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Association studies among promising mango (*Mangifera indica* L.) hybrids utilizing quantitative traits

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Abstract

The success of any crop improvement programme depends upon variability present at the genetic level, and knowledge of association between traits directly or indirectly influencing contributing traits is the prerequisite. Present study witnessed significant direct positive and direct negative effects between economically important traits among mango hybrids. The minimum difference between GCV and PCV was observed for fruit weight indicating very less environmental influence on this trait. Similarly, heritability (h^2_{BS}) ranged from 0.49 to 0.99 and highest value for genetic advance (GA) and heritability (h^2_{BS}) was noted for fruit weight. The principal component analysis (PCA) revealed a major proportion (91%) of variability was contributed by the first five components. Correlation at genotypic and phenotypic levels revealed that fruit weight is significantly and positively influenced by fruit length and fruit width. Similarly, path analysis demonstrated positive and direct effects of fruit length and leaf blade length on fruit weight. The information generated in present investigation has significance in selection of traits directly affecting the fruit weight, thus, very helpful in future mango improvement programmes.

Keywords: Heritability, hybrids, mango, path analysis and principal component analysis

Introduction

Mangifera indica L. (mango) is known as the king of fruits owing to its immense value in present scenario where India transitioning to become nutritionally secure country. Indian sub-continent is believed to be its primary center of origin. It belongs to family Anacardiaceae, which comprises about 81 genera (Pell *et al.*, 2010) [19]. The genus *Mangifera* itself consists of 69 valid species (Mukherjee, 1949; Kosterman & Bompard, 1993) [16]. The popularity of this fruit in the international market is due to its delicious taste, attractive peel colour, strong aroma and nutritional properties (Sivakumar *et al.*, 2011) [22]. India, the so-called "native home" of the mango, provides a wide range of diversity for this fruit crop due to its extreme cross-pollination behaviour, allopolyploidy and heterozygous nature. Today, all the commercially cultivated varieties have originated as natural chance seedling selection and later preserved through vegetative propagation (Ravishankar *et al.*, 2004) [20]. India acknowledged as the top mango producer in the world, produces 20.44 million MT of mangoes from an area of 2.29 million hectares (NHB, 2019-20) [18].

Assessment of genetic variability and identification of superior parents among a genotypically diverse population is the preliminary objective of any crop improvement programme (Gupta *et al.*, 2016) [6]. Further, estimation of genetic advance along with heritability also aids in selection criteria. Heritability is also helpful in estimating genetic gain of crop when studied in relation to correlation and path coefficient analysis Munda *et al.*, (2020) [17] and Begum *et al.*, (2022) [1]. Similarly, correlation and path coefficient analysis suggest the correlation between traits and determine their direct and indirect effects on trait of economic importance. The genotypic coefficient of variation (GCV) represents heritable traits while, phenotypic coefficient of variance (PCV) measures non-heritable traits in a population (Hamidou *et al.*, 2018) [7]. The principal component analysis (PCA) measures the percentage contribution to variability by an individual trait. The present investigation was undertaken with the objective of characterization and diversity assessment using different parameters of promising mango hybrids based on DUS guidelines.

Materials and Methods

Plant material

The present investigation was carried out using 24 promising mango hybrids bred at the ICAR- Indian Agricultural Research Institute, New Delhi and maintained under uniform culture practices (Table 1).

Morphological traits analysis

The experiment was laid out in randomized block design (RBD) with minimum 10 replications. The data pertaining to different quantitative parameters have been analyzed using analysis of variance (ANOVA) with the help of R software based on 11 quantitative traits. Heritability (h^2_{BS}) and genetic advance were calculated as suggested by (Begum *et al.*, 2022) [1].

Table 1: List of mango (*Mangifera indica* L.) hybrids used in the present study.

