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RESEARCH ARTICLE

EVALUATION AND GENETIC DIVERSITY ANALYSIS OF LOCAL MANGO GERMPLASM

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ABSTRACT

The experiment was conducted during 2019-2021 at Regional Agricultural Research Station, Akbarpur, Moulvibazar, Bangladesh with twenty-three local mango genotypes to assess the performance and genetic divergence for the identification of suitable parents for the future breeding program. Wide variations were observed regarding the number of fruits/plant, fruit weight, percent of edible portion, and TSS of different germplasms. The highest number of fruit per plant (610) was observed in MIAkb001, highest individual fruit weight /plant (759.7g) was obtained from MIAkb015. The higher fruit yield was recorded from MIAkb001 (162.07kg). The percent of the edible portion was higher in MIAkb014 (65.71%) whereas maximum TSS (18%) was obtained from MIAkb007 and MIAkb015 respectively. The genetic divergence was assessed in 23 mango genotypes through multivariate analysis. The genotypes under this study were grouped into five clusters and the diversity was influenced by the morphological characters. The highest number (8) of genotypes were in cluster-I and the lowest (1) number of the genotype was in cluster-III. From the PCA we found, the number of fruits per plant (FNPP), fruits yield per plant (FYPP), and individual fruit weight were positive across the two axes, and these were the main traits for genetic divergence.

KEYWORDS

Mango, multivariate analysis, genetic diversity

1. INTRODUCTION

Mango (*Mangifera indica* L.), a native of southeast Asia, is one of the important fruit crops in the tropical and subtropical regions of the globe (Duval et al., 2006; Majumder et al., 2013). Mango is known as the “King of fruits” in the tropical parts due to its popularity and economic importance (Asif et al., 2016; Jahurul et al., 2015; Litz, 2009). In Bangladesh, it occupies an area of 37,846 hectares of land with an annual production of 11,61,685 m tons (Statistics, 2017). The composition generally differs with cultivar and the stage of maturity. Commercial and good-quality mangoes are mostly grown in the north-western and south-western districts of the country (Ahmad, 1985). But there are different superior and local germplasm around the northeastern region that can be evaluated to release as a variety or to identify suitable mango genetic resource for purposeful breeding for the region (Majumder et al., 2013). Moreover, this germplasm may have some traits of interest for the mango improvement.

Multivariate technique such as principal component analysis is an efficient methodology for the clustering, distribution of genotypes, and assessment of genetic divergence of the genotypes with principal component biplot, and PC individual plot (Alam et al., 2020; Majumder et al., 2013). For any breeding program, the information about genetic diversity or the phylogenetic relationship of available germplasms in any crop is of greater importance (Arunachalam, 1981; Murty & Arunachalam, 1966). Which aids to select the best parents for establishing a new breeding population and better knowledge and understanding helps to get long-term selection gain (Chowdhury et al., 2002). If the parents are more diverse, it has the possibility of getting high heterotic offspring with larger segregating potential for the maximum utilization of plant genetic resources (Arunachalam, 1981). Though mango is widely grown in Bangladesh, but

still it is needed to improve mango through exploitation of local superior germplasms. Therefore, the objective of the study was to evaluate and find out the genetic diversity presents among the collected mango genotypes.

2. MATERIALS AND METHODS

2.1 Experimental Site

The experiment was conducted at Regional Agricultural Research Station, Akbarpur, Moulvibazar during 2019-2021. The orchard was located in the hilly region under the Northern and Eastern Hills (AEZ 29) of Bangladesh. Soil texture of the orchard was sandy clay (43-85%), silt (<50%), clay (>20%) and highland acidic soil with pH 4.0-5.0. Annual average rainfall was 256 cm at the experimental site.

2.2 Plant Materials and Their Management

Twenty-three local mango germplasm were identified and marked for this study. Ages of plant 25 to 30 years. A single plant has been considered as a unit plot. Fertilizer was applied with well decomposed cowdung 90 kg, Urea 3.5 kg, TSP 1.75 kg, Muriate of Potash 1.40 kg, Zypsum 0.875 kg, Zinc Sulphate 45.0 g, and Boric acid 90 g per plant, respectively. To manage soil pH. Dolomite were applied at the rate of 4.0 kg per decimil. Three full cover spray applications with Ripcord 10 EC @ 1 ml/L along with Tilt 250 EC @ 0.5ml/L were done; first at the flower initiation stage when the panicle is around two inches long; second at the pea stage of fruit and third spray at the marble stage. These sprays prevent the attack of mango hopper and anthracnose disease of mango. Intercultural operations such as weeding, spading, loosening of soil, irrigation were done as and when required.

