

Assessment of genetic diversity using D^2 statistics in brinjal of North Bengal

Abstract

Aim: Assessment of genetic diversity studies using D^2 statistics in Brinjal of North Bengal

Study design: Diversity D^2 analysis

Methodology: This study was undertaken to understand the genetic divergence of the 32 brinjal genotypes collected from different locations of North Bengal region. Through diversity D^2 analysis whole genotypes were categorized under seven groups with no evidence for geographical diversity as necessarily cause of genetic diversity.

Results and Conclusion: Highest genetic diversity was recorded in cluster I and V argued for their utilization to develop transgressive segregate lines. Genotypes under cluster VI and VII found to be effective for the improvement of yield related attributes. The cross combinations between cluster VI and V, cluster VI and II, cluster VI and VI, cluster VI and I, cluster VI and III, cluster VI and cluster VII could be effectively utilized to improve heterotic population or recombinant.

Keywords: Brinjal, Genotypes, Genetic diversity

1. INTRODUCTION:

Brinjal (*Solanum melongena* L.) also known as Eggplant in United States, Aubergine in France and England belongs to Solanaceae family is a kind of principle vegetable which has been cultivated worldwide (Bariket *al.* 2020). It is highly consumed vegetable of South East Asia grown throughout the year (Anbarasi and HariPriya, 2021). It is considered as poor man's crop (Praneetha, 2018; Nayaket *al.* 2020) originated and cultivated in India from long back. In India, it is popularly known as baigan, bhanta, badankai, vangi, etc (Ansari and Singh, 2014). It is grown extensively in India, Bangladesh, Pakistan, China, Japan and Philippines. In India major producing states are Orissa, Bihar, Karnataka, West Bengal,

Andhra Pradesh, Maharashtra and Uttar Pradesh (Sahana *et al.* 2020). Brinjal has high nutritional and medicinal values like decholesterolizing property primarily due to presence of oleic and linolenic fatty acids which are present abundantly in flesh and seeds (Hanchinmani and Imamsaheb, 2015) and minerals like Ca, Mg, P and fatty acids are present in the fruits. It has medicinal use like curing diabetics, asthma, cholera, bronchitis, diarrhea and liver complaints (Santhosha *et al.* 2017). Brinjal is a good source of protein, dietary fiber, and minerals like potassium, manganese, magnesium, and copper. It also contains good quantities of vitamin B1 (thiamine), vitamin B3 complex (niacin), vitamin B6 (pyridoxine), folate. In brinjal oblong fruited variety have high Total Soluble Solids (TSS), long fruited cultivars have high content of free reducing sugars, anthocyanin, phenols, glycoalkaloids (such as solasodine), dry matter, and amide proteins. Brinjal is used in the improvement of cardiovascular and liver health (Patel *et al.* 2013).

According to the national horticultural board data brinjal cultivated in 669000 ha with an annual production of 12777 MT in India (Anonymous, 2017). The demand for brinjal is increasing because of its high nutritional and medicinal values. Evaluation of brinjal genotypes helps in recommending particular genotype in terms of yield, quality and resistance to major pest and diseases and it also helps in developing a variety with high yield, colour, size, shape, weight, quality parameters and resistance to major pest and diseases. A large indigenous biodiversity exists in eggplant with variation in plant type, stem color, leaf size, leaf tip, midrib color, fruit size, fruit shape, fruit color, fruit yield, fruit quality, cooking quality, and tolerance to pests and diseases (Ullah *et al.* 2014). India is being primary centre of origin shows greater extent of variability and there will be high chances of effective selection for desirable types in the population with more variability (Vavilov, 1951). The varietal acceptance of brinjal is region specific. For the improvement of heritability the existence of variability in a particular trait is an important one. The estimation of genetic diversity has made it possible to choose genetically diverse parents for a successful hybridization program. Knowledge on genetic diversity, its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding programme. So,

based on this, the experiment was conducted to obtain information on genetic diversity among 32 genotypes of brinjal based on qualitative and quantitative characters respectively in the region of North Bengal, West Bengal, India.

