Variability of genetic - morphological traits of eleven seed strains of *Mangifera indica* L. growing in Upper Egypt

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Abstract: Mango (*Mangifera indica* L.) is one of the tastiest fruits in the world, with numerous advantages beyond their economic value. Eleven genotypes of mango various cultivars were examined for variability, heritability, and genetic advance, as well as multivariate analysis based on cluster and principal component analysis (PCA) for yield and some of its contributing traits during the two growing seasons, 2021 and 2022. All studied traits showed significant differences, and the phenotypic coefficients of variation (PCV) were found to be higher than genotypic coefficients of variation (GCV), supporting the idea that morphological (genetic) traits are more prevalent than environmental influence. All traits had substantial heritability ranging from 75.63 to 99.93 %, and the highest significant genetic advance (119.09 %) was for the number of fruits per tree than other traits. Four clusters were formed, *i.e.*, clusters I and IV had four genotypes, cluster II had two, and cluster III had one genotype. The highest cluster mean values for fruit diameter, fruit mass, yield per tree, and the number of fruits per tree were found in Cluster II, followed by cluster I. Greater genetic divergence was found between 'Zebda' or 'S9' or 'S10' with most other genotypes, indicating that these genotypes may be used to study the characters' broad range of variability and to yield high-quality recombinant lines. In light of the fact that mango is a very heterozygous crop, our current genetic results can be used for the selection of the appropriate parents in hybridization programs and in vegetative propagation to yield selective traits.

Key words: *Mangifera indica*; mango genotypes; genetic variation; principal component analysis; heritability

Spremenljivost genetskih (morfoloških) lastnosti sedmih semenskih linij manga (*Mangifera indica* L.) rastočega v Zgornjem Egiptu

Izvleček: Mango (*Mangifera indica* L.) je eden izmed najokusnejših sadežev na svetu s številnimi prednostmi poleg njihove cene. Preučevanih je bilo enajst genotipov manga različnih sort glede na njihovo variabilnost, dednost in genetsko prednost. Opravljena je bila multivariatna analiza, ki je temeljila na analizi grozdov in glavnih component (PCA) za pridelek in nekaterih z njim povezanih lastnosti v dveh rastnih sezonah, 2021 in 2022. Vse preučevane lastnosti so pokazale značilne razlike, kjer je imel fenotipski koeficient spremenljivosti (PCV) večje vrednosti kot genotipski koeficient raznolikosti (GCV), kar podpira idejo, da so morfološke (genetske) lastnosti prevladujoče nad okoljskimi vplivi. Vse lastnosti so imele znatno dednost, ki je znašala od 75,63 do 99,93 %. Največja značilna genetska prednost (119,09 %) je bila ugotovljena za za število plodov na drevo. Izoblikovale so se štiri skupine in sicer skupini I in IV s štirimi genotipi, skupina II je imela dva in skupina III en genotip. Največje poprečne vrednosti skupine za premer in maso plodu, pridelek na drevo in število plodov na drevo so bile določene v skupini II, ki ji je sledila skupina I. Med vsemi genotipi je bila večja genetska raznolikost ugotovljena pri sortah Zebda, S9 in S10, kar nakazuje, da bi se ti genotipi lahko uporabili za preučevanje značaja širše variabilnosti, kar bi privedlo do zelo kakovostnih rekombinantnih linij. Ob dejstvu, da je mango izredno heterozigotna kulturna rastlina, bi se ti rezultati lahko uporabili za odbiranje primernih staršev v programih križanja in pri vegetativnem razmnoževanju izbranih lastnosti.

Ključne besede: *Mangifera indica*; genotipi manga; genetska variabilnost; analiza glavnih komponent; dednost

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1 INTRODUCTION

Mango (*Mangifera indica* L.) is the king of fruits and, most important, occupies second place in terms of cultivated area after citrus in Egypt. The cultivated area of mango trees reached 265509 feddan (0.42 ha), producing 1,091,535 tons of fruits. The fruiting area in Egypt's Aswan Governorate, where the current study was conducted, got 13573 fed (5700.66 ha) and generated roughly 67076 tons of fruits (SIAERI, 2019). Mangoes are cultivated in over 100 countries, and the top-producing countries are India, China, Thailand, Indonesia, Mexico, and Nigeria (FAO, 2019). Mangoes are naturally heterogeneous and have a wide range of seed genotypes, demonstrating a wide genetic range in shape, color, bearing behaviors, maturation stage, and yield. Several factors, including selection, mutation, genetic drift, and recombination, provide sources of genetic diversity. Most mango cultivars, including some superior clones, are hybrids resulting from natural cross-pollination (Krishna & Singh, 2007; Ramírez & Davenport, 2016). Despite the level of genetic diversity among mango landraces and cultivars, many seeding strains have high productivity. Some of them outperform some of the mango varieties in some crop traits. However, in Egypt, wide mango varieties mainly arise from seedling strains. Mango is an allopolyploid, most probably amphidiploid, and outbreeding plant with chromosome number $2n = 40$ (Pierozzi & Rossetto, 2011) and is highly heterozygous as performance varies with the climate and resulting in a high level of genetic diversity. Vasugi et al. (2012) revealed that to develop new varieties, breeding programs that use germplasm with specific traits need precise information. Mangos have been classified based on fruit characteristics, including color, size, shape, mass, peel percentage, stone, pulp, and nutrient composition (Igbari et al., 2019; Arogundade et al., 2022). The morphological characteristics that distinguish mango cultivars make it difficult to distinguish between closely related varieties (Begum et al., 2016). Abdelsalam et al. (2018) presented some mango cultivars in Egypt by employing morphological properties of the fruits and molecular markers techniques to show the diversity of the collected cultivars.

Understanding the variability among a crop's genetic stocks is crucial to breeding programs. Moreover, genetic variability is essential to know the gene source for a particular trait within germplasm to identify desirable cultivars for commercial production and improve yield and other traits (Govindaraj et al., 2015). Also, the progress in breeding programs depends on the genetic variability in the breeding material. Most of the genetic characteristics are governed by more than one gene, which is highly affected by the environment. Hence, the coefficients of variation (both genotypic and phenotypic) and heritability (the degree to which a trait can be attributed to a particular gene) are crucial in determining the inheritance pattern of the traits. The heritability of a genetic character is important in determining the response to the selection (Piepho & Mohring, 2007). Because of the great heritability, the breeder can choose plants depending on how they display their traits (Holland, 2014).

