



ISSN (E): 2277-7695

ISSN (P): 2349-8242

NAAS Rating: 5.23

TPI 2023; 12(4): 773-781

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[www.thepharmajournal.com](http://www.thepharmajournal.com)

Received: 20-02-2023

Accepted: 31-03-2023

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## Genetic variability, correlation and path analysis for yield components in brinjal (*Solanum melongena* L.)

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**Abstract**

In the present study, variability, correlation and path coefficients analysis was carried out in fifty brinjal genotypes. The experiment was laid out in the Randomized Block Design with three replications. The observations were recorded on various yield and yield attributing characters. Correlation coefficients revealed that the fruit yield plant<sup>-1</sup> exhibited significant positive association with fruit length, fruit diameter, plant spread, average fruit weight and fruit yield hectare<sup>-1</sup> both at genotypic and phenotypic levels. Highest direct positive effect on fruit yield was recorded by average fruit weight followed by number of primary branches plant<sup>-1</sup> and plant spread. These characteristics could be employed as a selection trait breeding of high yielding brinjal genotypes. Estimates of divergence among 50 Brinjal genotypes revealed that significant divergence existed among them using Mahalanobis D<sup>2</sup> statistics. Fifty genotypes were grouped into eight different non-overlapping clusters. The crosses between the genotypes of cluster VIII with III, II and VII and Cluster I with those of III, II, VIII and VII and Cluster II with III, VIII and VI are likely to produce recombinants with desired traits. The genotypes selected on the basis of *per se* performance of fruit yield, yield contributing and quality traits can be used in brinjal improvement programme as elite germplasm lines or may be recommended as such for commercial cultivation after testing them over years and locations.

**Keywords:** Correlation, path analysis, genetic divergence, heritability, *Solanum melongena* L.

**Introduction**

Brinjal or eggplant or aubergine (*Solanum melongena* L.  $2n = 2x = 24$ ), a member of Solanaceae family, is the most common and popular vegetable crop of the world. It is an important source of revenue for large-scale, small-scale, and marginal farmers and is also known as the poor man's vegetable since it can be cultivated year-round in almost all parts of the world. (Kumar *et al.*, 2014) [34]. It is native to India, where it was initially found during 300 B.C. to 300 A.D. and South East Asia is regarded its secondary centre of diversity. *Solanum incanum*, a wild species with a wide distribution in at least 10 habitats across India, is thought to be the progenitor of the cultivated species *Solanum melongena*. (Vethamonai *et al.*, 2020) [94].

It is extensively grown in India, Pakistan, Bangladesh, China and the Philippines. India is the world's second-largest producer of brinjal, following China. (Ravali *et al.*, 2017) [67]. About 54.1 million tonnes of brinjal are grown on more than 1800 thousand hectares of land because to its great production potential and consumer availability (FAOSTAT, 2019) [22]. It's grown in West Bengal, Odisha, Andhra Pradesh, Gujarat and Bihar in India (Arti and Sharma, 2018) [4]. It is grown on about 735 thousand hectares and produces 12987 thousand metric tones per year, with productivity of 17.66 metric tonnes ha<sup>-1</sup> (NHB, 2018-19). It covers about 2.51 thousand hectares in Jammu and Kashmir, with an annual production of 45.62 thousand metric tonnes and a productivity of 18.17 metric tonnes ha<sup>-1</sup> (Horticultural Statistics at a glance, 2018) [27].

The most essential criteria for plant breeding is the exploitation of heritable genetic variation for the expression of beneficial traits in succeeding generations. Selection of genetically heterogeneous parents lead to the development of improved varieties, the basis of which is provided by estimation of genetic variation for selecting parental lines for their exploitation in hybrid development or increasing variation within breeding population. Yield is the most important parameter for plant breeders to consider while developing superior cultivars of any crop. High yield is the primary goal of all breeding programmes, however yield is generally low in heritability, thus direct selection is ineffective.

Some biometrical techniques aid in the selection of elite genotypes from the breeding population by providing information about the relative contribution of various component traits to yield. Correlation, path analysis are examples of such techniques.

## Materials & Methods

### Plant Material

Fifty diverse genotypes of brinjal were assessed for various yield and yield attributing traits at the Experimental field of

the Division of Vegetable Science SKUAST-K Shalimar Srinagar, during Kharif 2020. The genotypes, along with their sources, are listed in Table -1. Observations were recorded on five randomly selected plants of each genotype in each replication for various traits. The data thus obtained was analyzed as per method given by Mahalanobis, 1928 [45]. Criteria Toucher (Rao, 1952) [65] was used for determining the groups and clustering was done accordingly. Average inter and intra cluster distances were estimated as per method given by Singh and Chaudhary, 1985 [80].

