RESEARCHARTICLE





Assessment of Genetic Variability in Solanum lycopersicum L. Genotypes for Yield and Yield Attributing Traits

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Abstract

Tomato is a self-pollinated crop belongs to family Solanaceae. It is important for its fresh fruit market and is an ample source of vitamins A, C, and lycopene. Due to its nutritional value, tomato demand is continuously increasing. A study was conducted at the University of Agriculture, Faisalabad to study the genetic variability among tomato genotypes for fruit and yield related traits. Eighteen genotypes of tomato (Solanum lycopersicum L.) were studied in this experiment. The objectives of this study were to assess yield and yield attributing traits. Analysis of variance revealed highly significant amount of genetic variability among genotypes for traits under studied except plant height which showed significant results. High heritability was observed for no. of fruits/cluster, total fruit yield/plant, individual fruit weight, no. of fruits/plant, and no. of clusters/plant indicating that selection of these traits were effective for genetic improvement. Principal component analysis result exhibited that the first four principal components had Eigen value >1 out of six principal component analyses, contributing 84% of the total variance. Cluster analysis grouped 18 tomato genotypes into four clusters. Cluster I had the maximum cluster mean value for plant height while cluster III showed highest cluster mean value for pericarp thickness and cluster IV had the maximum cluster mean value for stem diameter. CLN-2001-A (2354.0), CLN-1621-L (2235.0), LO-4379 (1411.7) and PB-LO-2752 (1408) had better yield output among all the eighteen genotypes under studied.

KEYWORDS Tomato, Correlation, Genetic variability, Yield, Principle component analysis

1 | INTRODUCTION

Tomato, *Solanum lycopersicum* L. (2n=2x=24) is a mostly consumed vegetable in the world. Tomato is abundant in vital elements including vitamin C, potassium and antioxidants. Edible berry, Tomato is originated in western South America, Mexico and Central America (Gerszberg et al. 2014). Antioxidants such as beta-carotene, vitamin C, and lycopene are abundant in tomatoes. Tomatoes red colour is caused by the carotenoid pigment lycopene, a potent antioxidant that aids in scavenging dangerous free radicals from the body (Mallick et al. 2021). Lycopene may help lower the chance of developing some cancers, including those of the stomach, lung, and prostate (Kumar et al. 2020).

There are two types of growth tendencies for

tomato plants: determinate and indeterminate. With few side branches and a bushy growth style, determinate variations (Zushi et al. 2022). A tomato plant has green, pinnately complex leaves that are made up of several leaflets. Depending on the cultivar, there can be anywhere from 7 to 9 leaflets per leaf, but sometimes as many as 11 or more (Rakutko et al. 2018).

Inflorescences are the flower clusters that tomato plants generate. The reproductive organs of both males and females are present in the usually yellow blooms. They can be pollinated by their own pollen because they are self-pollinated. Nonetheless, pollinators like bees can enhance fruit set and quality through cross-pollination (Zizis, 2023). Tomato is an 302

important crop in Pakistan but it needs genetic improvement to create tomato varieties with excellent yields. The main causes of low yield of tomato in Pakistan are the absence of high-yielding cultivars and a lack of genetic diversity (Erika et al. 2022).

Tomato production is reduced in tropical and subtropical regions, due to adverse environmental factors including high temperatures (Nicola et al. 2009). Tomato plants may adapt to a variety of environmental circumstances. They grow best in regions with moderate temperatures, which are between 20 and 30°C (68 and 86°F) (Dholu et al. 2021). Because of their sensitivity to frost, tomatoes cannot withstand freezing temperatures. Although they can withstand slightly acidic to slightly alkaline environments, they prefer well-drained soil in the pH range of 6-7 (Dhaval et al. 2021).

Genetic analysis helps in identifying and understanding the genes associated with various important traits in tomatoes. These traits include fruit vield. size, shape. colour, flavour, nutritional composition. disease resistance, abiotic stress tolerance, and many others (Zhang et al. 2018). Genetic analysis enables breeders to make informed decisions during the breeding process (Chaudhary et al. 2019). Heritability for yield indicates that a greater number of environment trials are necessary for effective selection. Variability in population is determined using the phenotypic and genotypic coefficients of variation. Alone heritability estimation is insufficient to predict the effects of selection, so genetic improvement is also equally significant. The genetic diversity found in the genus Lycopersicon is responsible for the wide adaptation of tomatoes under contrasting environments (Rasheed et al. 2023).

