Studies on Genetic Diversity For Yield And Yield Contributing Characters In Sesame

Abstract: In the present investigation, sixty eight genotypes including three checks at RARS, Jagtial were evaluated for genetic diversity for selection of diverse parents. Divergence studies through D^2 statistic indicated the presence of substantial diversity by forming large number of clusters with wide range of inter-cluster distance.The 68 genotypes were distributed into eight clusters based on the D^2 values. Among the eight clusters, cluster I was the largest comprising of 30 genotypes followed by cluster II with 22 genotypes and Cluster III and V with six genotypes in each cluster remaining clusters IV, VI,VII,VIII were solitary. The data on character means for eight clusters indicated that, cluster III was having highest mean value for number of capsules per plant, capsule length, capsule width, number of seeds per capsule, seed yield per plant and 1000 seed weight. Cluster VIII for days to 50% flowering, plant height, days to maturity and number of branches per plant. The genotypes JCS 2611, JCS 2454 and JCS 3599 from these clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization programme.

Keywords: Sesame, diversity, yield, D^2 statistic, cluster analysis

Introduction:

Sesame (*Sesamum indicum* L.) (2n = 26), also known as Til or Gingelly, it is one of the most important oilseed crop of tropical and temperate regions. It is commonly known as “Queen of oilseeds” due to its resistance to oxidation and rancidity, also it plays an important role as an industrial food crop because of its high nutritional value.

Globally, sesame is produced over an area of 8.8 mha and annual production around 2.8 mt with average productivity of 382 kg/ha. India is still leading country with maximum (25.8 %) production from the largest (29.8 %) area and highest export (40 %) in the world. It is grown in India with an area of 15.80 lakh ha, 1.74 lakh tonnes production and 502 kg ha^{-1} productivity (AICRP annual report, 2019-20). Sesame occupies an area of 21,000 ha with production and productivity of 15,000 tonnes and 714 $kgha^{-1}$ respectively in Telangana (www.indiastat.com, 2020-21). It is grown as summer crop in Northern Telangana districts *viz.*, Adilabad, Jagtial, Karimnagar and Nizamabad. However, the development of improved plant cultivars and increasing the production is restricted mainly due to narrow genetic pool, which results in limited possibility to restructure the sesame crop.

Selection is the basis for crop improvement and efficiency of selection depends on the amount of variablity present in germplasm of crop. Genetic improvement of seed yield alone is not possible through phenotypic selection, because it is a complex character which is governed by polygenes and highly influenced by several quantitative traits.

Application of biometrical techniques in plant breeding has led to the greater understanding of genetics of quantitative characters and proved to be extremely useful to the plant breeder for systematic genetic analysis.

Genetic diversity is a ubiquitous feature of all species in nature. Genetic diversity is an inherited variation among and between populations, created, activated and maintained by evolution. Genetic divergence among the genotypes plays an important role in the selection of parents having wider variability for different characters and ultimately for rational use of genetic resources.

In addition, quantification of the degree of divergence in a given experimental material is of immense value in the identification of divergent genotypes for further use in hybridization programme. Mahalanobis D^2 statistic has been proven to be a powerful tool for quantifying genetic divergence in a given population. Divergent genotypes could be obtained by collection from different eco-geographical regions or it could be induced by combination breeding. Keeping in view the importance explained above, this study was undertaken to identify diverse parents for hybridization programme.

Material and methods:

The experiment was laid out at Regional Agricultural Research Station, Polasa, Jagtial, during *summer*, 2020. The experiment was laid out in Randomized Block Design (RBD) with two replications. Each genotype was sown in two rows of three meteres length, with inter-row spacing of 30 cm and intra row spacing of 15 cm. Sowing was done by dibbling the seed at 2-3 cm depth. All the standard package of practices were followed during crop growth period except spraying of insecticides. The experimental material used in the present investigation comprised of 68 genotypes (Table 1) of sesame including two checks *i.e.*, one National check (TKG 22) and two Local checks (YLM 11 and YLM 66). The data was recorded on yield and yield attributing characters *viz.*, days to 50% flowering (days), days to maturity (days), plant height (cm), number of branches per plant, number of capsules per plant, 1000 seed weight (g), seed yield per plant (g), capsule length (cm), capsule width (cm) and number of seeds per capsule from five randomly selected plants in each replication and the collected mean data was subjected to statistical analysis. In the present study genetic divergence was assessed by using Mahalanobis D^2 statistic. It is found to be useful in quantifying the degree of divergence between the biological population at genotypic level. D^2 statistic was estimated for 68 genotypes and the results obtained from the study presented below.

Results and Discussion:

Significant differences among the genotypes for individual characters were first determined and later the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the *Wilk's criterion* $^{\text{‘}\wedge\text{’}}$. The *Wilk's* criterion thus obtained was used in calculations of ‘V’ statistic. The statistic 1929.73 was highly significant (more than the tabulated χ^2 value) indicated that genotypes differed significantly when all the characters were considered simultaneously.