**Table 1:** List of brinjal (*Solanum melongena* L.) genotypes used in the present study

S. No.	Genotypes	Source	S. No.	Genotypes	Source	S. No.	Genotypes	Source
1.	IC-104082	SKUAST-K	23.	Pusa Ankur	SKUAST-K	45.	SB-45	SKUAST-K
2.	Arka Keshav	SKUAST-K	24.	IC-374892	SKUAST-K	46.	SB-46	SKUAST-K
3.	SB-3	SKUAST-K	25.	IC-413648	SKUAST-K	47.	SB-47	SKUAST-K
4.	IC-111010	SKUAST-K	26.	IC-099676	SKUAST-K	48.	SB-48	SKUAST-K
5.	SB-5	SKUAST-K	27.	SB-27	SKUAST-K	49.	SB-49	SKUAST-K
6.	SB-6	SKUAST-K	28.	Pusa Purple Long	SKUAST-K	50.	SB-50	SKUAST-K
7.	IC-261801	SKUAST-K	29.	IC-354867	SKUAST-K			
8.	SB-8	SKUAST-K	30.	IC-090981	SKUAST-K			
9.	SB-9	SKUAST-K	31.	SB-31	SKUAST-K			
10.	Azad Kranti	SKUAST-K	32.	IC-381562	SKUAST-K			
11.	SB-11	SKUAST-K	33.	SB-33	SKUAST-K			
12.	IC-374888	SKUAST-K	34.	SB-34	SKUAST-K			
13.	SB-13	SKUAST-K	35.	SB-35	SKUAST-K			
14.	SB-14	SKUAST-K	36.	SB-36	SKUAST-K			
15.	Annamalia	SKUAST-K	37.	IC-280952	SKUAST-K			
16.	SB-16	SKUAST-K	38.	SB-38	SKUAST-K			
17.	SB-17	SKUAST-K	39.	SB-39	SKUAST-K			
18.	IC-111018	SKUAST-K	40.	Arka Kusumkar	SKUAST-K			
19.	SB-19	SKUAST-K	41.	SB-41	SKUAST-K			
20.	Arka Nidhi	SKUAST-K	42.	SB-42	SKUAST-K			
21.	SB-21	SKUAST-K	43.	SB-43	SKUAST-K			
22.	Uttkal Keshri	SKUAST-K	44.	SB-44	SKUAST-K			

## Results and Discussion

### Grouping constellation using D<sup>2</sup> Statistics

The Mahalanobis D<sup>2</sup> statistics were used to investigate genetic divergence among the 50 brinjal genotypes. On the basis of genetic distance between genotypes, all genotypes were divided into various clusters. Fifty genotypes were grouped into eight different non-overlapping clusters (Table-2). The dendrogram and cluster diagram (Figs. 1 and 2) indicated that the cluster II has most genotypes (15), followed by cluster I (11), cluster VII (10), cluster III (6), cluster VIII (5) and the clusters IV (1), cluster V (1) and cluster VI (1) were having only one genotype in each respectively. The average intra and inter cluster distance (D<sup>2</sup>) values (Table-3) revealed that cluster VIII had the highest intra cluster distance (D<sup>2</sup>) value of 15322.62 followed by cluster VII (13498.64), cluster III (8720.61) and cluster II (8394.58). The inter cluster distance D<sup>2</sup> values was highest between cluster VIII and cluster III (103832.00) followed by cluster I and III (73700.02), cluster III and cluster VII (60425.96), cluster III and cluster VI (57670.67), cluster III and cluster V (57173.75), cluster III and cluster IV (45528.68) and cluster II and cluster VIII (41148.92). The maximum intra cluster distance suggested considerable heterogeneity in genetic constitution of genotypes in that cluster, whilst the minimum intra cluster distance indicated homogeneity in genetic constitution in that cluster. The maximum inter cluster distance value (cluster VIII and III) showed a more varied genetic structure of genotypes in both clusters. In contrast, minimum inter cluster