S. No.	Hybrid	Parentage
1	Amrapali	Dashehari x Neelum
2	H-1-11	Amrapali x Sensation
3	H-12-5	Amrapali x Sensation
4	H-1-5	Amrapali x Sensation
5	H-2-14	Amrapali x Alphonso
6	H-3-2	Amrapali x Sensation
7	H-4-8	Amrapali x Sensation
8	H-7-1	Amrapali x Sensation
9	Mallika	Neelum x Dashehari
10	NH-16-2	Amrapali x Sensation
11	NH-17-1	Amrapali x Sensation
12	NH-17-3	Amrapali x Sensation
13	NH-17-4	Amrapali x Sensation
14	NH-18-4	Amrapali x Sensation
15	NH-19-2	Amrapali x Sensation
16	NH-19-3	Amrapali x Sensation
17	NH-20-2	Amrapali x Sensation
18	Pusa Arunima	Amrapali x Sensation
19	Pusa Deepshikha	Amrapali x Sensation
20	Pusa Lalima	Dashehari x Sensation
21	Pusa Manohari	Amrapali x Sensation
22	Pusa Peetamber	Amrapali x Lal Sundari
23	Pusa Pratibha	Amrapali x Sensation
24	Pusa Shreshth	Amrapali x Sensation

H-hybrid, NH- New hybrids

Coefficient of variation (CV) was calculated in accordance with (Burton and De Vane, 1953) [2]. The genotypic and phenotypic correlation coefficients were analyzed as suggested by Begum *et al.* (2022) [1]. The path analysis was performed as per Dewey and Lu (1950) [4]. The Principal

Component Analysis (PCA) was carried out using IBM SPSS Statistics ver. 26 software.

Results

Analysis of variance (ANOVA)

Results pertaining to analysis of variance (ANOVA) for quantitative parameters revealed significant variation ($p \leq 0.001$) among 24 mango hybrids (Table 2). The highest coefficient of variation was observed for petiole length (13.80), leaf area (9.69), LBL/LBW (7.77), leaf blade width (6.79), inflorescence width (6.04), leaf blade length (5.65), fruit shape index (4.87), inflorescence length (4.35), fruit length (3.84), fruit width (2.51) and fruit weight (1.34). The genetic coefficient of variance (GCV) was recorded minimum (10.42) for LBL/LBW and maximum (35.71) for inflorescence width. Similarly, phenotypic coefficient of variance (PCV) was observed minimum (13.0) for LBL/LBW and maximum (36.21) for inflorescence width. Low heritability (h^2_{BS}) was recorded for the traits under consideration. It ranged from 0.49 to 0.99. Highest value for heritability (h^2_{BS}) and genetic advance (GA) was noted for fruit weight (0.99; 122.84). However, lowest heritability (0.49) and lowest genetic advance (0.46) were recorded for petiole length and fruit shape index, respectively.

Genotypic and phenotypic correlation

The correlation between genotype and phenotype helps in identification of efficient selection criteria for crop improvement. The present study revealed a high genotypic correlation coefficient as compared to phenotypic correlation coefficient (Table 3). Fruit weight was considered as a trait of economic importance which was significantly and positively correlated with the fruit length at both genotypic (0.777) and phenotypic (0.747) levels followed by fruit width (0.868; 0.852). However, fruit weight was noted to be significantly and negatively correlated with petiole length (-0.410; -0.290).

Path coefficient analysis

The direct and indirect effects of various traits on fruit weight has also been worked out. Results revealed a highest positive and direct effect of fruit length (1.609) and leaf blade length (1.366) of fruit weight (Table 4). The fruit width showed a positive indirect effect on fruit weight via traits like leaf blade length, LBL/LBW, petiole length, fruit length and fruit shape index. Similarly, fruit length showed an indirect positive effect on fruit weight via traits like leaf blade length, leaf blade width, petiole length, leaf area and inflorescence length (Table 3). However, petiole length presented an indirect negative effect on fruit weight.

Table 2: Analysis of variance (ANOVA) and estimation of genetic variability parameters for quantitative traits in mango hybrids.