Majumder et al. (2013) studied 60 mango genotypes to determine their variability, heritability, and genetic advance. They found that significant variations were observed in 20 traits. Also, there were considerable differences between the genotypic (GCV) and the phenotypic coefficients of variation (PCV) for almost all the characters, indicating the effect of the environment on the expression of these traits. However, among the studied characters, GCV and PCV were high for fruit yield per plant and the number of fruits per tree. All the studied traits showed considerably high heritability, ranging from 56.2 to 98.2 %, while the genetic advance was high for the top traits. Moreover, the combined influence of genetic advance and heritability offers the most effective conditions for selecting a specific trait.

Estimating each trait's contribution to the total observed variations in the genotypes is important; this enables the identification of the significant traits accounting for the greater share in the observed variations and then enables the breeder to focus on specific traits of interest for crop improvement. Consequently, the current work aimed to evaluate 11 mango genotypes by employing multivariate analysis based on cluster and principal component analysis (PCA) for yield and some of its contributing traits, as well as estimating the genetic variability, heritability, and genetic advance among the yield and its components.

2 MATERIALS AND METHODS

The present study was conducted on 12 years old mango trees grown on clay soil at Qus, Qena governorate, Egypt (25°54'56.2" N 32°45'30.7" E) during two successive seasons of 2021 and 2022. The experimental materials comprised 11 genotypes, *i.e.*, ten seeding strains and one check as the Zebda variety. The trees were spaced at 7 m x 7 m. The experimental design was intended in Randomized Complete Block Design with three replications. A single tree of both strains and varieties with the same uniform size is considered one replicate. Common cultural practices for orchards were provided with standard agronomic methods such as fertilization, irrigation, and pest management, as usual for mango farms. Data was recorded on ten quantitative characters in three rep-

lications and a single tree considered as replication for the studied traits as follows: yield per tree (Y), number of fruits per tree (NF), fruit mass (FM), fruit length (FL), fruit diameter (FD), fruit pulp (FP), seed mass (SM), total soluble solids (TSS), total sugars (TS g) and total acidity (AC). The yield per tree was recorded over the study period, fruit mass was measured by weighing balance, total soluble solids were measured by using a handy refractometer (AOAC, 2000), and total acidity was measured as g citric acid/ 100 g pulp according to (AOAC, 2000).

2.1 STATISTICAL ANALYSIS

The mean values of the data were analyzed according to (Sharma, 1998). Data were analyzed separately for each year and combined over two years (Steel & Torrir, 1980). The differences between the means for all studied traits were calculated using revised L.S.D. at 5 % and 1 %. Genotypic and phenotypic coefficient of variation (GCV and PCV) were computed by the formula suggested by Singh & Chaudhury (1985). Heritability, in a broad sense, was estimated according to Falconer (1989). The genetic advance was calculated as per the formula given by (Allard, 1960).

The hierarchical cluster analysis procedure of the program SPSS-V.13 for windows carried out cluster analysis. Principal component analysis (PCA) was performed using Minitab statistical software -V.17. The PCA was used to determine the extent of genetic variation. Eigenvalues were obtained from PCA, which were used to determine the axes' relative discriminative power and associated characters (Pradhan et al., 2015). The genotypes were categorized in a bi-plot figure and compared with the cluster analysis. Simple correlation coefficients between different traits under the study were analyzed by the method of Hayes et al. (1955).

3 RESULTS AND DISCUSSION

3.1 MEAN PERFORMANCE OF MANGO GENOTYPES

As shown in Table 1, it should be called that 2 out of 11 genotypes, *i.e.*, S9 and S10, were superior for the number of fruits per tree, yield per tree, fruit mass, and fruit diameter in the two years and showed significant (*p* < 0.01) compared to 'Zebda' (chick genotype No. 11), which was superior from the other genotypes in 5 out of 10 traits namely, fruit pulp, seed mass, TSS, total sugars, and total acidity in two years. Generally, the genotypes S9 and S10 were superior in yield traits, while 'Zebda' was

superior in all quality traits. Igbari et al. (2019) evaluated seven mango varieties using 13 morphological traits, and the results exhibited some variability in fruit sizes and shapes, leading to reliable discriminating characters. They demonstrated that while some mango fruit morphological traits showed the greatest diversity, others showed little to no variation and could not be effectively employed as a characterization tool.

3.2 ANALYSIS OF VARIANCE, GENOTYPIC AND PHENOTYPIC COEFFICIENTS OF VARIATION

The individual analysis of variance for each year and the combined analysis are shown in Table 2. The results indicated that mean squares of the studied genotypes were highly significant (*p* < 0.01) every two seasons and combined, indicating wide genetic diversity among the genotypes for all examined traits. Meanwhile, there were no significant differences in combined analysis among years for all traits except for the number of fruits/tree. However, the interaction of genotypes × years was significant (*p* < 0.01) for three out of ten studied traits: number of fruits/ tree, yield/ tree, and fruit mass. These results agree with Hamad (2021) and Serry et al. (2019).

Table 3 displays the heritability and predicted genetic advance, as well as the extent of variability within ten characters across different genotypes, as evaluated by range, genotypic coefficient of variation, and phenotypic coefficient of variation. The highest range of variation was recorded in the number of fruits per tree (141.77-488.73 and 146.90-496.63 fruits), followed by yield per tree (39.27-137.70 and 40.70 - 141.30 kg/tree), fruit mass (220.13-281.80 and 224.43-285.33 g) in first and second years, respectively among the characters (Table 3). A moderate range of variation was found in seed mass percentage (6.33-19.10 %) and (19.10-71.82 %), with a mean of 15.11 and 16.70 % in the first and second seasons, respectively. The remaining contributing characters had a narrow range of variation, indicating a small value of variability among the genotypes. The results of Jena et al. (2021) showed a marked variation in the fruit traits of mango genotypes, reflecting the highly heterozygous nature. Akhtar et al. (2007) stated that characters with a high range of variation should be prioritized in the selection. Galal et al. (2017) and Patel et al. (2015) obtained a wide range of phenotypic variations, high heritability, and genetic advance among the genotypes for the number of traits. Generally, population variability is essential for breeding programs, as substantial variation in the qualities of interest indicates an opportunity for successful improvement through selective breeding.