distance (cluster VI and VI) indicated closer relationship among the genotypes. Parallel findings were found by Silambarasan *et al.* (2020) [78] and Madhavi *et al.* (2015) [44]. The data of the cluster means for different traits (Table-4) indicated the wide difference between cluster means. Cluster V showed maximum mean values for days to first flower, days to first fruit set, days to first fruit picking and minimum mean values for fruit length, fruit diameter, average fruit weight, fruit yield plant<sup>-1</sup>, fruit yield hectare<sup>-1</sup>, dry matter content, total soluble solids and ascorbic acid content of fruit. Cluster IV showed maximum mean values for average fruit weight, fruit yield plant<sup>-1</sup>, fruit yield hectare<sup>-1</sup>, dry matter content, total soluble solids and minimum mean value for number of primary branches plant<sup>-1</sup>. Cluster VII showed maximum mean values for number of primary branches plant<sup>-1</sup>, fruit diameter and minimum mean values for days to first flower, days to first fruit set, days to first fruit picking. Cluster III showed maximum mean values for plant height, total phenols and minimum mean values for anthocyanin content of fruit peel, number of fruits plant<sup>-1</sup>. Cluster VI showed maximum mean values plant spread, fruit length, number of fruits plant<sup>-1</sup> and minimum mean value for plant height. Cluster VIII showed maximum mean values for ascorbic acid content of fruit, anthocyanin content of fruit peel and minimum mean value for total phenols. Cluster I showed minimum mean value for plant spread. Cluster II did not showed maximum and minimum mean values for any character. Thus, traits that contribute significantly to genetic

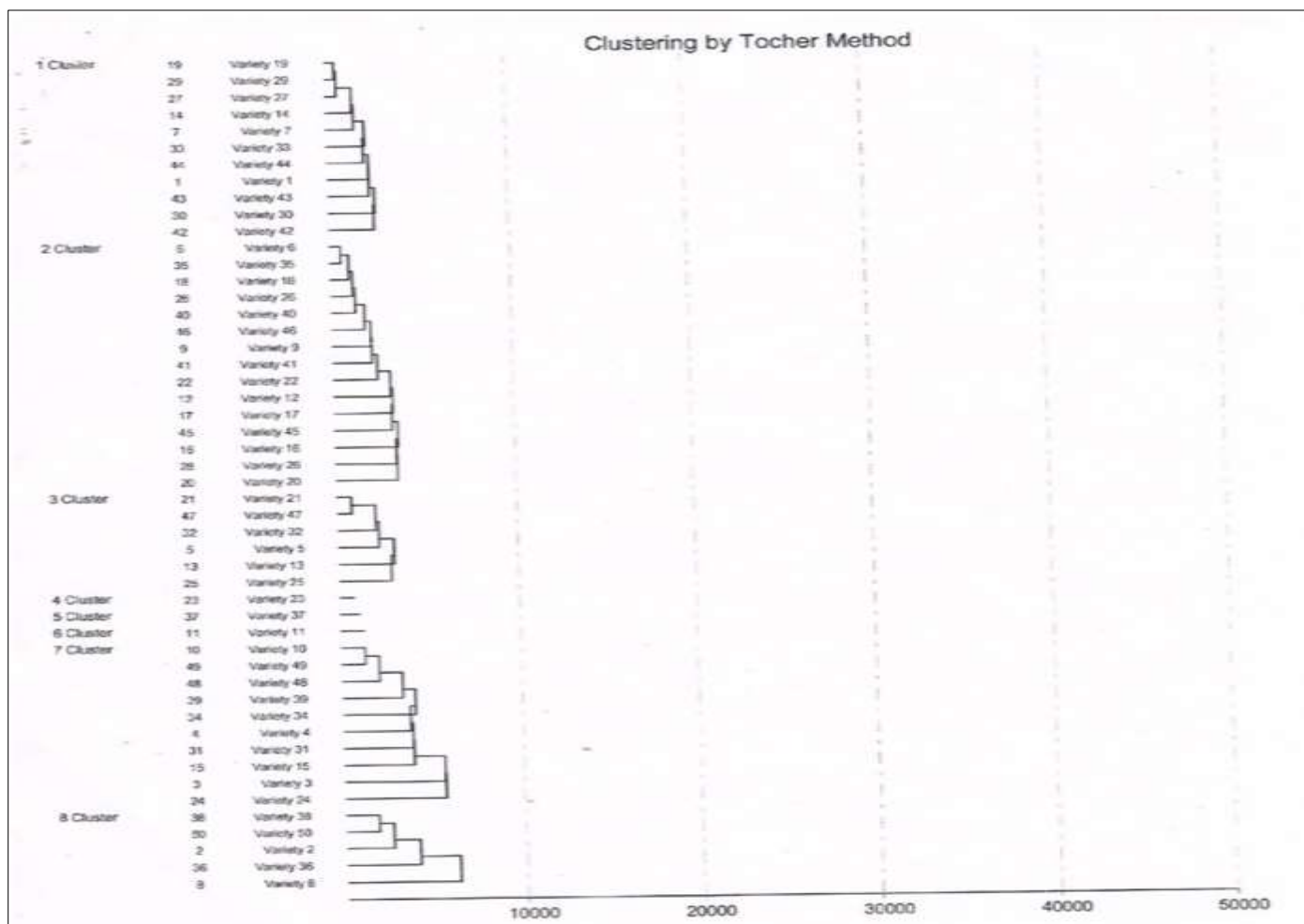
divergence can be improved by selecting genotypes from clusters with the highest cluster means for the relevant traits, which is dependent on the breeding program's objective. These findings are in consonance with the findings of the earlier work of Mishra *et al.* (2013) [48], Ahmad *et al.* (2014) [3] and Bhushan *et al.* (2018) [9].