2. MATERIAL AND METHODS:

The experiment was carried out at Experimental Farm of Uttar BangaKrishiViswavidyalaya, Pundibari, West Bengal, India during *Rabiseasons* of 2016-17 and 2017-18. The farm is situated at 26°19'86" N latitude and 89°23'53" E longitude, at an elevation of 43 meter above mean sea level. The list of the collected experimental material presented in Table.1 and fruit types are presented in Figure.1. Mahalanobis (1936) D^2 statistics was used for assessing the genetic divergence between brinjal genotypes. The original correlated unstandardised character mean values were transformed into standardised uncorrelated values to simplify the computational procedure. The D^2 values were obtained as the sum of squares of the differences between the pairs of corresponding uncorrelated (Y_s) values of any two genotypes. Using all D^2 values, the genotypes were grouped into clusters using Tocher's method as described by Rao (1952). The intra- and inter-cluster distances were calculated by the formula given by Singh and Chaudhary (1985). The character contribution towards genetic divergence was computed using the method given by Singh and Chaudhary (1977).

Plant height was measured at the time of the last harvest with help of measuring tape; the number of branches arising from the main stem above the ground level at final harvest was counted. Calyx length was measured individually with the help of a measuring tape, the number of days taken for the flower opening was recorded from the date of transplanting to the first flower opening, the number of days required to obtain harvestable maturity, the number of days taken for the first flowering to final harvest was calculated, fruit diameter was measured and data were collected after cutting horizontally into half, length of the fruit at horticultural maturity was measured with the help of a measuring scale from the base to the tip of fruits, weighed individual fruits and average was recorded in grams, the number of fruits harvested per plant during the harvesting period was recorded, the estimated average yield

per ha was recorded throughout the harvesting period based on the yield. To know anthocyanin content measured by Rangana, 1997 method, ascorbic acid content measured by AOAC, 1990 method, Mettler Toledo RE50 refractometer was used for the determination of total soluble solids and Phenol content of fruits measured by spectrophotometric method.

Data analysis

Cluster analysis classifies a set of observations into two or more mutually exclusive unknown groups based on combinations of interval variables. In this agglomerative hierarchical clustering technique was followed. The D^2 value obtained for a pair of population was taken as calculated value of χ^2 and was tested against the tabulated value of χ^2 for P (15) degrees of freedom where P (15) is the number of characters considered. The average intra cluster distances were calculated by the formula given by Singh and Chaudhary (1977). Square of intra cluster distance = $\sum D^2_i / n$. Using all D^2 values, the genotypes were grouped into clusters using Tocher's method as described by Rao (1952). The intra- and inter-cluster distances were calculated by the formula given by Singh and Chaudhary (1985).

$$\text{Inter-cluster distance} = \sqrt{\frac{D_{ij}^2}{n_i n_j}}$$

Table.1. List of experimental material included in the present study

Sl. No.	Genotypes	code	Location of Collection
1	Long and thick brinjal	UBB 1	Pundibari, West Bengal
2	KabraGol	UBB 2	Malda, West Bengal
3	Phasidewa local 2	UBB 3	Pundibari, West Bengal
4	AshpuriGhiaBrinjal	UBB 4	Malda, West Bengal
5	Long Brinjal	UBB 5	Pundibari, West Bengal
6	Chanda Tara Brinjal	UBB 6	Malda, West Bengal
7	Long Golden Brinjal	UBB 7	Dinhata, West Bengal
8	MukhtaBrinjal Green	UBB 8	Malda, West Bengal

9	AspuriChangaBrinjal	UBB 9	Malda, West Bengal		
10	Panjipara Local	UBB 10	Khoribari, West Bengal		
11	Phasidewa local 1	UBB 11	Malda, West Bengal		
12	Muktakeshi	UBB 12	Nadia, West Bengal		
13	JhosnaBrinjal	UBB 13	Malda, West Bengal		
14	Long Black	UBB 14	Pundibari, West Bengal		
15	HajipurBhastaBrinjal	UBB 15	Malda, West Bengal		
16	DebjhuriHajari	UBB 16	Malda, West Bengal		
17	Black Beauty	UBB 17	Nadia, West Bengal		
18	Kokila	UBB 18	Alipurduar, West Bengal		
19	Pusa Purple Long	UBB 19	Indian Agricultural Research Institute, New Delhi		
20	Ram Begun	UBB20	Malda, West Bengal		
21	Nababganj	UBB 21	North 24 Pargana, West Bengal		
22	Pundibari 2	UBB 22	Pundibari, West Bengal		
23	Jhuri Begun	UBB 23	Pundibari, West Bengal		
24	Thick Brinjal	UBB 24	Pundibari, West Bengal		
25	Tufanganj 1	UBB 25	Tufanganj, West Bengal		
26	Special Mukra	UBB 26	Nadia, West Bengal		
27	Shitali	UBB 27	Jateswar, West Bengal		
28	White Brinjal	UBB 28	Pudibari, West Bengal		
29	Swarna Mani	UBB 29	Vegetable science, BangaKrishiViswavidyalaya, West Bengal	Uttar	
30	PusaKranthi	UBB 30	Vegetable science, BangaKrishiViswavidyalaya, West Bengal	Uttar	
31	Punjab Sadabahar	UBB 31	Vegetable science, BangaKrishiViswavidyalaya, West Bengal	Uttar	
32	KasiTaru	UBB 32	Vegetable science,	Uttar	