Traits	Source of variation and mean squares (ANOVA)			Estimation of genetic parameter				Mean performance			
	Replication (DF = 9)	Genotypes (DF = 23)	Error (DF = 207)	GCV	PCV	h^2_{BS} (%)	GA 5%	Mean	CV	SE	CD 5%
Leaf blade length	0.93	64.84***	1.11	13.54	14.68	0.85	4.79	18	5.65	0.33	0.92
Leaf blade width	0.07	3.22***	0.10	11.52	13.37	0.74	0.99	4.84	6.79	0.10	0.29
LBL/LBW	0.07	1.71***	0.09	10.42	13.00	0.64	0.66	3.87	7.77	0.09	0.26
Petiole length	0.16	1.69***	0.15	13.75	19.48	0.49	0.57	2.85	13.80	0.12	0.34
Leaf area	18.99	2115.83***	40.56	21.92	23.97	0.83	27.14	65.70	9.69	2.01	5.61
Inflorescence length	4.11	451.91***	1.69	22.51	22.93	0.96	13.57	29.80	4.35	0.41	1.14
Inflorescence width	2.84	492.26***	1.40	35.71	36.21	0.97	14.23	19.61	6.04	0.37	1.04
Fruit length	0.05	19.00***	0.15	13.42	13.96	0.92	2.71	10.22	3.84	0.12	0.34
Fruit width	0.04	6.60***	0.02	13.39	13.62	0.96	1.64	6.05	2.51	0.04	0.17
Fruit shape index	0	0.57***	0	13.96	14.79	0.89	0.46	1.70	4.87	0.02	0.07
Fruit weight	11	35634***	6	31.59	31.62	0.99	122.84	188.93	1.34	0.80	2.24

DF= degree of freedom, GCV= genetic coefficient of variation, PCV= phenotypic coefficient of variation, h^2_{BS} (%) = heritability in broad sense, GA= genetic advance, CV= coefficient of variance, SE=standard error, CD= critical distance

Table 3: Phenotypic and Genotypic (Bold) correlation coefficient of quantitative traits among mango hybrids.

Traits	Leaf blade length	Leaf blade width	LBL/LBW	Petiole length	Leaf area	Inflorescence length	Inflorescence width	Fruit length	Fruit width	Fruit shape index	Fruit weight
Leaf blade length	1 **	0.6673 **	0.5319 **	0.2093 NS	0.9106 **	-0.0762 NS	-0.0572 NS	0.0815 NS	0.1992 NS	-0.1419 NS	0.1995 NS
Leaf blade width	0.5687 **	1 **	-0.2729 NS	-0.0364 NS	0.8531 **	0.1257 NS	-0.1982 NS	-0.0488 NS	0.2583 NS	-0.3569 NS	0.1975 NS
LBL/LBW	0.5139 **	-0.4064 **	1 **	0.3071 NS	0.2037 NS	-0.223 NS	0.1636 NS	0.1676 NS	-0.0494 NS	0.2424 NS	0.0279 NS
Petiole length	0.0791 NS	-0.0082 NS	0.1093 NS	1 **	0.1847 NS	-0.3403 NS	-0.0978 NS	-0.2962 NS	-0.4403 *	0.156 NS	-0.4117 *
Leaf area	0.8539 **	0.8178 **	0.0925 NS	0.1153 NS	1 **	-0.0005 NS	-0.2121 NS	-0.0125 NS	0.1305 NS	-0.159 NS	0.1037 NS
Inflorescence length	-0.0677 NS	0.1156 NS	-0.1839 **	-0.2425 **	0.0013 NS	1 **	0.4673 *	0.1868 NS	-0.0174 NS	0.2011 NS	0.0614 NS
Inflorescence width	-0.0496 NS	-0.1629 *	0.1262 NS	-0.0796 NS	-0.1871 **	0.4519 **	1 **	0.1442 NS	0.034 NS	0.077 NS	0.0381 NS
Fruit length	0.0741 NS	-0.0333 NS	0.1214 NS	-0.2338 **	-0.0072 NS	0.1792 **	0.145 *	1 **	0.5829 **	0.368 NS	0.7771 **
Fruit width	0.1744 **	0.2179 **	-0.0445 NS	-0.3112 **	0.1173 NS	-0.019 NS	0.0334 NS	0.5455 **	1 **	-0.5314 **	0.8681 **
Fruit shape index	-0.1146 NS	-0.2853 **	0.1856 **	0.0746 NS	-0.1347 *	0.1914 **	0.0798 NS	0.4114 **	-0.5292 **	1 **	-0.203 NS
Fruit weight	0.1831 **	0.1721 **	0.0189 NS	-0.2909 **	0.0957 NS	0.0599 NS	0.0378 NS	0.747 **	0.8527 **	-0.1912 **	1 **

*= significant at 5%, **= significant at 1%, NS= non-significant.