The percent contribution of the traits to total genetic divergence (Table-5) demonstrated that fruit yield hectare<sup>-1</sup> was the most important component, accounting for 15.71 percent of total genetic divergence, followed by fruit length

(15.67%), plant height (13.76%), fruit yield plant<sup>-1</sup> (11.24%), fruit diameter (8.76%), plant spread (7.35%), number of fruits plant<sup>-1</sup> (7.26%), average fruit weight (4.78%), days to first fruit set (4.41%) and days to first flower (3.07%). The traits that contribute the most towards the divergence should be emphasized for deciding the clusters to be chosen for hybridisation and the subsequent selection of the parents from the clusters be based on their individual performance. Parallel findings were found by Satesh *et al.* (2007) [75], Lokesh *et al.* (2013) [42] and Ravali *et al.* (2017) [67].

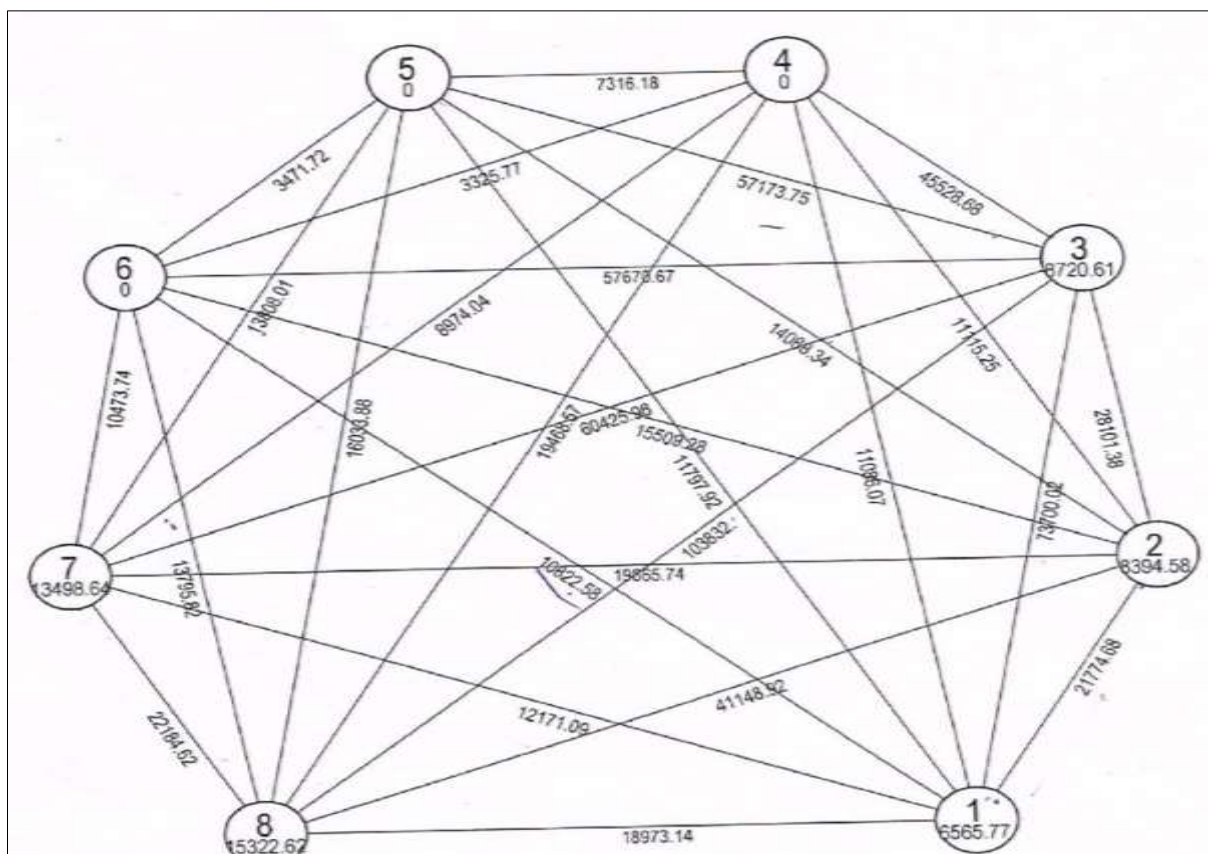
**Table 2:** Distribution of brinjal (*Solanum melongena* L.) genotypes into clusters based on D<sup>2</sup> Statistics