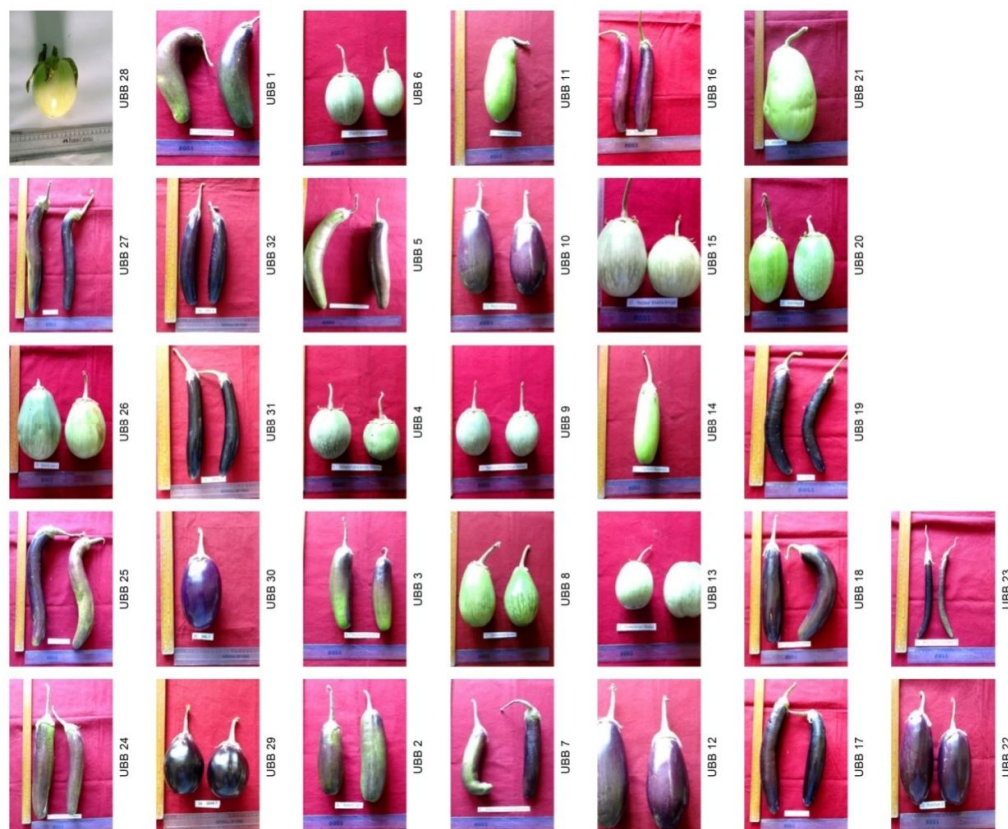


Figure 1: Fruits of the collected experimental material

3. RESULTS AND DISCUSSION:

3.1 Genetic divergence

Multivariate analysis serves as a useful tool to quantify the degree of divergence between the biological populations at genotypic level and to assess the relative contribution of different components to the total divergence both at intra and inter and cluster levels. D^2 technique of Mahalanobis based on multivariate analysis serves to be a good index for estimating genetic diversity (Gadekaret *al.*, 1992). Therefore, Genetic divergence among 32 genotypes of brinjal was assessed by adopting Mahalanobis D^2 statistic based on 15 characters viz., plant height (cm), number of primary branches, calyx length (cm), days to first flower, days to fruit maturity, fruiting span, fruit diameter(cm), fruit length (cm), fruit weight (g), number of fruit per plant, ascorbic acid (mg/100g), total soluble solids ($^{\circ}$ B), phenol (mg/100g), anthocyanin (mg/100g); yield per ha (t/ha).