A high magnitude of GCV percentage and PCV

Table 1: Means of the studied traits for eleven mango genotypes cultivated in Upper Egypt for the years 2021 and 2022

Genotypes	Number of fruits/tree	Yield/tree (kg)	Fruit mass (g)	Fruit length (cm)	Fruit diameter (cm)	Fruit pulp (%)	Seed mass (%)	TSS (%)	Total sugars (%)	Total acidity (%)
					1st Year					
S1	285.83 ± 15.72	61.23 ± 34.74	220.13 ± 26.17	8.57 ± 0.09	7.3 ± 0.07	62.17 ± 2.76	18.73 ± 0.24	13.93 ± 0.1	10.87 ± 0.44	0.34 ± 0.00001
S2	308.80 ± 51.87	69.8 ± 16.48	230.13 ± 9.77	8.7 ± 0.09	7.5 ± 0.04	61.97 ± 0.44	19.1 ± 0.01	14.17 ± 0.32	10.87 ± 0.25	0.31 ± 0.00003
S3	322.33 ± 46.97	70.63 ± 56.14	236.17 ± 11.32	8.97 ± 0.06	7.67 ± 0.06	62.23 ± 0.32	18.07 ± 0.3	14.83 ± 0.02	11.2 ± 0.12	0.305 ± 0.00003
S4	339.00 ± 25.04	82.07 ± 30.77	248.47 ± 10.17	8.67 ± 0.44	7.63 ± 0.09	62.4 ± 0.39	18.27 ± 0.03	15.33 ± 0.02	11.23 ± 0.02	0.291 ± 0.00001
S5	364.73 ± 37.76	91.50 ± 41.97	257.83 ± 4.42	8.93 ± 0.33	7.77 ± 0.06	63.47 ± 0.08	18 ± 0.21	15.27 ± 0.1	11.47 ± 0.04	0.277 ± 0.00005
S6	378.67 ± 38.58	98.80 ± 10.36	260.1 ± 4.81	9 ± 0.31	7.93 ± 0.06	63.87 ± 0.02	17.1 ± 0.36	15.87 ± 0.04	11.3 ± 0.13	0.275 ± 0.00003
S7	390.43 ± 34.40	102.93 ± 34.54	262.77 ± 25.9	9.43 ± 0.12	7.87 ± 0.2	64.4 ± 0.93	17.4 ± 0.16	15.9 ± 0.04	12.23 ± 0.09	0.257 ± 0.00001
S8	408.83 ± 33.82	107.47 ± 44.33	268.67 ± 10.89	9.57 ± 0.09	8.07 ± 0.09	65.23 ± 0.02	17.2 ± 0.16	16.2 ± 0.04	12.57 ± 0.17	0.25 ± 0.00003
S9	428.17 ± 17.42	120.80 ± 05.32	276 ± 24.25	10.03 ± 0.26	8.13 ± 0.06	66.67 ± 0.3	16.6 ± 0.16	16.23 ± 0.16	12.63 ± 0.02	0.252 ± 0.00001
S10	488.73 ± 19.33	137.70 ± 23.85	281.8 ± 9.25	10.67 ± 0.24	8.37 ± 0.02	68.23 ± 0.6	16 ± 0.17	17.13 ± 0.04	13.43 ± 0.15	0.245 ± 0.00001
Chick	141.77 ± 10.94	039.26 ± 0.96	247.17 ± 52.02	11.9 ± 0.04	7.63 ± 0.06	72.17 ± 0.16	6.33 ± 0.04	17.93 ± 0.143	14.47 ± 0.04	0.32 ± 0.0001
Means	350.66	89.29	253.57	9.49	7.81	64.8	15.11	14.99	11.47	0.26
LSD$_{0.05}$	12.97	4.97	4.58	0.38	0.34	1.3	0.7	0.51	0.59	0.05
LSD$_{0.01}$	17.68	6.77	6.25	0.52	0.46	1.77	0.96	0.7	0.8	0.07
					2nd Year					
S1	298.97 ± 13.33	68.6 ± 7.09	224.43 ± 14.16	8.77 ± 0.05	7.23 ± 0.04	62.2 ± 2.01	19.1 ± 0.16	14.53 ± 0.06	10.73 ± 0.24	0.338 ± 0.000112
S2	315.5 ± 22.21	73.2 ± 9.49	238.47 ± 5.97	8.83 ± 0.06	7.4 ± 0.09	62.33 ± 0.44	19 ± 0.25	15.33 ± 0.13	10.8 ± 0.13	0.315 ± 0.000025
S3	326.57 ± 55.44	78.27 ± 7.12	237.23 ± 18.13	9.03 ± 0.02	7.6 ± 0.07	62.13 ± 0.3	18.5 ± 0.16	15.17 ± 0.09	11.07 ± 0.09	0.31 ± 0.0001
S4	347 ± 28.99	88.2 ± 4.69	251.03 ± 7.7	8.97 ± 0.17	7.76 ± 0.06	63.23 ± 0.1	18.2 ± 0.09	15.86 ± 0.06	11.37 ± 0.02	0.295 ± 0.000025
S5	372.63 ± 42.8	94.27 ± 14.06	252.5 ± 23.59	9.13 ± 0.13	7.87 ± 0.1	63.67 ± 0.14	18 ± 0.16	16.1 ± 0.16	11.63 ± 0.003	0.27 ± 0.000025
S6	380.37 ± 35.1	98.5 ± 12.31	258.6 ± 6.31	9.57 ± 0.02	7.8 ± 0.16	64.03 ± 0.49	17.6 ± 0.09	16.03 ± 0.1	11.87 ± 0.04	0.258 ± 0.0000004
S7	410.07 ± 36.56	109.37 ± 10.17	265.43 ± 22.66	9.63 ± 0.06	7.9 ± 0.21	65.07 ± 0.44	17.3 ± 0.16	16.33 ± 0.16	12.37 ± 0.2	0.26 ± 0.000025
S8	421.53 ± 27.32	112.5 ± 10.93	269 ± 3.64	10 ± 0.28	7.6 ± 0.39	65.23 ± 0.14	17 ± 0.25	16.47 ± 0.08	12.5 ± 0.01	0.26 ± 0.000025
S9	444.1 ± 19.91	123.63 ± 11.96	275.63 ± 23	10.1 ± 0.36	7.96 ± 0.25	66.93 ± 0.17	16.5 ± 0.04	16.67 ± 0.02	13.13 ± 0.3	0.252 ± 0.00001
S10	496.63 ± 19.88	141.3 ± 31.92	285.33 ± 14.42	11 ± 0.21	8.27 ± 0.08	67.7 ± 0.11	15.77 ± 0.04	17.27 ± 0.02	13.4 ± 0.14	0.250 ± 0.00002
11(chick)	146.90 ± 54.27	40.7 ± 1.11	238.4 ± 15.97	11.53 ± 0.03	7.83 ± 0.01	70.67 ± 0.69	6.7 ± 0.16	17.43 ± 0.13	15.03 ± 0.06	0.323 ± 0.000132