The main objectives of this study was to assess the variability from the available germplasm to improve the selection process and identification of high yielding genotypes through the estimation of heritability, genetic variability, PCV, and GCV to initiate the tomato breeding program for the development of high yielding genotypes of tomato.

2 METERIALS AND METHODS

The experiment was conducted at the research area department of Plant Breeding and Genetics, University of Agriculture Faisalabad. A total of 18 genotypes of Solanum lycopersicum *L*. were evaluated under randomized complete block design (RCBD) with three replications. Row to Row and Plant to Plant distance was 2.5 feet and 2 feet respectively.

Parameters Recorded

Data were collected on six randomly selected plants for 12 quantitative traits [PH: Plant height(cm);

SD: Stem diameter(mm); FL: Fruit length(mm); FD: Fruit diameter(mm); PT: Pericarp thickness(mm) FFT: Fruit flesh thickness(mm); IFW: Individual fruit weight(g); FPP: No. of fruits/plant; CPP: No. of clusters/plant; FPC: No. of fruits/cluster; LPF: No. of locules/fruit; FYPP: Fruit yield/plant(g)].

Statistical Analysis

Analysis of variance for studied traits was performed by using Statistics 8.1 following Steel et al. 1997 to estimate the genotypic differences among all genotypes. Mean performance for all genotypes was estimated. Variability for each trait was calculated through coefficient of variation. Genotypic and phenotypic correlation coefficients were calculated by using R software. Principal component analysis and cluster analysis are the multivariate techniques that are used to analyses inter-relationship among several traits. PCA was used to estimate genetic divergence among different genotypes. Cluster analysis divides data set into some number of groups of genotypes. The divergence was calculated by PCA and cluster analysis following Pearson and Neyman (1928).

3 RESULTS & DISCUSSION

In this study, the analysis of variance was performed to assess the variability among 18 genotypes for 12 yield and yield-related traits of tomatoes. The mean square result revealed that significant differences as shown in Table 2. Mean performance for the trait plant height ranged from 95.1 to 131.17. CLN-1621-L (131.17) had maximum plant height while PB-LO-017906 (95.17) showed minimum plant height. The mean range for stem diameter was 10.00 to 13.50. Maximum stem diameter was recorded in the genotype LO-4379 and the minimum stem diameter was recorded for the genotype Sandal-F1. Compared the genotypes for fruit diameter, the mean ranged from 14.33 to 52.50. Genotype CLN-1621-L (52.50) recorded the maximum mean value and the minimum was recorded in BL-1176 (14.33). Data recorded for pericarp thickness ranged from 5.38 to 6.70. BL-1176 (6.70) had the maximum pericarp thickness, which is superior over other genotypes, while PB017895 (5.38), had the minimum pericarp thickness. No. of locules/fruit ranged from 2.00 to 4.83 among all the genotypes. In which Veepick (4.83) had maximum value, while BL-1176 (2.00) had minimum value. The mean values for individual fruit weight ranged from 4.17 to 94.50. Among all the genotypes studied Kanatoo (94.50) had the maximum value while BL-1176 (4.17) had the lowest value. Total fruit yield/plant was ranged from 317.5 to 2354.0. The minimum value for total fruit yield/plant was recorded in BL-1176 (317.5), while the maximum value was noted

in CLN-2001-A (2354.0). The no.	of fruits/plant ranged
Table 1: List of genotypes used in th	e present study

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Sr. No.	Genotypes	Sr. No.	Genotypes
1	CLN-1621-L	10	Veepick
2	CLN-2001-A	11	PB-LO-017903
3	Hybrid-B	12	V-676
4	BL-1176	13	Sultan
5	LO-4379	14	PB-LO-017906
6	PB017895	15	Kanatoo
7	Su Kong Tsao Feng	16	Sandal-F1
8	BGH-24	17	Bambino-F1
9	BL-1173	18	PB-LO-2752

 Table 2: Mean squares for morphological and yield-related traits of tomato

Source	Replication	Genotypes	Error
Degree of freedom	2	17	34
Plant height	101.8	304.9*	120.3
Stem diameter	1.01	2.3**	0.72
Fruit yield/plant	15514	1015684**	18656
Individual fruit weight	112.9	2254.3**	53.8
No. locules/fruit	0.24	1.6**	0.47
Pericarp thickness	1.32	0.4**	0.16
Fruit length	34.4	319.5**	34.4
Fruit flesh thickness	104.1	200.3**	25.4
No. of clusters/plant	0.43	8.5**	0.70
No. of fruits/cluster	0.29	11.6**	0.42
Fruit diameter	87.6	311.1**	27.5
No. of fruits/plant	0.48	1067**	23.8
* ~			