3.2 Grouping of genotypes into different clusters

Result obtained from D² analysis presented in the table.2 showed that all the 32 genotypes under study were broadly categorized into seven different clusters. Among the entire, cluster I showed to be consisting of maximum number of genotypes viz., UBB 1, UBB 2, UBB 3, UBB 4, UBB 5, UBB 6, UBB 7, UBB 8, UBB 9, UBB 10, UBB 11, UBB 12, UBB 13, UBB 14, UBB 15, UBB 16, UBB 17, UBB 18, UBB 19, UBB 20, UBB 29, UBB 30. Other than this, total four number clusters i.e., cluster II, cluster III, cluster IV and cluster V were consisting of two genotypes in each. Two remaining clusters, cluster VI and cluster VII were comprised of single genotype in each.

After evaluating the source of collection of genotypes and the pattern of cluster distribution indicated that, the geographical diversity need not necessarily be related to the genetic diversity. Among the genotypes from one geographical area, parallelism was not noticed between geographical diversity and genetic diversity. Similar finding was earlier reported by the Vanajaet *al.* (2003), Arunkumar and Biradar (2004), Sreelathakumary and Rajmony (2004), and Senapathiet *al.* (2005).

Table.2. Clustering pattern of 32 genotypes of Brinjal

Sl. No.	Cluster number	Total number of genotypes	Name of genotypes
1	I	22	UBB 1, UBB 2, UBB 3, UBB 4, UBB 5, UBB 6, UBB 7, UBB 8, UBB 9, UBB 10, UBB 11, UBB 12, UBB 13, UBB 14, UBB 15, UBB 16, UBB 17, UBB 18, UBB 19, UBB 20, UBB 29, UBB 30
2	II	2	UBB 23, UBB 28
3	III	2	UBB 22, UBB 25
4	IV	2	UBB 27, UBB 32
5	V	2	UBB 24, UBB 31
6	VI	1	UBB 21

3.3 Mean intra and inter cluster distance

Mean intra and inter cluster distances were presented in table 3. It was observed that average inter cluster distance was higher than the average intra cluster distance indicated wide genetic diversity among the genotypes of different groups than those of same cluster. Similar results were reported by Mahesha *et al.* 2006, Kumar *et al.* (2007), Dutta *et al.* (2009), Sekharet *et al.* (2008) and Islam *et al.* (2011) in brinjal. The intra cluster D^2 values ranged from 0.000-1932.26. Highest intra cluster distance was recorded for cluster I (1932.26) followed by cluster V (1033.35), cluster IV (734.35), cluster III (728.95), cluster IV (734.35) and cluster II (516.00). Whereas, there was no intra cluster distance observed for cluster VI and cluster VII.

In the present study, inter cluster distance found to be maximum for combination between cluster VI and cluster V (9459.58) followed by cluster VI and II (8576.57), cluster VI and cluster VI (8513.05), cluster VI and cluster I (7474.44), cluster VI and cluster III (7027.58) and cluster VI and cluster VII (5953.15). However, minimum inter cluster distance was recorded for combination between cluster IV and cluster II (636.51) followed by cluster VII and cluster III (1172.78), cluster V and cluster II (1205.75) and cluster V and cluster IV (1227.81).

However, the reason of no intra distance in the cluster VI and cluster VII in the present investigation was that both clusters were comprises of single genotype in each case. Highest cluster distance of cluster I and cluster V indicated existence of genetic divergence among these genotypes in these each cluster and thereby could be used for improvement of yield through recombination breeding and also could be used to develop transgressive segregating lines or heterotic population due existence of high level heterogeneity (Mehta and Asati, 2008). The lowest magnitude of inter cluster distance was recorded for the combination between cluster IV and II followed by cluster VII and III indicated that there were

no significant genetic diversity among the genotypes of these clusters and could not be possible to utilize in cross breeding improvement programme.