Table 4: Genotypic path analysis showing direct (bold) and indirect effect of various quantitative traits on fruit weight in mango hybrids.

Traits	Leaf blade length	Leaf blade width	LBL/LBW	Petiole length	Leaf area	Inflorescence length	Inflorescence width	Fruit length	Fruit width	Fruit shape index	Fruit weight
Leaf blade length	1.36663	-0.39145	-0.38645	-0.01907	-0.51042	-0.00162	0.0079	0.13118	-0.15609	0.15891	0.1995 NS
Leaf blade width	0.91197	-0.58661	0.19832	0.00332	-0.47815	0.00267	0.02736	-0.07857	-0.20249	0.39974	0.1975 NS
LBL/LBW	0.72684	0.1601	-0.72662	-0.02799	-0.11416	-0.00474	-0.02258	0.26977	0.03869	-0.27138	0.0279 NS
Petiole length	0.28604	0.02135	-0.22319	-0.09112	-0.10354	-0.00723	0.0135	-0.47687	0.34511	-0.17477	-0.4107 *
Leaf area	1.24451	-0.50043	-0.14799	-0.01683	-0.5605	-0.00001	0.02927	-0.02009	-0.1023	0.17806	0.1037 NS
Inflorescence length	-0.10414	-0.07374	0.16204	0.03101	0.0003	0.02124	-0.06449	0.30073	0.01361	-0.22521	0.0614 NS
Inflorescence width	-0.07821	0.11628	-0.1189	0.00891	0.11889	0.00993	-0.13801	0.23215	-0.02668	-0.08624	0.0381 NS
Fruit length	0.11137	0.02863	-0.12177	0.02699	0.007	0.00397	-0.0199	1.6098	-0.45688	-0.41208	0.7771 **
Fruit width	0.27216	-0.15155	0.03587	0.04012	-0.07316	-0.00037	-0.0047	0.93837	-0.7838	0.59515	0.8681 **
Fruit shape index	-0.19392	0.20939	-0.17608	-0.01422	0.08912	0.00427	-0.01063	0.59236	0.41654	-1.11988	-0.203 NS

Residual=0.0902, Significance * and ** at 5% and 1% respectively.

Principal component analysis

Principal component analysis indicating the percent variance contributed by each trait to the total variance. Eigen values of five Principal Components (PC) were considered since they represent a value greater than 1 with cumulative variance of 91.005% (Table 5 and Fig 1). High variance was depicted by PC1 (28.29%) and PC2 (23.57%), respectively. The highest contributor of variability in PC1 was fruit weight (19.43%) followed by fruit width (17.74%), leaf blade width (16.62%) and leaf blade length (15.78%), respectively. In contrast, leaf

area (16.13%), petiole length (15.40%) and fruit length (14.71%) were the largest sources of variability in PC2 (Table 6). The 16.51% variance depicted in PC3 was majorly presented by LBL/LBW (36.01%) and fruit shape index (24.71%); whereas 13.37% variance in PC4 was shown by inflorescence length (49.66%) and inflorescence width (15.92%). In PC5 chief contributor was inflorescence width (39.41%) and fruit shape index (30.60%). As per the biplot analysis (Fig. 2), it was evident that selection of genotypes with high fruit weight requires high PC1 and low PC2.

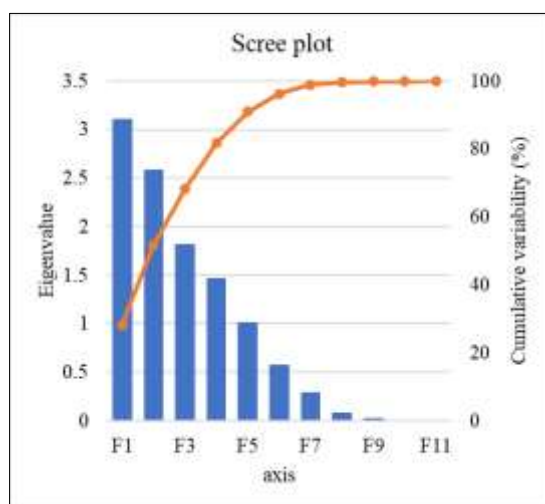


Fig 1: Scree plot representing Eigen value with respect to principal components.