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2.3 Data Collection and Analysis

Data were recorded on fruit yield and morphological traits as and when necessary. Recorded data for studied traits were assigned to analysis of variance as per procedure described by Steel & Torrie (Steel & Torrie, 1960). Multivariate analysis of the principal components was also derived. All the data were subjected to analysis with R statistical package. (De Mendiburu & Simon, 2015; Kassambara & Mundt, 2017; Team, 2013; Vu, 2011).

3. RESULTS AND DISCUSSION

A wide variation was observed regarding the number of fruits/plant/year, individual fruit weight (g), fruit yield (kg/plant) different germplasm tested (Table 1). A higher number of fruits per plant (610) was observed in MIAkb001 and the lowest was in MIAkb015. The higher individual fruit weight (759.7g) was obtained from MIAkb015 and the lower one is MIAkb009.

Table 1: Qualitative and quantitative characters of selected 23 local mango germplasm

Acc. No.	No. of Fruits/Plant/Year	Individual Fruit wt. (g)	Fruit Shape			Fruit Yield (Kg/plant)
			Length (cm)	Breadth (cm)	Width (cm)	
MIAkb001	610	265.7	9.1	7.4	6.8	162.07
MIAkb002	398	252.1	9.5	7.6	6.4	100.33
MIAkb003	432	114.7	7.1	5.4	5.1	49.55
MIAkb004	571	170.2	7.7	6.3	5.9	97.18
MIAkb005	431	98.4	6.6	5.3	4.8	42.41
MIAkb006	232	107.3	6.9	5.3	4.7	24.89
MIAkb007	222	141	7.8	5.7	5.2	31.3
MIAkb008	403	104	6.4	5.1	4.7	41.91
MIAkb009	143	94	5.4	4.4	4.2	13.44
MIAkb0010	361	137.5	6.9	6.2	5.7	49.63
MIAkb0011	126	182.2	7.6	6.4	6.4	22.95
MIAkb012	156	128.5	6.5	6.4	5.5	20.04
MIAkb013	109	103.9	7.1	5.6	5.1	11.32
MIAkb014	98	306.3	10.3	7.7	7.1	30.01
MIAkb015	87	759.7	13.5	10.8	9.6	66.09
MIAkb016	143	200.8	8.9	7.2	6.1	28.71
MIAkb017	87	220.2	8.9	6.7	6.3	19.15
MIAkb018	310	245.4	10.6	9.2	6.4	76.07
MIAkb019	221	167.7	7.9	6.2	5.5	37.06
MIAkb020	175	209.7	8.2	7.2	6.1	36.69
MIAkb021	209	167.2	8.6	6.8	5.6	34.94
MIAkb022	132	184.9	8.7	6.5	5.9	24.4
MIAkb023	310	220.9	11.5	7.7	7.1	68.47
Mean	231.08	174.31	7.08	9.74	9.11	41.47
Min.	87	94	5.4	4.4	4.2	11.32
Max.	610	759.7	13.5	10.8	9.6	162.07

Higher fruit yield was recorded from MIAkb001 (162.07kg/plant) and the lowest (11.32 kg/plant) one is MIAkb013. The highest weight of fruit skin was obtained from MIAkb015 (182.8 g) and the lowest one in MIAkb005 (18.7 g). The higher percent of edible portion was obtained in MIAkb014 (65.71%) and the lowest (33.09%) was recorded in MIAkb010. The highest

soluble solid was from MIAkb007(18%) and MIAkb015 (18%) and the lowest was recorded in MIAkb013(7%). A marvelous color was observed in MIAkb001, MIAkb002, MIAkb006 and MIAkb011.

Table 1 Continued...