Again, the combinations of cluster VI and V followed by cluster VI and II, cluster VI and VI, cluster VI and I, cluster VI and III, cluster VI and cluster VII these showed greater extent of inter cluster distance which indicated on inter-cross hybridization among the genotypes under each cluster combinations might result in a wide spectrum of segregating population as genetic diversity is very distinct among the groups and there by predicted the possibility of using these genotypes under each cluster to improve heterotic population or recombinant

Table.3. Inter and Intra cluster (Diagonal) distance of Brinjal

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	1932.26	1872.88	1447.69	1822.12	2547.82	7474.44	1953.74
Cluster II		516.00	1674.34	636.51	1205.75	8576.57	2670.44
Cluster III			728.95	1590.35	2532.40	7027.58	1172.78
Cluster IV				734.35	1227.81	8513.05	2596.60
Cluster V					1033.35	9459.58	3562.85
Cluster VI						0.00	5953.15
Cluster VII							0.00

N.B: Bold values indicate inter cluster distance

3.1.3 Cluster mean of individual characters and their contribution towards diversity

The mean performance of 32 genotypes from 7 different clusters for 15 characters under study was presented in table.4. Cluster VI registered highest mean for plant height (115.94 cm) followed by cluster VII (107.65 cm) while lowest mean was noticed in cluster II (69.40 cm). Highest mean for number of primary branches was recorded in cluster III (7.21) followed by cluster VII (7.15) and lowest mean was found in cluster V (4.68). Highest mean for calyx length was recorded in cluster IV (5.35cm) followed by cluster V (4.49cm) and lowest mean was found in cluster I (3.95cm). Cluster I recorded lowest mean for days to

first flowering (63.67 days) followed by cluster V (63.82 days) whereas highest mean was observed in cluster II (72.18 days). Cluster VII showed minimum mean for days to fruit maturity (37.36 days) followed by cluster I (38.58 days) while maximum mean was noticed in cluster VI (48.10 days) followed by cluster V (43.81 days). Highest mean for fruiting span was noticed in cluster II (103.08 days) followed by cluster IV (102.36 days) and lowest mean was observed in cluster VII (95.15 days) followed by cluster I (98.04 days). Cluster VI recorded maximum mean for fruit diameter (13.22 cm) followed by cluster VII (10.73 cm) and minimum mean was recorded in cluster II (4.76 cm) followed by cluster III (7.14 cm). Mean for fruit length was highest in cluster IV (25.02 cm) followed by cluster III (22.25 cm) and lowest in cluster VII (12.53 cm) followed by cluster II (13.62 cm). Cluster VI recorded maximum mean for fruit weight (899.27 g) followed by cluster VII (428.32 g) and minimum mean was recorded in cluster II (80.73 g) followed by cluster V (161.32 g). Cluster II has shown highest mean for number of fruits per plant (34.96) followed by cluster V (15.57) while lowest mean was observed in cluster VI (2.30) followed by cluster VII (4.34). Highest mean for ascorbic acid was recorded in genotypes of cluster II (11.69 mg/100g) followed by cluster III (9.79 mg/100g) while lowest mean was shown by cluster VII (8.43 mg/100g) followed by cluster I (9.26 mg/100g). Cluster II showed highest mean for total soluble solid (5.89 °B) followed by cluster VI (5.74 °B) while lowest mean was recorded in cluster VII (5.35 °B). Highest mean for Anthocyanin (IU) was recorded in genotypes of cluster V (120.05 IU) followed by cluster III (113.70 mg/100g) while lowest mean was shown by cluster VII (13.50 mg/100g) followed by cluster VI (14.05 mg/100g). Highest mean for Phenol (mg/100g) was recorded in genotypes of cluster II & VI (1.43 mg/100g) followed by cluster IV (1.32 mg/100g) while lowest mean was shown by cluster VII (1.02 mg/100g) followed by cluster III (1.15 mg/100g). Highest mean for Yield/ha (t/ha) was recorded in genotypes of cluster IV (46.10 t/ha) followed by cluster VII (42.25 t/ha) while lowest mean was shown by cluster VI (32.42 t/ha) followed by cluster III (33.17 t/ha).