S. No.	Cluster	No. of genotypes in the cluster	Name of genotypes
1.	I	11	SB-19, IC-354867, SB-27, SB-14, IC-261801, SB-33, SB-44, IC-104082, SB-43, IC-090981, SB-42
2.	II	15	SB-6, SB-35, IC-111018, IC-099676, Arka Kusumkar, SB-46, SB-9, SB-41, Uttkal Keshri, IC-374888, SB-17, SB-45, SB-16, Pusa Purple Long, Arka Nidhi
3.	III	6	SB-21, SB-47, IC-381562, SB-5, SB-13, IC-413648
4.	IV	1	Pusa Ankur
5.	V	1	IC-280952
6.	VI	1	SB-11
7.	VII	10	Azad Kranti, SB-49, SB-48, SB-39, SB-34, IC-111010, SB-31, Annamalia, SB-3, IC-374892
8.	VIII	5	SB-38, SB-50, Arka Keshav, SB-36, SB-8



19=SB-19, 29=IC-354867, 27= SB-27, 14=SB-14, 7=IC-261801, 33= SB-33, 44=SB-44, 1=IC-104082, 43=SB-43, 30=IC-090981, 42=SB-42, 6=SB-6, 35=SB-35, 18=IC-111018, 26=IC-099676, 40=Arka Kusumkar, 46=SB-46, 9=SB-9, 41=SB-41, 22=Uttkal Keshri, 12=IC-374888, 17=SB-17, 45=SB-45, 16=SB-16, 28=Pusa Purple Long, 20=Arka Nidhi 21=SB-21, 47=SB-47, 32=IC-381562, 5=SB-5, 13=SB-13, 25=IC-413648, 23=Pusa Ankur, 37=IC-280952, 11=SB-11, 10=Azad Kranti, 49=SB-49, 48=SB-48, 39=SB-39, 34=SB-34, 4=IC-111010, 31=SB-31, 15=Annamalia, 3=SB-3, 24=IC-374892, 38=SB-38, 50=SB-50, 2=Arka Keshav, 36=SB-36, 8=SB-8

**Fig 1:** Clustering by Tocher method (Dendrogram)



**Fig 2:** Tocher Method (Mahalanobis Euclidean Distance; Not to the Scale)

**Table 3:** Average intra-cluster (Diagonal) and inter cluster (Above Diagonal) distance values in brinjal (*Solanum melongena* L.)

S. No.	Cluster	I	II	III	IV	V	VI	VII	VIII
1.	I	6565.77	21774.68	73700.02	11086.07	11797.92	10822.58	12171.09	18973.14
2.	II		8394.58	28101.38	11115.25	14088.34	15509.28	19865.74	41148.92
3.	III			8720.61	45528.68	57173.75	57670.67	60425.96	103832.00
4.	IV				0.00	7316.18	3325.77	8974.04	19468.57
5.	V					0.00	3471.72	13808.01	16033.88
6.	VI						0.00	10473.74	13795.82
7.	VII							13498.64	22184.62
8.	VIII								15322.62

**Table 4:** Cluster means for various yield characters in different clusters of brinjal (*Solanum melongena* L.) genotypes (Tocher Method)