Acc. No.	Skin Thickness (cm)	Wt. of Skin (gm)	Wt. of Stone (gm)	Edible Portion (%)	Stone			TSS	Attractiveness	Organoleptic Taste
					Length (cm)	Breadth (cm)	Width (cm)			
MIAb001	0.2	35.6	61.7	63.37	6.7	4.2	1.9	15	Excellent	Good
MIAb002	0.2	46.5	58.9	58.19	7.4	4.1	1.9	15	Excellent	Good
MIAb003	0.1	19.8	28.6	57.8	5.8	3.1	1.7	13	Good	Intermediate
MIAb004	0.2	42.1	44	49.41	5.5	3.1	1.8	9	Intermediate	Intermediate
MIAb005	0.1	18.7	32.2	48.27	5.5	2.9	1.9	12	Poor	Intermediate
MIAb006	0.2	25.6	27.5	50.51	5.6	3.1	1.9	14	Excellent	Good
MIAb007	0.2	22.3	51.1	47.94	6.4	3.5	2.2	18	Good	Good
MIAb008	0.1	20.8	35.2	46.15	5.6	3.2	2.2	16	Good	Good
MIAb009	0.1	19.7	27.2	50.1	5.4	2.8	2.2	16	Poor	Good
MIAb010	0.1	43.8	48.2	33.09	5.5	3.2	1.8	15	Poor	Good
MIAb011	0.2	35.2	48.4	54.11	5.5	2.8	1.9	15	Excellent	Good
MIAb012	0.1	30.5	25.5	48.63	4.5	3.4	1.6	16	Poor	Good
MIAb013	0.2	23.9	37.5	40.9	5.1	3.1	1.7	7	Poor	Poor
MIAb014	0.2	55.8	49.2	65.71	6.9	3.8	2.4	12	Good	Good
MIAb015	0.2	182.8	155.3	55.49	10.2	4.9	2.1	18	Good	Good
MIAb016	0.2	46.2	30.9	61.6	6.2	3.4	1.9	10	Good	Poor
MIAb017	0.1	39.8	35.9	65.62	5.7	3.5	2.3	17	Good	Good
MIAb018	0.2	51.7	57.2	55.62	8.5	3.5	2.4	11	Poor	Poor
MIAb019	0.2	35.1	48.3	50.26	6.1	3.3	1.9	12	Poor	Good
MIAb020	0.1	38.5	55.6	55.12	6.9	4.4	2.5	11	Good	Poor
MIAb021	0.2	38.6	62.5	39.53	6.5	3.7	1.5	17	Poor	Good
MIAb022	0.2	32.5	39.9	60.84	6.9	3.5	1.8	14	Poor	Good
MIAb023	0.2	88.9	48.8	37.66	9.2	4.6	1.5	10	Poor	Poor
Mean	0.12	30.83	34.66	38.99	4.5	2.52	1.45	10	-	-
Min.	0.1	18.7	25.5	33.09	4.5	2.8	1.5	7	-	-
Max.	0.2	182.8	155.3	65.71	10.2	4.9	2.5	18	-	-

3.1 Principal Component Analysis (PCA)

In the PCA-biplot for the it was found that the two PCs (PC1 and PC2) described 52.6 % and 14 % of the variance (Figure 2). Eigen values of the principal component axis, percent of total variation and cumulative variation accounted for them obtained from the principal component analysis are presented in Table 2. The results showed that the first principal axis, the number of fruits per plant (FNPP) largely accounted for the variation among the genotypes which alone contributed 52.58% of the total variation. The first seven characters of the principal component axes

with eigen values above unity accounted for 96.69 % of the total variation among the fourteen characters. The rest seven characters contributed the remaining 3.31 % of the total variation. Similar findings were also reported by another studies (Alam et al., 2016; Salim et al., 2013). A group of researchers studied genetic diversity of acid lime through morphological characters and reported that fruits per tree, yield per plant, juice volume and juice percentage were major contributor towards divergence (Ranpise & Desai, 2003).The character contributed the maximum to the divergence should be given greater emphasis for selection in breeding (Jagadev & Samal, 1991).

