -1	*Mangifera indica*	Thirthahalli, Shimoga
Kuntehole Appe-2	*Mangifera indica*	Thirthahalli, Shimoga
Kuntehole Appe -3	*Mangifera indica*	Thirthahalli, Shimoga
Anantha Bhatta Appe	*Mangifera indica*	Sagar, Shimoga
Appemidi	*Mangifera indica*	Sagar, Shimoga
Dodderi Jeerige	*Mangifera indica*	Sagar, Shimoga
Sadamidi	*Mangifera indica*	Sagar, Shimoga
Karpoora Jeerige	*Mangifera indica*	Ripponpet, Shimoga
Sudoor Appe -1	*Mangifera indica*	Ripponpet, Shimoga
Sudoor Appe -2	*Mangifera indica*	Ripponpet, Shimoga

Table 2. Estimates of variability, heritability and genetic advance among 50 Appemidi genotypes

Traits	GCV (%)	PCV (%)	h^2 (%)	GA (%)
Fruit weight (gm)	68.1167	69.532	0.9597	137.4643
Fruit length (cm)	23.6371	24.3874	0.9394	47.1946
Fruit width (cm)	33.3942	33.8257	0.9747	67.9146
Fruit thickness (cm)	35.5982	36.257	0.964	71.9998
Firmness	32.1608	39.6455	0.6581	53.7436
Phenolics (mg/100ml)	44.2296	50.8435	0.7568	79.2608
Flavonoids (mg/100ml)	36.7929	40.7065	0.817	68.5062
Sap Burning (sec)	42.0792	57.9201	0.5278	62.9758
Leaf area (sq.cm)	51.6307	60.5308	0.7276	90.7209

Table 3. Average intra (bold) and inter cluster (off diagonal) D^2 values among three clusters in 50 Appemidi genotypes

Cluster	1	2	3
1	186.821	207.328	186.805
	(13.668)	(14.399)	(13.668)
2		18.703	221.05
		(4.325)	(14.868)
3			167.646
			(12.948)

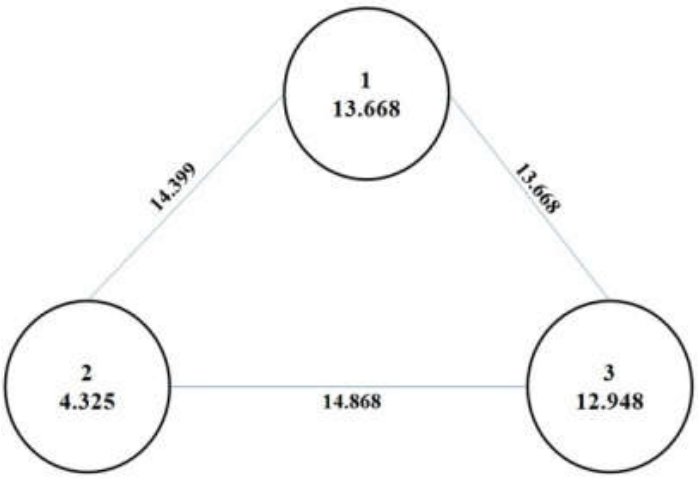

Figure 2. Genetic distance among 50 genotypes of Appemidi

Table 4. Distribution of 50 Appemidi genotypes into three clusters based on D^2 analysis

Cluster	No. of Genotypes	Name
I	36	Adderi Jeerige, Admundga, Ananthabhatta Appe, Appemidi, Aruna Gowda Appe, Attigadde Appe-2, Balekoppa Appe, Gidagana mane, Mahabalagiri Appe, Manibhatta Appe,Chanshi Appe, Dannalli Appe, Dodderi Jeerige, Gaddahalli Appe, Gidaganamavu, Gorana Appe, Gurumurthy Appe, Haldota Appe, Hithalahalli Appe, Holekoppad Appe, Honasgadde Appe, Huli Appekai, Isagoor Appe, Jeerige, Jeerige Neermavu, Kadikai, Kalakai, Kalkundi Appe, Kalkuni, KalwaGudda, Nandgar Appe, KangaraMatha, Karigal Appe, Karpoora Jeerige, Kashimidi, Manadoorkatta Appe
II	2	Kove Sara, Modur Appe
III	12	Kuntehole Appe-1, Kuntehole Appe-2, Kuntehole Appe -3, Kutumba Appe, Malanji Appe , Mandmane, Murgeer, Sadamidi, Shidadakke Appe, Sudoor Appe-1, Sudoor Appe-2 , Thumbebeedu.