*=Significant, **=Highly Significant

from 6.00 to 75.50. Among all genotypes, BL-1176 (75.50) had a maximum value and Veepick (6.00) had a minimum value. Fruit length ranged from 14.17 to 60.17 among all the genotypes. In which Veepick (60.17) had highest while BL-1176 (14.17) had the lowest value. Fruit flesh thickness was ranged from 13.55 to 44.87. BL-1173 (13.55) had minimum value while Sukong Tsao Feng (44.87) had maximum value. The mean value for no. of fruits/cluster was ranged from 2.67 to 10.17 among all genotypes. Hybrid-B (10.17) had maximum value while Veepick (2.67) had minimum value. The mean value for the no. of clusters/plant ranged from 2.33 to 8.33. Among all the studied genotypes, Sukong Tsao Feng (8.33) had maximum value while minimum value was recorded in PB-LO-017906 (2.33). Estimation of heritability is the best indicator to determine heritable proportion of variation. The effectiveness of phenotypic-based selection was assessed by the high heritability which could be useful for the breeding program. The heritability estimated for traits ranged from 39.74 to 94.68. High heritability recorded for Fruit yield/plant (94.68%) followed by no. of fruits/plant (93.59%), Individual weight of fruit (93.16%), no. of fruits/cluster (89.69%), no. of clusters/plant (77.94%), Fruit diameter (77.42%), Fruit length (73.40%), Fruit flesh thickness (69.57%), no. of locules/fruit (44.33%), Stem diameter (42.62%), and Plant height (39.74%),

followed by Pericarp thickness (37.05%) as shown in Table 3.

Correlation

The correlation coefficient measured statistics frequently employed in research to demonstrate a relationship between variables (Janse et al. 2021). Utilizing correlation analysis improves comprehension of the relationships between various characters. As indicated by Singh and Chaudhry (1985), elementary correlation analysis can be categorized into genotypic and phenotypic coefficients. The genotypic and phenotypic association of plant height were positive and highly significant with fruit length (0.72**, 0.36*) and fruit yield/plant (0.79 **, 0.44**) respectively. The genotypic and phenotypic correlation of individual fruit weight were negative and highly significant with no. of fruit/plant (-0.78**,-0.77**), no. of cluster/plant (-0.64**,-0.60**) and no. of fruits/cluster (-0.88**,-0.82**) respectively as in Table 4.

Principle Component Analysis

Principle component analysis had been widely used for the evaluation of tomato genotypes, observing the characteristics of the plants that caused the genotype variance and selecting the desirable genotypes for breeding purposes (Chávez-Servia et al. 2018; Tembe et al. 2018; Figàs et al. 2018; Tripodi et al. 2021; Jin et al. 2019). The results exhibited that the first four principal components had Eigen value >1 out of six principal component analyses, contributing 84% of the total variance (Table 5). Brejda et al. (2000) reported that Eigen values represented the traits among the principal components because they explain a variance minimum 10%. The contribution of the first principal component recorded the maximum variability (44.72), followed by the second principal component which contributed (16.97) towards variability, the third principal component demonstrated (11.98) variability and four principal components showed (10.41) of the total variability. All the studied traits showed a significant difference for the first four principal components.

Biplot

Biplot principal component analysis showed that the first two principal component was developed to determining the associations between the PCs and each of the genotypes and traits (Yan and Rajcan 2002; Yan and Kang 2003). The PCA Biplot divided studied traits into four groups. The first groups included no. of clusters/plant, no. of fruits/plant and no. of fruits/cluster which were positively correlated with the first two PCs. The second group included fruit diameter, fruit yield/plant, plant height, fruit flesh thickness and fruit length which were correlated the l positively with the PC-1 and correlated negatively with indiv Table 2. Estimation of Constitution and Constitution and the length of the length