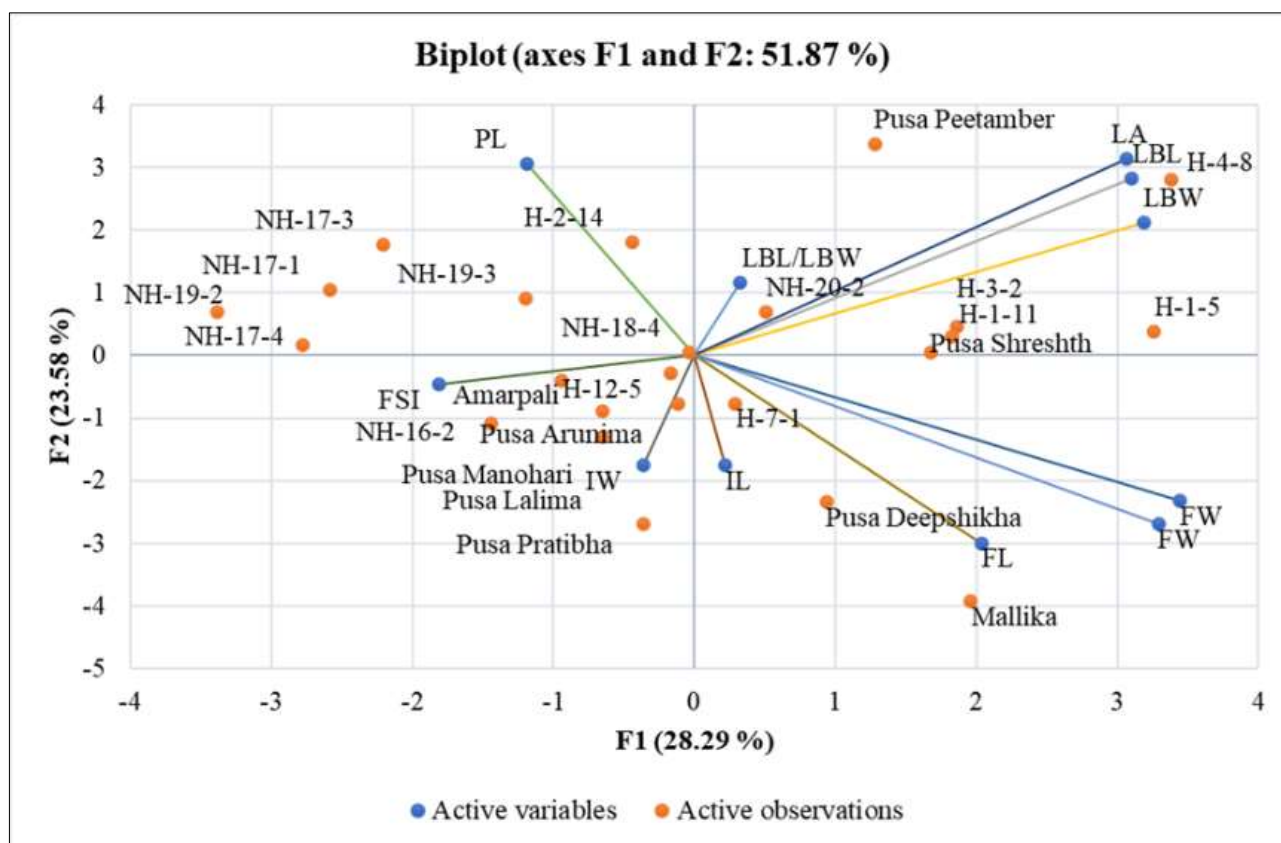


Fig 2: PCA biplot representing morphological traits and 24 hybrids of mango. LBA: leaf blade length, LA: leaf area, LBW: leaf blade width, FW: fruit weight, FW: fruit width, FL: fruit length, IL: inflorescence length, FSI: fruit shape index, IW: inflorescence width, PL: petiole length.