Table 2: Latent roots (eigen values) and percent of variation in respect of 14 characters of 23 mango genotypes

Principal Component Axis	Eigen Values	Percentage	
		Total Variation Accounted For	Cumulative
FNPP	7.361281	52.58058	52.58058
IFW	1.965852	14.0418	66.62238
FL	1.415981	10.11415	76.73653
FB	1.224613	8.747236	85.48377
FWD	0.716	5.114285	90.59805
SKT	0.461794	3.298529	93.89658
SKW	0.391862	2.799017	96.6956
STW	0.17741	1.267215	97.96281
EP	0.137384	0.981313	98.94412
LST	0.070922	0.506589	99.45071
BST	0.035898	0.256411	99.70712
WDST	0.027165	0.194037	99.90116
TSS	0.012104	0.086454	99.98761
FYPP	0.001734	0.012385	100

3.2 Non- Hierarchical Clustering

Non-hierarchical clustering was done using a covariance matrix where 23 mango genotypes were grouped into five clusters. The clustering pattern obtained through different techniques coincided with the grouping patterns done by principal component analysis. So, it can be safely stated that the results obtained through PCA were established by non-hierarchical clustering. It is interesting to note that 34.78 % of genotypes were included in cluster I and 30.43% in cluster II, and 17.39% were in

cluster IV, and the remaining 17.39% were in the other two clusters. The composition of clusters with different genotypes including their source of the collection is presented in Table 3. Cluster I obtained the highest number of genotypes (08) which was followed by cluster II (07), cluster IV (04), cluster V (03), and cluster III (1). The lowest number of genotypes (1) was observed in cluster III (Figure 1). In another study similar clustering pattern were also observed in Mango (Majumder et al., 2013; Rymbai et al., 2014; Tewodros et al., 2019)

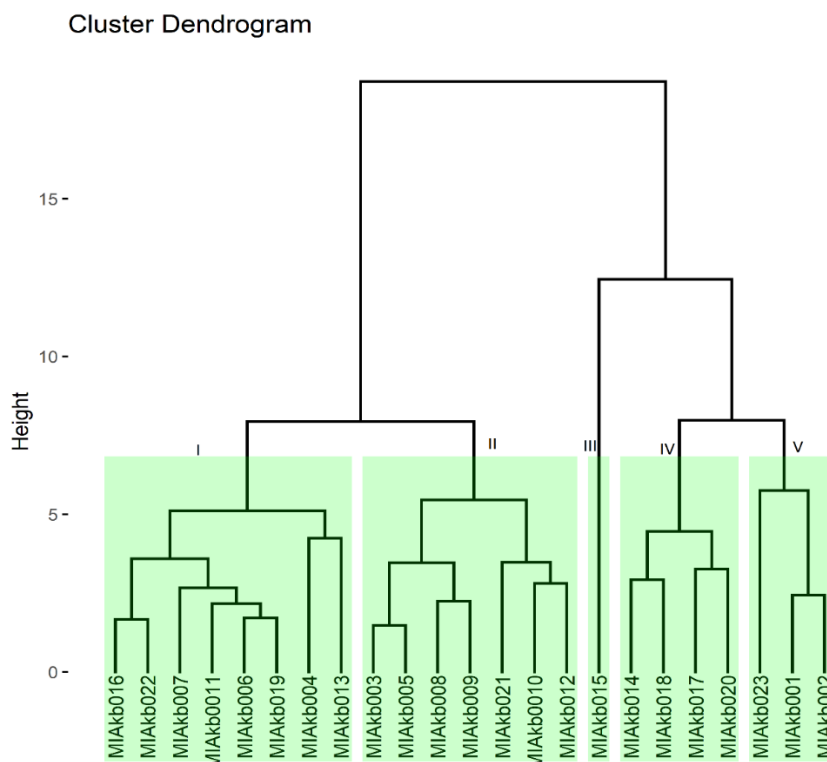


Figure 1: Non-hierarchical clustering of 23 mango genotypes considering 14 morphological traits

A two-dimensional scatter plotting diagram (Z1-Z2) constructed using component score 1 on X-axis and component score 2 on the Y-axis exhibited that the genotypes fall into five clusters (Fig. 2). All the studied mango genotypes were distributed on the individual biplot based on the principal component score. The genotypes with wider distance were supposed to be more genetically diversified. For the selection of parents.