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Table 2: Mean squares of variance analyses for the studied traits of eleven mango genotypes cultivated in Upper Egypt for the years years 2021 and 2022 and combined analysis for the two years

S. O. V	df	NF	Y (kg/tree)	FM (g)	FL (cm)	FD (cm)	FP (%)	SM (%)	TSS (%)	TSg (%)	AC (%)
Year 1											
Replications	2	119.09	226.37	121.26	1.73	0.44	0.58	0.2	0.15	0.38	0.001
Genotypes	10	24464.9**	2405.4**	1113.2**	3.14**	0.28**	30**	37.4**	4.3**	4.0**	0.003**
Error	20	57.95	8.5	7.24	0.05	0.04	0.58	0.17	0.09	0.12	0.0001
Year 2											
Replications	2	39.18	86.9	96.664	0.79	0.94	0.22	0.14	0.58	0.35	0.001
Genotypes	10	25503.8**	2373.4**	1043.2**	2.47**	0.24**	21.57**	36.12**	2.29**	5.10**	0.003**
Error	20	19.03	4.99	6.61	0.07	0.06	0.49	0.14	0.04	0.1	0.0002
Combined analysis											
Years (Y)	1	1445.8**	292.74	6.37	0.62	0.62	0.02	0.1	2.64	1.82	1.82
Error (a)	4	1264.46	229.82	110.55	1.42	1.42	0.41	0.2	1.02	0.46	0.46
Genotypes (G)	10	27219.3**	4769.1**	2123.5**	5.53**	5.53**	50.93**	73.42**	6.27**	9.02**	9.02**
G × Y	10	22749.4**	9.61**	32.82**	0.09	0.09	0.59	0.12	0.27	0.11	0.11
Error (b)	40	2.35	0.57	6.76	0.04	0.04	0.53	0.16	0	0.1	0.1
Means		360.02	88.72	254.19	9.69	7.75	64.84	16.7	16.11	12.17	0.28
LSD$_{0.05}$		7.43	3.8	4.37	0.45	0.42	1.19	0.64	0.34	0.54	0.05
LSD$_{0.01}$		10.13	5.19	5.97	0.61	0.57	1.63	0.87	0.46	0.73	0.07

percentage were observed in the number of fruits per tree, followed by yield per tree and fruit mass in both seasons. Meanwhile, the other traits recorded less difference between GCV and PCV and less influence by environmental conditions (Table 3). High estimates of broad sense heritability for these variables show little to no environmental influence, even though they exhibit a little mismatch between PCV and GCV, as evidenced by these results. GCV's high value can be exploited through proper selection. Galal et al. (2017) reported that the higher the genotypic coefficient of variation value, the more potential for character improvement. These findings agree with Majumder et al. (2012); Patel et al. (2015); Sridhar et al. (2018), and Das et al. (2021). They found significant heritability and genetic advance among the genotypes and tiny variations between the genotypic and phenotypic coefficients of variation for practically all variables, indicating that environmental influences were minimal. The high PCV and GCV were obtained for fruit mass, seed width, seed mass, acidity, TSS, and yield/plant. The high PCV and GCV were obtained for fruit mass, seed width, seed mass, acidity, TSS, and yield/plant.

3.3 HERITABILITY AND GENETIC ADVANCE

As our understanding of genetics continues to expand, we can utilize heritability to forecast how choosing superior genotypes will ultimately pan out. From the results presented in Table 3, the heritability percentage ranged from 75.63 (fruit diameter) to 99.93 % (number of fruits per tree). High heritability percentage estimates coupled with the high genetic advance in the number of fruits per tree (99.76 and 119.09 %) in the first season indicate that the environment less influenced this character, showing that these traits were controlled by a small number of genes or, alternatively, that there was an additive genetic influence even if they were polygenic in nature. As this is the case, selecting certain characteristics would be more useful for increasing yield. The high value

Table 3: Range of values and genetic parameters for all studied traits of mango genotypes cultivated in Upper Egypt during the years 2021 and 2022