Contributions of the characters towards total diversity of the genotypes were represented in the table.4. It indicate that characters viz., total yield per hectare (30.04 %),

number of fruit per plant (28.83) and fruit weight (20.97%) were principal contributing characters towards total divergence. However, comparatively moderate contribution was recorded for fruit diameter (8.47%), plant height (4.44%) and calyx length (3.63%). Other than these, low contributions were recorded for ascorbic acid (1.21%), total soluble solid (1.21%), anthocyanin (0.60%), fruit length (0.20%) and number of primary branch (0.20%). Whereas, for rest of the characters viz., phenol content, days to first flowers and days to fruit maturity did not showed any contribution towards the total diversity. Similar results were reported by Manju and Sreelathakumary (2002) and Senapatiet *al.* (2003) in chilli and Sharma and Maurya (2004), Kumar *et al.* (2007), Duttaet *al.* (2009), Das *et al.* (2010) and Islam *et al.* (2011) in brinjal.

However, on the basis of mean of cluster performance cluster VI and VII were important for plant height, fruit diameter, primary branches, fruit weight, total soluble solid and total yield. Whereas, for the for the quality traits viz., anthocyanin, phenol and ascorbic acid as well as calyx length, number of fruit plant cluster II and cluster III could be consider as important. So, selection of the genotype from these cluster as crossing breeding parent could emerged most effective. In the other hand, total yield per hectare, number of fruit per plant and fruit weight showed maximum contribution towards the diversity followed by fruit diameter, plant height and calyx length. Result indicated that **diverse genotypes** can be utilized for improvement of yield productivity. The greater diversity in the present materials was due to these characters which will offer a good scope for improving the yield through rational selection of parent's genotypes for brinjal. The genotypes of highly divergent clusters may also be utilized in a breeding programme for development of high yielding varieties with desirable attribute and can also be utilized in heterosis breeding programme for development of F₁ hybrids with superior yield and quality characters.

Table.4. Cluster mean of individual characters and their percent of contribution

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Number of first rank	% contribution
PH	99.90	69.40	99.22	104.75	85.42	115.94	107.65	22	4.44
PB	5.27	5.71	7.21	6.75	4.68	6.29	7.15	1	0.20
CL	3.95	4.14	4.41	5.35	4.49	3.99	4.12	18	3.63
DFF	63.67	72.18	64.61	69.15	63.82	70.86	70.35	0	0.00
DFM	38.58	41.03	41.74	38.80	43.81	48.10	37.36	0	0.00
FS	98.04	103.08	101.89	102.36	102.19	101.14	95.15	1	0.20
FD	7.95	4.76	7.14	8.88	8.39	13.22	10.73	42	8.47
FL	18.86	13.62	22.25	25.02	22.19	17.93	12.53	1	0.20
FW	311.40	80.73	307.38	177.55	161.32	899.27	428.32	104	20.97
FPP	11.35	34.96	6.53	14.78	15.57	2.30	4.34	143	28.83
VC	9.26	11.69	9.79	9.40	9.35	9.74	8.43	6	1.21
TSS	5.60	5.89	5.39	5.60	5.54	5.74	5.35	6	1.21
PHOL	71.22	54.68	113.70	111.84	120.05	14.05	13.50	3	0.60
ANTH	1.16	1.43	1.15	1.32	1.21	1.43	1.02	0	0.00
YP	42.18	33.76	33.17	46.10	35.07	32.42	42.25	149	30.04

PH: Plant height (cm); PB: Number of primary branches; CL: Calyx length (cm); DFF: Days to first flower; DFM: Days to fruit maturity; FS: Fruiting span; FD: Fruit diameter (cm); FL: Fruit length (cm); FW: Fruit weight (g); FPP: Number of fruit per plant; VC: Ascorbic acid (mg/100g); TSS: TSS (°B); PHOL: Phenol (mg/100g); ANTH: Anthocyanin (mg/100g); YP: Yield per ha (t/ha).

4. CONCLUSION:

It emerged conclusively from the present investigation on evaluation of brinjalgermplasm for winter season that all the 32 genotypes collected from different locality of north Bengal were highly diversified and were less effected by the environment. Selection of the characters under study, specifically number of fruit per plant, fruit weight, fruit diameter, calyx length and plant height will likely to be effective in increasing fruit yield per plant due to having effect of more additive gene action and will be effective in developing heterotic population due to having more diversity. Genotypes under cluster VI and VII will be most effective for the improvement of yield related attributes. The cross combinations between cluster VI and V, cluster VI and II, cluster VI and VI, cluster VI and I, cluster VI and III, cluster VI and cluster VII can be effectively utilized to develop improved heterotic population or recombinant.

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