Table 3: Distribution of 23 mango genotypes in 5 clusters			
Cluster	No. of Genotype	Genotypes	Percentage
I	08	MIAkb004, MIAkb006, MIAkb007, MIAkb011, MIAkb013, MIAkb016, MIAkb019, MIAkb022,	34.78
II	07	MIAkb003, MIAkb005, MIAkb008, MIAkb009, MIAkb010, MIAkb012, MIAkb021	30.43
III	01	MIAkb015	4.35
IV	04	MIAkb014, MIAkb017, MIAkb018, MIAkb020,	17.39
V	03	MIAkb001, MIAkb002, MIAkb023	13.04

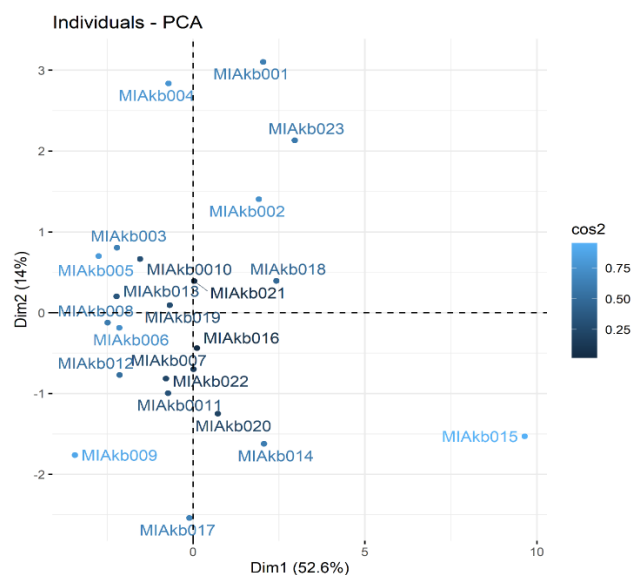


Figure 2: Principal component individual plot of 23 mango genotypes considering 14 morphological traits

3.3 Contribution of Different Characters Towards Divergence

Contributions of different characters responsible for genetic divergence are presented in Table 4. It was revealed that in vector I (Z1), the important characters responsible for genetic divergence in the major axis of differentiation were individual fruit weight (IFW), fruit length, and breadth. In vector II (Z2) number of fruits per plant (FNPP), fruits yield per plant (FYPP), and width of stone (WDST) were important traits for genetic divergence. In both the vectors, number of fruits per plant (FNPP)

(0.2278 and 037.823), fruits yield per plant (FYPP) (2.558 and 29.824), and individual fruit weight (12.197 and 1.383) were positive across the two axes indicating the important component of genetic divergence among the studied characters. Similar findings were also found by other researchers (Majumder et al., 2013; Rymbai et al., 2014; Toili et al., 2016). Alam et al. (2016) also reported that number of fruits per plant, %TSS, fruit weight, and yield per plant played a major role in both axes for determining the genetic divergence of Pummelo (Alam et al., 2016).

Table 4: Relative contributions of the 14 characters towards genetic divergence of 23 mango genotypes

Character	Vector 1	Vector 2
FNPP	0.227895	37.82338
IFW	12.19778	1.383828
FL	12.45732	0.05331
FB	12.22179	0.000179
FWD	12.45925	0.027963
SKT	2.986385	3.939926
SKW	11.36828	0.391056
STW	10.82402	0.162301
EP	1.081388	4.053567
LST	11.12868	0.294384
BST	9.836747	0.438249
WDST	0.436727	14.32826
TSS	0.214851	7.27863
FYPP	2.558897	29.82497

4. CONCLUSION

The indigenous and local plant genetic resources are priceless treasure for us. The existence of genetic diversity in crops is important for breeding new varieties or hybrids. Mango is very popular fruit and has greater diversity in Bangladesh due to its wider cultivation and adaptation. So, there is a considerable scope for mango improvement by utilizing existing local mango genetic resources. In the present study MIAkb001, MIAkb002, MIAkb006, MIAkb011, MIAkb014 and MIAkb015 performed better considering the studied morphological and fruit traits. There was wide variability of the studied 14 traits of 23 mango genotypes and all genotypes were grouped in five clusters. Genotypes of cluster I and V located in wider distance in the individual PCA biplot. So, crossing between the genotypes of these two clusters have the possibility to get maximum heterotic combination for future breeding program. Moreover, further genetic studies with a large set of mango germplasm and utilization of advanced molecular techniques are suggested for improvement of mango.

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