the PC-2. While third group include stem diameter, individual weight of fruit

Table 3: Estimation of Genetic Components of different studied traits in 18 genotypes of Tomato								
Traits	Maximum	Minimum	ECV (%)	PCV (%)	GCV (%)	h2 (%)	GA (%)	
Plant height	131.17	95.17	9.70	12.20	7.69	39.74	9.99	
Stem diameter	13.50	10.00	7.60	10.03	6.54	42.62	8.80	
Fruit length	60.17	14.17	17.33	33.60	28.79	73.40	50.81	
Fruit diameter	52.50	14.33	15.53	32.70	28.77	77.42	52.14	
Pericarp thickness	6.70	5.38	7.99	8.49	5.17	37.05	6.48	
Fruit flesh thickness	44.87	13.55	18.97	34.38	28.67	69.57	49.26	
Individual fruit weight	94.50	4.17	16.03	61.31	59.17	93.16	117.66	
No. of fruits/plant	75.50	6.00	16.75	66.17	64.01	93.59	127.57	
No. of clusters/plant	8.33	2.00	16.82	35.82	35.87	77.94	57.52	
No. of fruits/cluster	10.16	2.67	12.56	38.51	36.47	89.69	71.16	
No. of locules/fruit	4.83	2.33	22.05	29.55	19.67	44.33	26.98	
Fruit yield/plant	2354	317.50	13.19	57.22	55.68	94.68	111.62	

ECV= Genotypic coefficient of variance **PCV**= Phenotypic coefficient of variance **GCV**= Genotypic coefficient of variance **h2** = Heritability **GA** = Genetic advance

Table 4: Genotypic (rg) and Phenotypic (rph) correlation coefficients among the different pair of traits in 18 genotypes

Traits	R	Stem	Fruit	Fruit	Pericarp	Fruit	Individual	Fruit	No.of	No.of	No.of	Locules/
		diameter	length	diameter	thickness	flesh	fruit	yield/	fruits/	clusters	fruits	fruit
						thickness	weight	plant	plant	/plant	/cluster	
Plant height	r _g	0.56	0.72	0.490*	-0.07	0.16	0.53 *	0.79 **	-0.27	-0.22	-0.33	0.38
-	r ph	0.36	0.36	0.22	0.04	0.15	0.27	0.44**	-0.15	-0.11	-0.16	0.05
Stem diameter	rg		0.41	-0.28	-0.36	-0.09	0.18	-0.13	-0.22	-0.15	-0.39	0.92 **
	r ph		0.29*	-0.06	-0.08	0.02	0.12	0.04	-0.09	-0.002	-0.19	0.21
Fruit length	r _g			0.40	-0.61**	0.59*	0.78**	0.26	-0.66**	-0.49*	-0.79**	1.01**
	r ph			0.44**	-0.25	0.40**	0.64**	0.27*	-0.59**	-0.45**	-0.63**	0.31*
Fruit diameter	rg				-0.33	0.70**	0.30	0.63**	-0.44	-0.30	-0.34	0.46
	r _{ph}				-0.13	0.51**	0.33*	0.61**	-0.44**	-0.29*	-0.37**	0.09
Pericarp thickness	rg					-0.49*	-0.29	-0.14	0.33	-0.30	0.50^{*}	-0.33
	r ph					-0.29*	-0.13	0.05	0.17	-0.02	0.24	-0.21
Fruit flesh thickness	r _g						0.13	0.50*	-0.05	0.22	-0.21	0.42
	r ph						0.12	0.41**	-0.02	0.15	-0.14	0.20
Individual fruit weight	r _g							0.26	-0.78	-0.64**	-0.88	0.70
	r _{ph}							0.30	-0.77	-0.60	-0.82	0.39
Fruit yield/plant	r _g								-0.07	0.10	-0.11	0.06
	r ph								-0.14	0.01	-0.22	-0.02
No. of fruits/plant	r _g									0.92	0.92	-0.71
	r ph									0.85	0.89	-0.39
No. of clusters/plant	r _g										0.73	-0.66
	r ph										0.57	-0.24
No. of fruits/cluster	r _g											-0.79
	r ph											-0.45

*=Significant, **=Highly Significant

and no. of locules/fruit correlated negatively with the PC-1 and correlated positively with the PC-2. The fourth group consists of pericarp thickness which were positively correlated with the PC-1 and negatively correlated with the PC-2. Genotypes BGH-24, Unknown-2, BL-1173, Bambino-F1, Kanatoo, PB-LO-2752, PB017895, Sandal-F1 and V-676 were nearest to the origin point of the biplot showed the less genetic diversity for the studied attributes and the genotypes such as Hybrid-B, BL-1176, PB-LO-017906, Sultan, Veepick, LO-4379, CLN-1621-L, CLN-2001-A and Su Kong Tsao Feng.