Discussion

Eleven quantitative traits studied were highly significant ($p \leq .001$) which indicates presence of huge variations among the 24 mango hybrids. Confirmation of considerable genetic variability is based on critical differences (CD), mean, coefficient of variation (CV) and standard errors (SE). Both genetic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) further confirmed significant diversity at the genetic level thus offering potential for selection of important traits for mango improvement. Our results are in agreement with the findings of Beghum *et al.* (2022) [1]. They also reported higher phenotypic coefficient values compared to genotypic values which is mainly due to less environmental effects on the studied traits. It was also observed that minimum difference between GCV and PCV was for fruit weight (31.59; 31.62) and fruit width (13.39; 13.62) traits, resulting in easy expression of genes without environmental effects (Munda *et al.*, 2020) [17]. However, maximum difference between GCV and PCV was recorded for petiole length (13.75; 19.48) and LBW/LBW (10.42; 13.00) indicating significant environmental effects on

expression of these traits. This relationship between GCV and PCV play a pivotal role in making selections for these traits. The highest GCV and PCV were found in Inflorescence width (35.71; 36.21) and fruit weight (31.59; 31.62). These findings are in accordance with the findings of Elaiyaraja *et al.* (2021) [5] and Indian *et al.*, (2022) [9] who have reported a high PCV than GCV for each yield-attributing trait in mango. Earlier reports from Das *et al.* (2021) [3] based on study in mango (*Mangifera indica* L.) high values of GCV and PCV were observed for stone weight, fruit weight, peel weight, yield, total flavonoid and total phenols offering a wide scope for selection among genotypes. Another investigation pertaining to mango by Sridhar *et al.* (2018) [23] revealed that both GCV and PCV were high in inflorescence width (28.42; 27.74), fruit weight (40.81; 39.10) and yield/plant (45.70; 44.92). A trait with a high GCV has substantial potential for crop improvement due to its high genetic variability. According to Singh and Kumar (2005) [21] selection for a particular trait is more effective if it has both a high GCV and a high heritability.

Table 5: Percentage variability and cumulative variance for each principal component.

	F1	F2	F3	F4	F5
Eigenvalue	3.112	2.593	1.817	1.472	1.016
Variability (%)	28.292	23.577	16.517	13.378	9.241
Cumulative %	28.292	51.869	68.386	81.764	91.005

Table 6: Percentage contribution of each trait in different principal components in mango hybrids.

Traits	PC1		PC2		PC3		PC4		PC5	
	FL1	% Contribution	FL2	% Contribution	FL3	% Contribution	FL4	% Contribution	FL5	% Contribution
Leaf blade length	0.701	15.783	0.581	13.007	0.362	7.206	0.087	0.520	0.110	1.185
Leaf blade width	0.719	16.621	0.438	7.385	-0.301	4.981	0.370	9.303	-0.171	2.881
LBL/LBW	0.073	0.173	0.240	2.225	0.809	36.018	-0.285	5.536	0.325	10.373
Petiole length	-0.268	2.306	0.632	15.400	0.281	4.344	-0.186	2.357	0.046	0.209
Leaf area	0.693	15.431	0.647	16.137	0.104	0.600	0.239	3.867	-0.115	1.303
Inflorescence length	0.050	0.079	-0.361	5.020	0.076	0.318	0.855	49.667	-0.002	0.000
Inflorescence width	-0.083	0.219	-0.362	5.050	0.339	6.323	0.484	15.927	0.633	39.419
Fruit length	0.461	6.819	-0.618	14.719	0.501	13.838	-0.093	0.583	-0.330	10.699
Fruit width	0.778	19.437	-0.479	8.834	-0.136	1.020	-0.284	5.468	0.174	2.966
Fruit shape index	-0.410	5.390	-0.095	0.347	0.670	24.715	0.212	3.046	-0.558	30.607
Fruit weight	0.743	17.743	-0.555	11.876	0.108	0.636	-0.234	3.727	-0.060	0.357

PC= Principal component, FL= Factor loading.