S. No.	Cluster	Days to first flower	Days to first fruit set	Days to first fruit picking	Plant height (cm)	Plant spread (cm)	Number of primary branches plant <sup>-1</sup>	Fruit length (cm)	Fruit diameter (cm)
1.	I	40.15	46.72	69.96	69.89	50.74	3.81	11.60	5.30
2.	II	47.72	54.38	81.26	67.60	52.67	3.70	10.73	5.02
3.	III	48.48	55.12	76.26	80.30	54.16	3.64	13.71	5.50
4.	IV	43.73	51.60	76.30	64.83	66.67	2.52	11.73	5.68
5.	V	56.57	62.20	88.53	73.49	52.61	2.57	8.21	3.57
6.	VI	47.10	57.20	82.13	57.47	58.49	3.74	14.56	3.64
7.	VII	37.77	44.95	68.34	74.69	58.36	3.86	11.07	5.92
8.	VIII	44.34	52.71	81.31	73.96	58.96	3.69	11.34	4.04

S. No.	Cluster	Average fruit weight (g)	No of fruits plant <sup>-1</sup>	Fruit yield plant <sup>-1</sup> (kg)	Fruit yield ha <sup>-1</sup> (q)	Dry matter content (%)	Total soluble solids (°brix)	Ascorbic acid content of fruit (mg 100 g <sup>-1</sup> )	Anthocyanin content of fruit peel mg 100g <sup>-1</sup>	Total phenols (mg 100g <sup>-1</sup> )
1.	I	94.86	7.58	0.67	248.11	11.50	4.27	2.39	2.43	69.10
2.	II	73.44	9.11	0.65	241.34	10.11	4.52	2.63	1.87	94.48
3.	III	93.18	7.56	0.72	269.37	10.22	4.08	1.93	1.73	131.32
4.	IV	129.93	7.67	0.99	370.16	13.59	5.24	3.43	3.67	87.57
5.	V	40.10	9.67	0.38	142.07	7.52	3.05	1.08	3.31	71.54
6.	VI	62.83	10.67	0.66	246.90	10.50	3.15	1.44	4.59	78.35
7.	VII	88.66	8.33	0.71	263.28	10.05	4.55	2.72	3.71	81.60
8.	VIII	54.56	9.60	0.47	177.74	9.09	4.81	3.64	5.33	60.12



**Table 5:** Percent contribution of individual traits towards total genetic divergence in brinjal (*Solanum melongena* L.)

S. No.	Traits	Contribution %
1.	Fruit yield hectare <sup>-1</sup> (q)	15.71
2.	Fruit length (cm)	15.67
3.	Plant height (cm)	13.76
4.	Fruit yield plant <sup>-1</sup> (kg)	11.24
5.	Fruit diameter (cm)	8.76
6.	Plant spread (cm)	7.35
7.	Number of fruits plant <sup>-1</sup>	7.26
8.	Average fruit weight (g)	4.78
9.	Days to first fruit set	4.41
10.	Days to first flower	3.07
11.	Total phenols (mg100g <sup>-1</sup> )	1.96
12.	Total soluble solids (°Brix)	1.65
13.	Dry matter content (%)	1.33
14.	Ascorbic acid content (mg100g <sup>-1</sup> )	1.07
15.	Anthocyanin content of fruit peel (mg100g <sup>-1</sup> )	1.03
16.	Days to first fruit picking	0.87
17.	Number of primary branches plant <sup>-1</sup>	0.08

**Correlation coefficients**

Correlation coefficient study determines the mutual relationship between two plant characters and the yield components that should be selected for yield improvement. In present study (Table-6) the genotypic and phenotypic correlation coefficient were worked out for all the seventeen traits. In general, the genotypic correlation values were slightly greater than the phenotypic correlation, indicating that environmental masking effects were minimal, demonstrating the presence of inherent association between various traits. Results obtained in present study are in agreement with the findings of Dhaka *et al.* (2014) [20], Lakshmi *et al.* (2014) [39]

and Srivastava *et al.* (2018) [82]. Correlation coefficients disclosed that the economically important trait i.e. fruit yield plant<sup>-1</sup> exhibited significant positive association with fruit length ( $r_g=0.4276$ ,  $r_p=0.4119$ ), fruit diameter ( $r_g = 0.4829$ ,  $r_p=0.4544$ ), plant spread ( $r_g =0.2736$ ,  $r_p=0.2633$ ), average fruit weight ( $r_g=0.7268$ ,  $r_p=0.6830$ ), fruit yield hectare<sup>-1</sup> ( $r_g=0.9991$ ,  $r_p=0.9990$ ) both at genotypic and phenotypic levels. Similar results were observed by Arunkumar *et al.* (2013) [5], Nayak and Nagre (2013) [55] and Banerjee *et al.* (2018) [8]. These mentioned traits may be treated as prime traits during the course of selection to enhance the yield of brinjal.