Characters	Min	Max	GCV (%)	PCV (%)	Hb (%)	GA
			Year 1			
Number of fruits/tree	141.77 ± 10.94	488.73 ± 19.33	2320.07	2325.58	99.76	119.09
Yield/tree (kg)	39.26 ± 0.96	137.7 ± 23.85	894.78	897.95	99.65	17.44
Fruit mass (g)	220.13 ± 26.17	281.8 ± 9.25	145.38	146.33	99.35	14.82
Fruit length (cm)	8.57 ± 0.09	11.9 ± 0.04	10.86	11.03	98.46	0.1
Fruit diameter (cm)	7.3 ± 0.07	8.37 ± 0.02	1.03	1.2	85.85	0.07
Fruit pulp (%)	61.97 ± 0.44	72.17 ± 0.16	15.11	15.41	98.08	1.17
Seed mass (%)	6.33 ± 0.04	19.1 ± 0.01	74.69	75.04	99.54	0.35
TSS (%)	13.93 ± 0.1	17.93 ± 0.143	8.84	9.03	97.83	0.18
Total sugars (%)	10.87 ± 0.44	14.47 ± 0.04	10.88	11.21	97.07	0.24
Total acidity (%)	0.245 ± 0.00001	0.34 ± 0.00001	0.35	0.35	99.3	0.0002
			Year 2			
Number of fruits/tree	146.90 ± 54.27	496.63 ± 19.88	2359.54	2361.3	99.93	39.18
Yield/tree (kg)	40.7 ± 1.11	141.3 ± 31.92	844.32	846.1	99.79	10.26
Fruit mass (g)	224.43 ± 14.16	285.33 ± 14.42	135.93	136.8	99.37	13.53
Fruit length (cm)	8.77 ± 0.05	11.53 ± 0.03	8.27	8.51	97.15	0.14
Fruit diameter (cm)	7.23 ± 0.04	8.27 ± 0.08	0.78	1.02	75.63	0.09
Fruit pulp (%)	62.13 ± 0.3	70.67 ± 0.69	10.84	11.09	97.73	0.99
Seed mass (%)	6.7 ± 0.16	19.1 ± 0.16	71.82	72.11	99.6	0.29
TSS (%)	14.53 ± 0.06	17.43 ± 0.13	4.64	4.73	98.06	0.08
Total sugars (%)	10.73 ± 0.24	15.03 ± 0.06	13.67	13.94	98.07	0.2
Total acidity (%)	0.250 ± 0.00002	0.338 ± 0.000112	0.36	0.36	98.45	0.0004

Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (Hb), and genetic advance (GA)

of heritability coupled with a moderate degree of genetic advance was recorded for yield per tree, fruit mass in the two seasons, and the number of fruits per tree in the 2nd season. Thus, selection would be sufficient in situations of high heritability value and high or moderate value of genetic advance. This condition develops because of the interaction of additive genes (Das et al., 2021). Sridhar et al. (2018) concluded that high heritability implies that the environment's influence was negligible, allowing the breeder to choose plants based on their phenotypic expression. Hence the selection of the characters would be suitable for improving mango.

Because strong heritability does not always reflect high genetic progress, high heritability coupled with a lower degree of genetic advance was seen in the results of fruit length, fruit diameter, fruit pulp percentage, seed mass percentage, TSS percentage, total sugars, and total acidity, demonstrating that environmental factors and non-additive gene effects (dominance and epistasis) played a more significant role in determining these characteristics than did additive genetic factors (Sridhar et al., 2018; Getachew et al., 2021). All of the analyzed traits of mango genotypes with high heritability in the Das et al. (2021) study had high genetic advance values, indicating that additive genes controlled these qualities, and that selection would favor their improvement. In addition, Jena et al. (2021) concluded that the high heritability of mango traits and closeness of GCV and PCV values indicate they are less environmentally effective. Consequently, a reliable selection is made for breeding based on phenotypic characteristics (Bally and De Faveri, 2021).

3.4 PRINCIPAL COMPONENT ANALYSIS AND GENETIC DISTANCE

Figure 1 shows the various components and the eigenvalues calculated by principal components analysis (PCA). The principal component analysis revealed that four principal components, PC1, PC2, PC3, and PC4, with eigenvalues 4.70, 2.12, 0.12, and 0.06, respectively, have accounted for the total cumulative variability among genotypes. The first two principal components, PC1 (67.1 %) and PC2 (30.25 %), showed eigenvalues of more than one, and cumulatively they explained 97.35 % variability (the highest variance when correlating the most relevant components), where the contribution of PC1 towards variability was the highest (67.1 %). The results showed that fruit mass and total sugars in PC1 and fruit mass and number of fruits in PC2 had the highest loadings. Many authors as Lawson et al. (2019) and Sridhar et al. (2022), established the effectiveness of PCA, proving it could classify mangoes. Lal et al. (2019) reported that
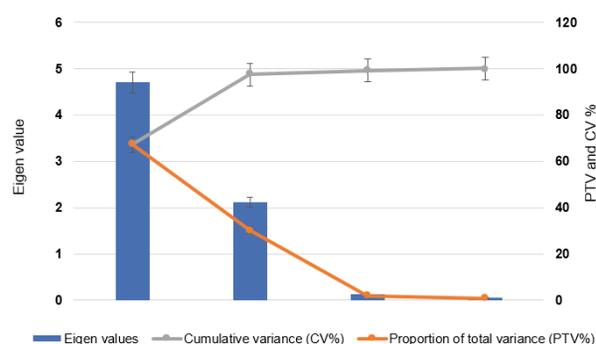

Figure 1: Scree plot of Eigenvalues, variability proportion (PTV), and cumulative variability (CV) for studied traits of eleven mango genotypes

PCA for 17 traits of 60 mango genotypes was reduced to six principal components with eigenvalues up to 1.0, presenting a cumulative variance of 78.78 % variation among the genotypes.

As shown in Table 4 and Figure 2, PC1 has a positive association with total sugars and fruit mass and a negative association with total acidity. The second PC has a positive association with fruit mass and the number of fruits while the negative association with total sugars. The third PC has a positive association with fruit diameter and the number of fruits while a negative association with yield per tree. PC4 has a positive association with fruit mass and a negative association with yield per tree.

The current investigation indicated that five major characters contributed one hundred percent to genetic divergence out of a total of seven yield and contributing traits. The number of fruits per tree and the yield per tree were found to contribute 87.8 % and 8.4 %, respectively, to genetic divergence out of the five major traits studied (Figure 3).