Heritability (h^2_{BS}) ranged from 0.49 to 0.99 for the traits in the present study. Heritability (h^2_{BS}) is helpful in predicting the various genotypic effects e.g. epistasis and dominance and their effect on selection process through phenotypic performance (Ullah *et al.*, 2011) [24]. Heritability (h^2_{BS}) and genetic advance (GA) are important factors in predicting specific phenotypical traits (Johnson *et al.*, 1955) [10]. Thus, the traits having high value for heritability and genetic advance must be considered in selection procedure for crop improvement. In present study, the highest heritability (h^2_{BS}) and genetic advance (GA) was recorded for fruit weight (0.99; 122.84). According to Ibrahim and Hussain, (2006) [8], additive gene action leads to high heritability and high genetic advance, while environmental influence and non-additive gene action indicate low heritability and genetic advance. As per study conducted by Latheef *et al.* (2022) [14] in mango, high heritability with high genetic advance was recorded for number of fruits /tree (97.74, 43.03), number of panicles/tree (98.91, 46.84) and fruit yield /tree (99.43, 62.91) indicating a wide scope of improving these traits by selection. The genotypic correlations in the current study appear to be stronger than the phenotypic correlations, demonstrating the existence of an inherent relationship between different traits. The fruit weight is an economic trait in mango which directly linked to crop yield. In the present study, the fruit weight was found to be significantly and positively correlated with fruit length and fruit width at both genotypic and phenotypic level. Thus, selecting and utilizing these traits in mango improvement will automatically improve fruit weight.

Sridhar *et al.* (2018) [23] also observed that fruit length, fruit weight, fruit diameter, stone weight, stone length, stone width, pulp content and ascorbic acid are significantly and positively correlated both at genotypic and phenotypic levels (In addition, mango exhibited a strong positive and significant correlation with respect to fruit yield and fruit weight, fruit width, fruit length, panicle width, stone weight and pulp weight at both genotypic and phenotypic levels (Elaiyaraja *et al.*, 2021) [5]. Our results are also in agreement with Karuna *et al.* (2018) [11] and Majumder *et al.* (2012) [15].

Results in the present study revealed the highest positive and direct effect on fruit weight by fruit length and leaf blade length. Similar results were also recorded for fruit yield per tree in mango where number of fruits per tree represent a highest positive direct effect whereas panicle length had a moderate and direct positive effect on fruit yield (Latheef *et al.*, 2022) [14]. Our results indicated that fruit width showed a positive indirect effect whereas, fruit length showed indirect positive effect on fruit weight. Thus these traits can be

directly selected for fruit weight improvement. Similar kinds of results have already been published by many researchers for fruit weight presenting a direct positive effect on fruit yield per tree Majumder *et al.*, (2012) [15]; Lal *et al.*, (2017) [13] and Kishore *et al.*, (2021) [12].

A total of five principal components were observed with a cumulative variance of 91.005%. Based on highest contributor of variability traits like fruit weight, fruit width, leaf blade width, leaf blade, leaf area, petiole length, fruit length, LBL/LBW, fruit shape index, inflorescence length and inflorescence width are contributing 91% variability in mango hybrids under study.

Conclusion

Twenty-four mango hybrids have been characterized based on DUS guidelines for estimation of diversity using genetic variability parameters, i.e., ANOVA, correlation analysis, phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), path analysis and principal component analysis has helped in understanding the prevailing genetic variability among hybrids. Genotypic and phenotypic coefficient of variations was recorded highest for inflorescence width. Fruit length and leaf blade length showed a positive correlation with fruit weight indicating a direct effect of these traits on increased fruit weight. Biplot using principal component of analysis helpful in identification of superior hybrids in fruit weight, i.e., Mallika and Pusa Deepshikha. Genetic relatedness of hybrids provided useful information for utilization of these hybrids in future breeding programmes as a source of important desirable traits.

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References

1. Begum T, Munda S, Pandey SK, Lal M. Estimation of selection criteria through multi-year assessment of variability parameters, association studies and genetic diversity of *Solanum khasianum* CB Clarke. *Scientia Horticulturae*. 2022;297:110923.
2. Burton GW, de Vane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*. 1953;45:474-481.