Cluster Analysis and Mean Performance

Cluster analysis grouped 18 tomato genotypes into four clusters as shown in Table 7 and mean values of all traits in each cluster is presented in Table 6.Cluster I consisted of maximum number of 11 genotypes (CLN-1621-L, CLN-2001-A, LO-4379, PB017895, Su Kong Tsao Feng, BGH-24, BL-1173, Unknown-2, V-676, Kanatoo and PB-LO-2752), followed by cluster IV (Veepick, Sultan, PB-LO-017906 and Bambino-F1), cluster II (Hybrid-B and Sandal-F1) and cluster III (BL-1176) Table 7. According to the mean values of clusters in Table 6 cluster I had maximum cluster mean for plant height (115.21), fruit diameter (36.96), fruit flesh thickness (29.56) and fruit yield/plant (1359.06). However, cluster III showed highest cluster mean value for pericarp thickness (6.70), No. of fruits/plant (75.50), no. of clusters/plant (8.17) and no. of fruits/cluster (9.50). While cluster IV had maximum cluster mean value for stem diameter (11.67), fruit length (38.38), individual fruit weight (61.25) and no. of locules/fruit (3.67).

 Table 5: Eigen Value, Variability, Cumulative Variability and

 Factor Loadings of First Six Principal Component Axis to

 Variation for Studied Attributes in Tomato Genotypes

Parameters	PC-I	PC-II	PC-III	PC-IV	PC-V	PC-VI
Eigenvalue	5.37	2.04	1.44	1.25	0.66	0.45
Variability (%)	44.72	16.97	11.99	10.41	5.47	3.73
Cumulative %	44.72	61.70	73.68	84.09	89.56	93.29
Plant height	-0.48	0.31	0.33	0.68	-0.17	0.08
Stem diameter	-0.35	-0.23	0.83	0.16	0.05	0.17
Fruit length	-0.89	0.07	0.19	-0.07	0.00	-0.20
Fruit diameter	-0.64	0.53	-0.36	-0.05	0.15	0.36
Pericarp thickness	0.37	-0.19	-0.30	0.65	0.53	-0.15
Fruit flesh thickness	-0.45	0.71	0.06	-0.38	0.28	-0.13
Individual fruit weight	-0.86	-0.19	-0.15	0.12	-0.13	-0.35
No. of fruits/plant	0.87	0.34	0.29	0.03	0.07	-0.13
No. of clusters/plant	0.69	0.54	0.35	-0.09	-0.03	-0.23
No. of fruits/cluster	0.90	0.23	0.12	0.07	0.09	0.12
No. of locules/fruit	-0.70	-0.22	0.36	-0.17	0.45	0.02
Fruit yield/plant	-0.46	0.71	-0.13	0.37	-0.10	-0.02

 Table 6:
 Mean
 Performance
 of
 Clusters
 for
 Studied

 Morphological and Yield-Related Traits
 Tra

Characters	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Plant height	115.21	108.33	100.33	111.92
Stem diameter	11.35	10.42	10.17	11.67
Fruit length	35.97	23.08	14.17	38.38
Fruit diameter	36.96	33.92	14.33	29.92
Pericarp thickness	5.91	6.18	6.70	6.26
Fruit flesh thickness	29.56	22.65	17.78	22.75
Individual fruit weight	50.05	12.08	4.17	61.25
No. of fruits/plant	28.58	44	75.50	11.63
No. of clusters/plant	5.55	5.33	8.17	3.04
No. of fruits/cluster	4.92	8.33	9.50	3.75
No. of locules/fruit	3.09	2.83	2	3.67
Fruit yield/plant	1359.06	453	317.50	615.67

 Table 7: Distribution of Studied Genotypes into Four Clusters

 Class Frequency Genotypes

01033	Trequency	Genotypes
1	11	CLN-1621-L, CLN-2001-A, LO-4379,
		PB017895, Su Kong Tsao Feng, BGH-24,
		BL-1173, Unknown-2, V-676, Kanatoo, PB-
		LO-2752
2	2	Hybrid-B, Sandal-F1
3	1	BL-1176
4	4	Veepick, Sultan, PB-LO-017906, Bambino-
		F1

Table 8: D² Statistics among different clusters

Central Object	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	0	857.40	1012.45	627.52
Cluster 2	857.40	0	155.88	236.16
Cluster3	1012.45	155.88	0	390.13
Cluster 4	627.52	236.16	390.13	0

In contrary cluster II had minimum mean value for plant height (108.33), pericarp thickness (6.18) and cluster III showed minimum mean value for stem diameter (10.17), fruit length(14.17), fruit diameter(14.33), fruit flesh thickness(17.78), individual fruit weight(4.17), no. of locules/fruit(2) and fruit yield/plant(317.50). However cluster IV had the minimum cluster mean value for no. of fruits/plant (11.63), no. of clusters/plant (3.04) and no. of fruits/plant (3.04).