**Path coefficient analysis**

Correlation analysis shows the pattern of association between component traits and yield; it simply depicts the overall influence of a trait on yield rather than establishing a cause-and-effect link. It does not specify the relative importance of direct and indirect influences of different yield variables. In order to understand the cause of a link between two variables, path coefficient analysis provides information about the cause and effect situation. It serves as a foundation for selecting superior genotypes from a large breeding population. The path coefficient analysis (Table-7) demonstrated that highest direct positive effect on fruit yield was recorded by average fruit weight (0.6778) followed by number of primary branches plant<sup>-1</sup> (0.1693), plant spread (0.1418), fruit length (0.1168), dry matter content (0.0774), plant length (0.0396) and days to first fruit set (0.0328) indicate that these traits can be used to generate an optimum reliable selection index for increasing brinjal fruit yield. This was in agreement with the study of Dharwad *et al.* (2009) [21], Nayak and Nagre (2013) [55] and Patel *et al.* (2015) [58].

**Table 6:** Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among different growth traits in brinjal (*Solanum melongena* L.)

Parameters	DFP	DFFS	PH	FL	FD	PS	NPB	DFFP	AFV	DMC	TSS	ACC	AC	NFP	FYP	FY	TPC
Days to first flower	1.0000	0.9654**	0.0232	-0.1995	-0.0324	-0.3633**	-0.1101	0.7299**	-0.0337	-0.2548*	-0.2302*	-0.2812*	-0.2077*	-0.1008	-0.1001	-0.0998	0.2144*
Days to first fruit set	0.9641**	1.0000	-0.0216	-0.2169*	-0.0243	-0.3278*	-0.1550	0.7650**	-0.0661	-0.2268*	-0.2327*	-0.2989*	-0.1303	-0.0611	-0.1065	-0.1061	0.2075*
Plant height	0.0231	-0.0215	1.0000	0.1175	0.0847	0.1037	0.1441	-0.1348	0.1019	0.0090	-0.0898	-0.0928	-0.0715	-0.0058	0.1462	0.1500	0.0996
Fruit length	-0.1989	-0.2164	0.1173	1.0000	0.0723	0.2417*	0.1997	-0.2415*	0.3817**	-0.0923	0.1179	0.1305	0.0397	-0.1163	0.4276**	0.4268**	0.1369
Fruit diameter	-0.0312	-0.0230	0.0838	0.0704	1.0000	0.1979	0.2661*	-0.2179*	0.5948**	0.0547	-0.0052	0.0935	0.0189	-0.2289*	0.4829**	0.4813**	0.1832
Plant spread	-0.3629**	-0.3276*	0.1036	0.2414*	0.1946	1.0000	0.2201*	-0.1830	0.1074	-0.0069	0.2076*	0.1805	0.1540	0.2361*	0.2736*	0.2740*	0.0651
No. Of primary branches/ plant	-0.1093	-0.1540	0.1440	0.1984	0.2626*	0.2191*	1.0000	-0.0967	-0.0247	0.0398	0.1025	0.2140*	0.0120	0.2626*	0.1938	0.1921	0.0346
Days to first fruit picking	0.7289**	0.7642**	-0.1350	-0.2410*	-0.2140*	-0.1830	-0.0960	1.0000	-0.2379*	-0.3617**	-0.1422	-0.0770	-0.0581	0.0605	-0.2269*	-0.2248*	0.0919
Average fruit weight	-0.0332	-0.0654	0.1011	0.3780**	0.5807**	0.1064	-0.0249	-0.2359*	1.0000	0.0633	-0.0800	-0.0597	-0.1914	-0.5847**	0.7268**	0.7247**	0.1022
Dry matter content	-0.2545*	-0.2266*	0.0089	-0.0924	0.0533	-0.0068	0.0396	-0.3615**	0.0620	1.0000	0.2147*	0.0048	-0.1487	-0.0174	0.1164	0.1153	0.1190
Total soluble solids	-0.2297*	-0.2319*	-0.0897	0.1174	-0.0037	0.2070*	0.1025	-0.1414	-0.0790	0.2140*	1.0000	0.2450*	0.0588	0.0084	-0.0923	-0.0907	-0.0247
Ascorbic acid content	-0.2807*	-0.2983*	-0.0928	0.1295	0.0912	0.1799	0.2128*	-0.0770	-0.0588	0.0051	0.2439*	1.0000	0.3546**	0.1591	0.0580	0.0570	-0.1475
Anthocyanin content	-0.2076*	-0.1302	-0.0715	0.0395	0.0186	0.1539	0.0120	-0.0581	-0.1900	-0.1487	0.0587	0.3541**	1.0000	0.1826	-0.0948	-0.0940	-0.4109**
No. Of fruits/plant	-0.0869	-0.0549	-0.0031	-0.1003	-0.1966	0.2113*	0.2367*	0.0543	-0.5491**	-0.0144	0.0063	0.1398	0.1631	1.0000	0.1863	0.0996	-0.0522
Fruit yield/ plant	-0.1000	-0.1032	0.1419	0.4119**	0.4544**	0.2633*	0.1866	-0.2181*	0.6830**	0.1121	-0.0893	0.0530	-0.0910	0.1818	1.0000	0.9991**	0.1825
Fruit yield/Ha	-0.0949	-0.1030	0.1458	0.4121**	0.4544**	0.2643*	0.1858	-0.2164*	0.6825**	0.1113	-0.0880	0.0523	-0.0905	0.1830	0.9990**	1.0000	0.1823
Total phenol content	0.2142*	0.2074*	0.0996	0.1367	0.1804	0.0651	0.0345	0.0918	0.1013	0.1190	-0.0246	-0.1473	-0.4109**	-0.0464	0.1753	0.1755	1.0000