Previous studies (Rajan et al., 2009; Majumder et al., 2012; Singh, 2016; Sridhar et al., 2022) have also reported the maximum contribution of the number to genetic divergence in mango genotypes. Therefore, the

Table 4: Principal component analysis for different traits in mango genotype

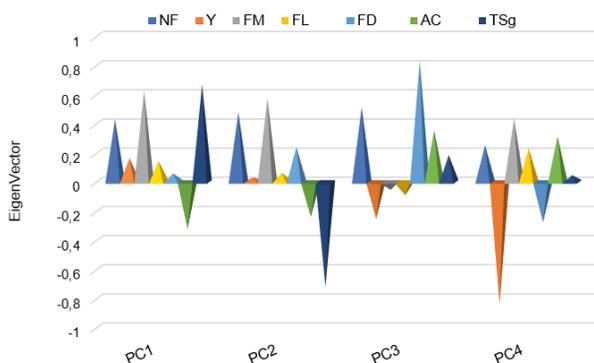| Variables	PC1	PC2	PC3	PC4
NF	0.429	0.479	0.515	0.254
Y	0.165	0.0316	-0.254	-0.838
FM	0.627	0.571	-0.054	0.435
FL	0.144	0.0630	-0.092	0.233
FD	0.058	0.240	0.829	-0.278
AC	-0.323	-0.239	0.356	0.313
TS g	0.669	-0.719	0.185	0.047

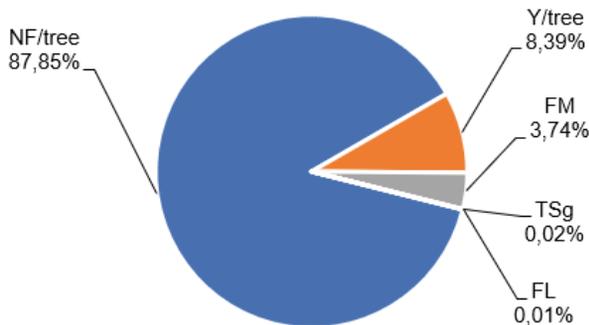**Figure 2**: Scree plot of Eigenvector for studied traits of 11 mango genotypes in Upper Egypt

Figure 3: Graphical representation of the proportionate contribution of studied major traits towards genetic divergence

number of fruits would be the critical parameter for selecting divergent genotypes. Clusters I and II exhibited the highest cluster mean values for most studied physical traits (Table 5). The highest cluster mean values for fruit diameter, fruit mass, yield per tree, and number of fruits per tree were found in Cluster II, followed by cluster I. Cluster III represented the highest cluster mean value for total acidity, total sugars, TSS, fruit pulp, and fruit length. Although cluster IV had the maximum number of genotypes (4), no remarkable feature was noticed in this cluster for most different characters, and it had the lowest mean values for fruit diameter, fruit length, fruit mass, total sugars, total soluble solids, and fruit pulp.

In order to decipher the variation among the genotypes, a principal component analysis (PCA) was carried out. Moreover, a scattered diagram of the genotypic distribution pattern on the axis is shown in Figure 4. The scree plot indicates most of the variation is derived from the first and second components in the eigenvalue of the genotypes data. The results of biplot-PCA stated the presence of high genetic variations among genotypes based

Table 5: Average (av) of studied traits for each cluster along with standard deviation (SD), as well as the difference (dif) between each cluster, mean, and total mean

| Cluster No.		Fruit diameter (cm)	Fruit length (cm)	Fruit mass (g)	Yield/tree (kg)	Number of fruits/tree	Total acidity (%)	Total sugars (%)	TSS (%)	Seed mass (%)	Fruit pulp (%)
I	av ± SD	7.86 ± 0.001	9.41 ± 0.11	261.86 ± 34.88	101.91 ± 58.42	390.91 ± 43.39	0.26 ± 0.00003	12 ± 0.25	16.03 ± 0.08	17.45 ± 0.15	64.37 ± 0.56
	dif	0.08	-0.18	7.99	10.52	35.56	-0.02	-0.11	0.12	0.79	-0.45
II	av ± SD	8.19 ± 0.04	10.46 ± 0.3	279.7 ± 30.03	130.86 ± 49.3	464.41 ± 59.95	0.25 ± 0.00	13.15 ± 0.15	16.83 ± 0.22	16.22 ± 0.22	67.39 ± 0.68
	dif	0.4	0.86	25.82	39.46	109.06	-0.03	1.05	0.91	-0.44	2.57
III	av ± SD	7.73 ± 0.00	11.72 ± 0.00	242.78 ± 0.00	39.98 ± 0.00	144.33 ± 0.00	0.32 ± 0.00	14.75 ± 0.00	17.68 ± 0.00	6.52 ± 0.00	71.42 ± 0.00
	dif	-0.05	2.13	-11.1	-51.42	-211.01	0.04	2.65	1.77	-10.14	6.6
IV	av ± SD	7.52 ± 0.04	8.82 ± 0.02	235.76 ± 26.82	74 ± 7.93	318 ± 45.06	0.31 ± 0.00029	11.02 ± 0.06	14.9 ± 0.32	18.63 ± 0.18	62.33 ± 0.11
	dif	-0.27	-0.78	-18.12	-17.4	-37.34	0.03	-1.08	-1.02	1.97	-2.49
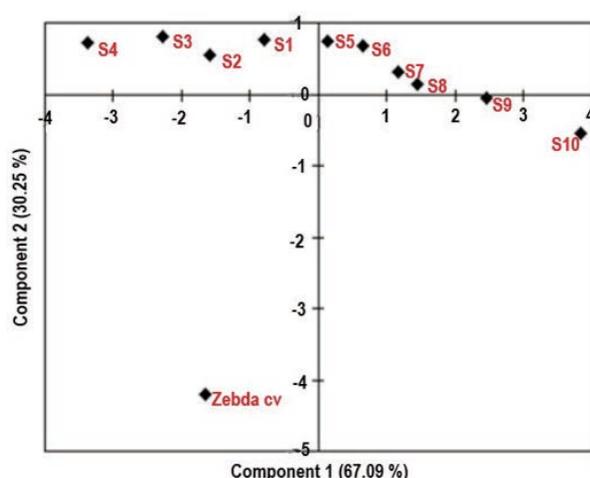
Figure 4: Principal component analysis (PCA) based on the first and second components for the eleven mango genotypes

on the data of studied traits (Figure 4). The first and fourth clusters had four genotypes accounting for 72.8 % of total genotypes (36.4 % each), beside two and one genotypes were classified in the second and third clusters accounting for 18.1 % and 9.1 % of total genotypes, respectively (Table 6).