Dendrogram and Distance between Clusters

The distance between the clusters presented in Table 8. The results showed that distance among clusters I and II (857.40) which contained 13 genotypes, clusters I and III recorded the maximum distance (1012.45) and showed the maximum genetic divergence both contained 12 genotypes and distance between the clusters I and IV (627.52) contained 11 genotypes. While the distance among clusters II and III was (155.88) both clusters contained 3 genotypes and the distance among clusters II and IV (236.16) that demonstrated the lowest genetic divergence both contained 6 genotypes. Moreover, the distance among the cluster III and IV (390.13) both consisted of 5 genotypes. The highest distance was present among the clusters I and III which exhibited that maximum genetic divergence was present between these clusters and these clusters improve the selection criteria for the improvement of crops for studied morphological and attributes associated with yield. So, the genotypes were involved in these clusters could be used in the creation of high-yielding varieties for future breeding program. Narolia and Reddy (2012) indicated the maximum divergence among the studied genotypes of tomato.

The findings of this experiment was also confirmed by Kumar et al. (2016) which demonstrated that maximum divergence was present among clusters I and IV and the genotypes of these clusters could be utilized in the hybridization process for selecting the sergeants from the segregating populations. Results were also confirmed by (Verma and Patel, 2023). The dendrogram was performed using Ward's method, where 18 accessions were classified into four clusters (Fig. 3). Cluster I consisted of 11 genotypes (CLN-1621-L, CLN-2001-A, LO-4379, PB017895, Su Kong Tsao Feng, BGH-24, BL-1173, Unknown-2, V-676, Kanatoo and PB-LO-2752) cluster II contained 2 genotypes (Hybrid-B and Sandal-F1), cluster III consisted of 1 genotype (BL-1176) and cluster IV contained 4 genotypes (Veepick, Sultan, PB-LO-017906 and Bambino-F1) respectively according to the Fig. 3. Akhter et al. (2021) done an experiment on 15 tomato genotypes and that genotypes were grouped into three clusters. The maximum 7 genotypes were present in the cluster I which showed the maximum divergence.

biplot for contribution of traits

(Kumar et al. 2016b) conducted an experiment on 35 genotypes of tomato and found 4 clusters. Their results showed that cluster III had maximum number

of genotypes (10). Henareh et al. (2015) characterized the 97 accessions into the five clusters which were performed by Ward's method.



Fig. 2: Distribution of Studied Morphological and Yield-Related Traits and Genotypes across



Fig. 3: Dendrogram Showing Clustering Pattern of 18 Studied Genotypes of Tomato



Conclusion

The analysis of variance showed that significant difference was observed among genotypes for plant height while highly significant difference were observed for the no. of fruits/plant, no. of clusters/plant, no. of fruits/cluster, fruit length, fruit diameter, individual fruit weight, pericarp thickness, fruit flesh thickness, no. of locules/fruit, fruit yield/plant and stem diameter. The traits had higher heritability (>80%) makes the selection easier. The traits with high heritability generate high response to selection whereas the traits had low heritability (<60%) make selection difficult. Fruit yield/plant, no. of fruits/plant, individual fruit weight and no. of fruits/cluster displayed high heritability. Correlation studies showed that fruit vield/plant was positively highly significant association with plant height and fruit diameter while showed significant positive correlation with fruit flesh thickness at genotypic level. At phenotypic level fruit yield/plant was positively significant correlated fruit length, individual fruit weight and highly significant positive correlated plant height, fruit diameter and fruit flesh thickness. Principle component analysis exhibited that BL-1176, Hybrid-B, Veepick, CLN-1621-L and PB-LO-017906 contributed maximum to total genetic variability. The traits that showed maximum contribution to total divergence includes fruit yield/plant, fruit flesh thickness, no. of clusters/plant, no. of fruits/plant, no. of fruits/cluster and fruit diameter.

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