**Table 7:** Path Matrix showing direct (diagonal) and indirect (off diagonal) effects of different yield parameters on yield in brinjal (*Solanum melongena* L.)

S. No.	Parameters	Days to first flower	Days to first fruit set	Plant height (cm)	Fruit length (cm)	Fruit diameter (cm)	Plant spread (cm)	No of primary branches <sup>-1</sup> plant	Days to first fruit picking	Average fruit weight (g)	Dry matter content (%)
1.	Days to first flower	-0.2693	-0.2600	-0.0062	0.0537	0.0087	0.0978	0.0296	-0.1965	0.0091	0.0686
2.	Days to first fruit set	0.3169	0.03283	-0.0071	-0.0712	-0.0080	-0.1076	-0.0509	0.2511	-0.0217	-0.0745
3.	Plant height (cm)	-0.0009	-0.0009	0.0396	0.0047	0.0034	0.0041	0.0057	-0.0053	0.0040	0.0004
4.	Fruit length (cm)	-0.0233	-0.0253	0.0137	0.1168	0.0085	0.0282	0.0233	-0.0282	0.0446	-0.0108
5.	Fruit Diameter (cm)	0.0005	0.0004	-0.0013	-0.0011	-0.0156	-0.0031	-0.0042	0.0034	-0.0093	-0.0009
6.	Plant spread (cm)	-0.0515	-0.0465	0.0147	0.0343	0.0281	0.1418	0.0312	-0.0259	0.0152	-0.0010
7.	No of primary branches <sup>-1</sup> plant	-0.0186	-0.0263	0.0244	0.0338	0.0451	0.0373	0.1693	-0.0164	-0.0042	0.0067
8.	Days to first fruit picking	-0.0129	-0.0136	0.0024	0.0043	0.0039	0.0032	0.0017	-0.0177	0.0042	0.0064
9.	Average fruit weight (g)	-0.0228	-0.0448	0.0691	0.2587	0.4032	0.0728	-0.0167	-0.1612	0.6778	0.0429
10.	Dry matter matter (%)	-0.0197	-0.0176	0.0007	-0.0071	0.0042	-0.0005	0.0031	-0.0280	0.0049	0.0774
	Genotypic correlation with Fruit yield	-0.0999	-0.1061	0.1500	0.4268**	0.4813**	0.2740*	0.1922	-0.2248*	0.7247**	0.1153

### Conclusion

From the study, it can be concluded that for future breeding programme in brinjal, genotypes the crosses between the genotypes of cluster VIII with III, II and VII and Cluster I with those of III, II, VIII and VII and Cluster II with III, VIII and VI are likely to produce recombinants with desired traits. The genotypes selected on the basis of *per se* performance of fruit yield, yield contributing and quality traits can be used in brinjal improvement programme as elite germplasm lines or may be recommended as such for commercial cultivation after testing them over years and locations.

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