3. Das SS, Kishore K, Lenka D, Dash DK, Samant D, Panda CM, et al. Studies on genetic variability, heritability and character association of yield and quality traits in mango germplasm in eastern tropical region of India. *Agricultural Research Journal*. 2021;58(6):998-1005.
4. Dewey DI, Lu KH A. correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*. 1959;51:515-518.
5. Elaiyaraja R, Rajangam J, Parthiban S, Santha S, Vani V. Assessment of genetic variability, heritability and character association in yield and yield attributing traits of pickling mango (*Mangifera indica* L.) genotypes. *Journal of Pharmaceutical Innovation*. 2021;10(11):305-311.
6. Gupta AK, Mishra R, Singh AK, Srivastava A, Lal RK. Genetic variability and correlations of essential oil yield with agro-economic traits in Mentha species and identification of promising cultivars. *Industrial Crops and Products*. 2016;95:726-732.
7. Hamidou M, Souley AKM, Kapran I, Souleymane O, Danquah EY, Ofori K, et al. Genetic variability and its implications on early generation sorghum lines selection for yield, yield contributing traits, and resistance to sorghum midge. *International Journal of Agronomy*; c2018. p. 1-10.
8. Ibrahim MM, Hussein RM. Variability, heritability and genetic advance in some genotypes of roselle (*Hibiscus sabdariffa* L.). *World Journal of Agricultural Sciences*. 2006;30(2): 345.
9. Indian G, Sankaranarayanan R, Murugesan S, Rajangam J. Studies on genotypic and phenotypic variability in mango (*Mangifera indica* L.). *Journal of agriculture and ecology research international*. 2022;13:121-130.
10. Johnson WW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*. 1995;47:314-318.
11. Karuna K. Correlation Coefficient Analysis of Some Mango (*Mangifera indica* L.) Hybrids. *Chemical Review and Letters*. 2018;7(26):490-495.
12. Kishore K, Rupa TR, Samant D. Influence of shade intensity on growth, biomass allocation, yield and quality of pineapple in mango-based intercropping system. *Scientia Horticulturae*. 2021;278:109868.
13. Lal S, Singh SK, Singh AK, Srivastav M, Singh A, Singh NK. Character association and path analysis for fruit chromatic, physicochemical and yield attributes in mango (*Mangifera indica*). *Indian journal of agricultural sciences*. 2017;87(1):122-131.
14. Latheef A, Pugalendhi L, Rani A, Jeyakumar P, Kumar M, Devi M. Genetic Analysis of Mango (*Mangifera indica* L) Genotypes for Year-round Flowering and Yield Characters. *Madras Agricultural Journal*. 2022;109:23-27.
15. Majumder DAN, Hassan L, Rahim MA, Kabir MA. Correlation and path coefficient analysis of mango (*Mangifera indica* L.). *Bangladesh Journal of Agricultural Research*. 2012;37(3):493-503.
16. Mukherjee SK. A Monograph on the genus *Mangifera* Linn. *Lloydia*. 1949;12:73-136.
17. Munda S, Dutta S, Lal M. Variability estimation and genetic divergence in *Cymbopogon winterianus* for development of superior genotype. *Agronomy Journal*. 2020;113(2):993-1007.
18. NHB Indian Horticulture Database. [Weblink: <http://www.nhb.com>]. [Visited on 27 Nov 2022].
19. Pell SK, Mitchell JD, Miller JD, Lobova TA. *Anacardiaceae In: Flowering Plants. Eudicots*. 2010;7-50.
20. Ravishankar KV, Chandrashekara P, Sreedhara SA, Dinesh MR, Anand L, Saiprasad GVS. Diverse genetic bases of Indian polyembryonic and monoembryonic mango (*Mangifera indica* L.) cultivars. *Current science*. 2004;87:870-871.
21. Singh O, Kumar J. Variability, heritability and genetic advance in brinjal. *Indian Journal of Horticulture*. 2005;62:265-267.
22. Sivakumar D, Jiang Y, Yahia EM. Maintaining mango (*Mangifera indica* L.) fruit quality during the export chain. *International food research journal*. 2011;44(5):1254-1263.
23. Sridhar D, Ghosh B, Kundu S, Hasan MA, Das NC. Genetic variability and heritability studies of mango cultivars. *International journal of current microbiology and applied sciences*. 2018;7(9):752-756.
24. Ullah MZ, Bashar MK, Bhuyain MSR, Khalequazzaman M, Hasan MJ. Interrelationship and cause-effect analysis among morpho-physiological traits in birain rice of Bangladesh. *International Journal of Plant Breeding and Genetics*. 2011;5:246-254.