Pairwise comparisons were conducted between all genotypes, and the mean dissimilarity values were calculated based on five traits of the studied mango fruit. The distance between all eleven mango genotypes was evaluated. The Euclidean distance coefficient ranged from 0.539 (between S1 and S2) to 16.334 (between S2 and ''Zebda'), where the mean distance between groups was found with a maximum (16.334), as shown in Table 7, which indicates to a reasonable variance between the genotypes. Zebda cultivar was found to be much distanced genetically from other genotypes (>10 DC), followed by S10 [from S1 (7.6 DC), S2 (7.5 DC), S3 (7 DC), and S4 (6.3 DC)], S9 [from S1 (6 DC) and S2 (5.9 DC)] as well as both S10 [from S5, (5.4 DC)] and S9 [from S3, (5.4 DC)] that distanced from the genotypes under study. Most other genotypes were scattered over the plot with a medium or close genetic distance. There may have been shared ancestors between the genotypes, as evidenced by the close distance between them and their grouping within a common cluster (Lal et al., 2019). When there is a lot of variance between individuals' genes, it might cause phenomena known as allelic amplitudes to appear in the population's phenotypes. Using varieties from various clusters with high to moderate genetic distances in crossing programs may be advised to create new recombinants with desirable characteristics (Majumder et al., 2013).

Table 6: Optimization grouping between 11 mango genotypes, obtained by cluster analysis, based on five fruit characteristics, using the Euclidian distance

Clusters	No. of genotypes	Percentage	Genotypes included
I	4	36.4 %	GROUP1 (Y1 > = 0, Y2 > = 0): S5, S6, S7 and S8
II	2	18.1 %	GROUP2 (Y1 > = 0, Y2 < 0): S9 and S10
III	1	9.1 %	GROUP3 (Y1 < 0, Y2 < 0): Check
IV	4	36.4 %	GROUP4 (Y1 < 0, Y2 > = 0): S1, S2, S3 and S4

Table 7: Euclidean distance coefficient (DC) among 11 Mango genotypes

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	'Zebda'
S1	0	0.539	1.052	1.732	2.34	3.031	3.846	4.483	6.019	7.642	16.329
S2		0	0.855	1.428	2.123	2.852	3.682	4.325	5.91	7.518	16.334
S3			0	0.893	1.631	2.263	3.16	3.805	5.432	7.023	15.625
S4				0	0.831	1.509	2.39	3.032	4.682	6.253	15.085
S5					0	0.798	1.586	2.229	3.858	5.44	14.409
S6						0	1.068	1.66	3.268	4.817	13.641
S7							0	0.647	2.317	3.879	13.057
S8								0	1.702	3.238	12.527
S9									0	1.631	11.268
S10										0	10.085

The hybridization program would be sensible if performed with 'Zebda' combined with any other studied genotypes and between S10 with S1, S2, or S3 due to higher observed distances to obtain higher values of essential characteristics, as well as a mitigation of the speed of primitive extinction and adaptive genes between genotypes (Govindaraj et al., 2015). Small distances between S1 and S2 (0.539 DC) or S2 and S8 (0.647) may correspond to originating from a common ancestor, or some genetic material may be substituted between the parental roots of these genotypes, making them all combined into one main group (Davis, 1997; Tahir et al., 2021).

3.5 UPGMA CLUSTERING DENDROGRAM

Figure 5 presents the UPGMA tree diagram generated by cluster analysis based on five fruit traits of mango genotypes. Generally, it shows two large classes: low seed mass (SM) trait ('Zebda') and high or medium SM trait (other genotypes). Four groups were formed in a complex selection across the approved cut-off point; 'Zebda' formed a single cluster within a class with a low SW trait and the other ten genotypes in the other class. Genotypes clustered similarly in the dendrogram, cluster analysis, principal component analysis (PCA) graph, and along the two axes of the PCA graph (Figure 4). Once more, 'Zebda' created a single cluster that was very different from the other clusters, suggesting that this genotype could be crossed with others to produce offspring with the desired characteristics. The perusal of the results revealed that the number of fruits per tree and fruit mass exhibited higher estimates of GCV, heritability, and genetic advance, indicating additive gene effects controlling these traits. Therefore, individual plant selection for these traits would be effective in the mango crop. Accordingly, non-additive control the inheritance of all studied traits except the two above traits (number of fruits per tree and fruit mass); hence, other methods used in the breeding that traits other than selection like hybridization, mutations, and vegetative propagation, especially mango is a highly heterozygous crop. The results of genetic studies can be used for the selection of parents in hybridization programs. Hence, direct selection may be followed to im-
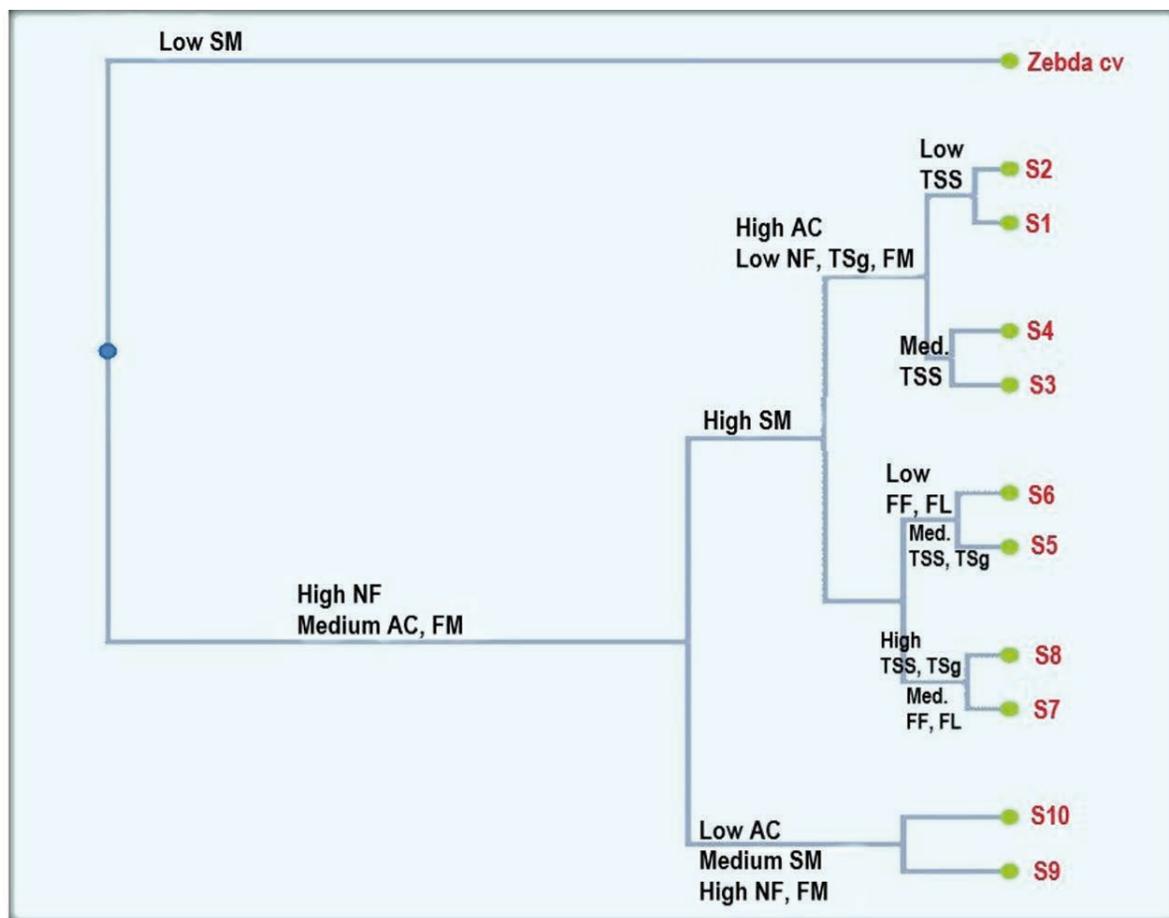