Table 5. Relative contribution of different characters to genetic divergence of 50 Appemidi genotypes

Character	Contribution %
Fruit weight (gm)	10.44
Fruit length (cm)	9.46
Fruit width (cm)	15.26
Fruit thickness (cm)	4.40
Firmness	1.63
Phenolics (mg/100ml)	14.36
Flavonoids (mg/100ml)	14.85
Sap Burning (sec)	6.44
Leaf area (sq.cm)	23.10

investigation consequently revealing the presence of appreciable magnitude of genetic variance among the experimental material. The genetic parameter PCV was slightly higher than the GCV for all the nine characteristics studied indicating the role of environment (Table 2.). High heritability with high genetic advance was observed for fruit characters, leaf area, sap test, phenols and flavonoids. This showed that these characters have additive inheritance and are amenable for selection. The progenies derived from these genotypes would have similar characteristics like the parents due to the high heritability. High heritability has been reported in mango (Iyer, 1991; Sharma and Majumder, 1988a; Singh *et al*., 2004). Mango being highly heterozygous the genetic parameters and heritability estimates can vary with the population size.

Genetic divergence

The genetic divergence was high and 50 genotypes were grouped into 3 clusters (Figure 2; Table 3 & 4).Cluster I was observed to have 36 varieties of which 20 belonged to one region (Sirsi) with maximum diversity within the cluster (13.668). The intra-cluster distance was observed to be least in the III cluster (12.948) with majority of genotypes belonging to one region (Sirsi). The difference observed between these two populations is less. The genetic diversity within the clusters can be attributed to propagation by seeds and the existence of heterozygosity, indicating that most of the varieties have narrow genetic base and are descendant from a single source, although they are grouped into two clusters. The maximum inter-cluster distance was observed between cluster II and cluster III (14.868) and I and II (14.399), the distance being almost same. The 28 genotypes in these clusters belonged to one region (Sirsi), which substantiates the statement made earlier. The distance between clusters I and III was comparatively less (13.668) and these genotypes belonged to three nearby regions (Sirsi, Sagara, Siddapura) spread over a distance of 30-40 sq km, which also indicates that the diversity is essentially due to the heterozygosity and their origin is from a single source with the seed getting dispersed through flowing water. Thus cluster distance varied from 4.325 (cluster II) to 13.668 (cluster I).This shows the presence of more diversity among the genotypes within the clusters. Hence, importance should be given to the components of cluster I and cluster III for breeding programme. Thereby, selection within these clusters may be utilized based on suitable traits in crop improvement. Majumder *et al*. (2013), in an earlier study assessed genetic divergence through D^2-statistics and principal component analysis in 60 mango genotypes observed eight

clusters and concluded that the morphological characters influenced the diversity but not by the geographical distribution of the genotypes, which is similar to the results obtained here. Himabindu (2015) evaluated the genetic diversity in 34 mango cultivars through D^2 analysis and observed large variability for several morphological characteristics. This very clearly shows that the rich diversity in *M. indica* needs to be exploited by conservation and evaluation. The contribution of different characters towards the expression of genetic divergence has been given in (Table 5.). The maximum participation in manifestation of genetic divergence was exhibited by leaf area (23.10%), fruit width (15.26%), total flavonoids (14.85%), and total phenols (10.08%). Himabindu (2015), in her studies on indigenous mango varieties observed that total phenols contributed the maximum (20.68%) to the diversity followed by fruit skin thickness (19.79%), indicating that the characters with maximum contribution towards diversity should also be given due consideration for crop improvement. Hence, the characters contributing towards the expression of genetic divergence needs to be considered as a criteria in the selection of parents for breeding programme.

Conclusion

The study showed that diversity exists in the indigenous genotypes of "Appemidi". The genetic divergence analysis utilizing D^2 Mahalanobis test with data from 50 Appemidi genotypes resulted in three clusters indicating wide range of genetic diversity between the clusters based on morphological character. The clustering was not on the basis of their geographic locations, which showed the importance to seed dispersal mechanism by streams and rivers. The morphological components as well as certain biochemical compounds contribute to diversity. The high heterozygosity present has resulted in large variability for morphological characters. Estimation of volatiles in the parents and in the progenies can help in the screening of the progenies at the nursery stage thus helping in the selection. Conservation of indigenous types is a must to identify desirable traits in these genotypes for further use in the breeding programme. Evaluation of these types can help in the identification of better genotypes for products viz., pickle, which are gaining commercial importance.

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Conflict of interest

The authors declare that they have no conflicts of interest.

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