Figure 5: Dendrogram, using average linkage (Between Groups), for eleven mango genotypes based on five fruit traits

prove mango for these characters. Sridhar et al. (2018) and Das et al. (2021) both find results consistent with these conclusions.

3.6 CORRELATION COEFFICIENTS

Understanding how different traits are linked is crucial during the crop improvement selection process (Fasahat et al., 2016). Simple correlation coefficients between different traits in eleven mango genotypes for nine traits in two years (above and below) are demonstrated in Table 8.

In the present study, the highest significantly positive correlation coefficients were obtained between yield per tree and number of fruits per tree (0.987 and 0.995), followed by fruit mass (0.966 and 0.971), fruit pulp (0.905 and 0.940), fruit length (0.865 and 0.910) and total sugars % (0.819 and 0.911) in first and second seasons, respectively. This finding implied that selection procedures aimed at increasing yield per tree would improve these characteristics automatically. On the other hand, seed mass demonstrated a negative and significant correlation with each yield per tree (-0.838 and -0.883), no of fruits per tree (-0.860 and -0.954), fruit mass (-0.833 and -0.913) and fruit pulp (-0.850 and -0.868) as well as TSS % (-0.400 and -0.885) and total sugars (-0.802 and -0.913) in first and second seasons, respectively. The number of fruits per tree showed positive and highly significant with fruit mass (0.955 and 0.973), fruit length (0.868 and 0.911), and fruit pulp (0.910 and 0.942), while it demonstrated insignificant with seed mass (-0.860 and-0.954) in first and second seasons, respectively. These results agree with Samal et al. (2012) and Igbari et al. (2019). They used the Pearson correlation coefficient for mango varieties quality parameters and found positive and

negative correlations between many fruit traits. Lawson et al. (2019) also used Pearson's correlation coefficient to explore the relationship between the postharvest quality parameters during mango fruit ripening. A real picture of the genetic relationships between various traits and the direct and indirect contributions of one trait to another is provided by correlation analysis (Jena et al., 2021). In our investigation, positive and negative correlations between quantitative characteristics were strongly reflected.

4 CONCLUSIONS

Eleven genotypes of mango exhibited substantial genetic diversity. The highest range of variation was recorded in the number of fruits per tree, followed by yield per tree and fruit mass. High heritability estimates coupled with a high or moderate degree of genetic advance in the number of fruits per tree, yield per tree, and fruit mass. The correlation was positive and significant between yield per tree, with each of number of fruits per tree, fruit mass, fruit length, fruit pulp, and total sugars. In contrast, seed mass demonstrated a negative and significant correlation with yield per tree, number of fruits per tree, fruit mass, and fruit pulp in the two years of study. For the future experiment, traits contributing maximum to genetic diversity, such as fruits per tree, fruit mass, and yield per tree, should be prioritized as selection parameters, and diverse genotypes identified in the present study may be utilized for attempting heterotic cross combinations and developing hybrid varieties.

5 ACKNOWLEDGEMENT

Table 8: Simple correlation coefficients between each pair of nine traits in 1st (above diagonal) and 2nd year (below diagonal) in eleven mango genotypes

Traits	Y (kg)	NF	FM (g)	FL (cm)	FD (cm)	FP (%)	SM (%)	TSS (%)	TSg (%)
Y (kg)		0.987**	0.966**	0.865**	0.846**	0.905**	-0.838**	0.469	0.819**
NF	0.995**		0.955**	0.868**	0.847**	0.910**	-0.860**	0.466	0.847**
FM (g)	0.971**	0.973**		0.773	0.805**	0.850**	-0.833**	0.397	0.788
FL (cm)	0.91**	0.911**	0.869**		0.859**	0.817**	-0.693	0.473	0.711
FD (cm)	0.649**	0.646	0.637	0.662		0.755	-0.638	0.382	0.627
FP (%)	0.94**	0.942**	0.929**	0.856**	0.546		-0.850**	0.639	0.879**
SM (%)	-0. 883**	-0.954**	-0.913**	-0.828**	-0.595	-0.868**		-0.400	-0.802**
TSS (%)	0.883**	0.891**	0.901	0.698	0.45	0.808**	-0.885**		0.483
TSg (%)	0.911**	0.912**	0.889**	0.745	0.428	0.895**	-0.913	0.867**	

**. The mean difference is significant at the 0.01 level

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6 AUTHOR CONTRIBUTIONS

The study's planning and design included the participation of all authors. Mansour, MM, and Osman, SOA, prepared the materials and collected the data; Hussein, NRA, and Zaki H analyzed the data. Mansour, MM, Osman, SOA, and Zaki H wrote the original and subsequent versions of the manuscript. All authors have reviewed and approved the final manuscript.

7 DECLARATIONS

7.1 CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

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