Relative contribution of different traits towards divergence

The per cent contribution towards genetic divergence by all the yield and yield contributing traits is presented in Table 2 and Fig 1. The maximum contribution towards genetic divergence was by days to 50 % flowering (27.30 %), number of capsules per plant (22.78 %), number of seeds per capsule (14.04 %), number of branches per plant (14.04 %) seed yield per plant (10.49 %), capsule width (4.82 %), 1000 seed weight (3.81 %), days to maturity (2.45 %), capsule length (0.08 %) and plant height (0.13 %) respectively. The days to 50 % flowering (27.30 %), number of capsules per plant (22.78 %) and number of seeds per capsule (14.04 %) together contributed more than 60% towards genetic divergence, therefore, the characters should be given importance during selection. These results were in accordance with the reports of Rajani Bisen *et al.* (2013), Ajay Tanwar and Rajani Bisen (2018) and Gogoi *et al.* (2018).

Grouping of genotypes into various clusters

Based on the D^2 values, the distribution patterns of genotypes done into eight clusters are presented in Table 3. The genotypes belonging to same cluster had an average low D^2 value than those belonging to different clusters. The diagrammatic representation of eight clusters consisting of different genotypes is shown in Fig 2. Among the eight clusters, cluster I was the largest comprising of 30 genotypes followed by cluster II with 22 genotypes. cluster III and cluster V with 6 genotypes in each cluster and clusters IV, VI, VII and VIII were solitary. The IV, VI, VII and VIII were represent by a single genotype indicate high degree of heterogeneity among the genotypes. Solitary clusters may be of distinct recombinant or rare segregants. More number of cluster formation is an indication of higher divergence.

The pattern of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that there is no parallelism between geographical diversity and genetic diversity. This suggests forces such as exchange of breeding material, natural and artificial selection, genetic drift, migration, gene flow and variation in environment may be responsible for this diversity (Singh *et al.*, 1999; Bharadwaj *et al.*, 2001; Sood., 2005)

Average intra and inter cluster distance

The average intra and inter-cluster values estimated as per the procedure given by Singh and Choudhary (1977). The average D^2 values of intra and inter cluster distances are presented in Table 4. The maximum intra cluster distance was recorded for cluster I (70.86) followed by cluster V (69.48), cluster III (58.06) and cluster II (44.26) indicating that some diversity still existed among genotypes. This could be made use of in the yield improvement through recombination breeding. The results were in conformity with Venkatesh *et al.* (2011) and Ahadu Menzir (2012).

From the inter cluster D^2 values of eight clusters it can be seen that the highest inter cluster distance (585.57) was found between clusters VI and VIII followed by cluster IV and cluster VIII (330.23). Cluster I and cluster VIII (325.13) suggesting that the crosses involving varieties from these clusters may be used in hybridization programme to produce useful segregants for yield improvement in recombination breeding programmes.

It is assumed that the maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated that the hybridazation between cluster VI (JCS 4151) cluster VIII (Swetha thil) is sugested to produce promising segregants for yield and yield contributing characters. The genotypes of these clusters may be used as parents in the crossing programme to generate breeding material with high diversity.

Cluster mean

The cluster means in respect of ten yield and yield contributing traits across eight clusters are presented in Table 5. In case of days to 50% flowering, cluster means ranged between 42.50 (cluster VI) and 57.50 days (cluster VIII). Genotypes of cluster VI showed early flowering habit with 42.50 number of days to flowering while, genotypes of cluster VIII had late flowering habit with 57.50 days.

Cluster mean for days to maturity ranged between cluster VI (85.50) and cluster VIII (97.50) days. Genotypes under cluster VI was of early maturity type with number of days to mature being 85.50 days. While, that under cluster VIII were of late maturity types (97.50 days).

With regard to plant height, the genotypes of cluster VIII exhibited the highest mean plant height (105.50 cm). Cluster II comprised of genotypes with a lowest mean plant height (78.85 cm). The mean values of remaining clusters were intermediate.

Cluster mean for number of branches per plant ranged between 2.00 and 5.00. The sesame genotypes under cluster VI had 2.00 branches per plant cluste followed by cluster VIII (5.00), cluster VII (3.00), cluster III (3.00). Cluster I, II, IV and V had less number of branches.

Cluster mean for number of capsules per plant ranged between 23.00 (cluster II) and 57.00 (cluster III). Genotypes under cluster II (23.00) had less number of capsules per plant and those in cluster III (57.00) had more number of capsules per plant.

With respect to 1000 seed weight, cluster III had the highest mean value (3.83 g) followed by cluster IV (3.41 g) and cluster II had lowest 1000 seed weight (2.86).

Cluster mean for seed yield ranged between 3.07 g (cluster VIII) to 10.37 g (cluster III). Genotypes under cluster VIII (3.07 g) showed lowest seed yield those in cluster III (10.37 g) has highest seed yield per plant.

With regard to the capsule length, the cluster means ranged between 2.17 and 2.35. Genotypes under cluster V (2.17 cm) showed lowest mean of capsule length while, genotypes of cluster V and VII (2.35 cm) had capsules with maximum length.

Ccluster VI had the lowest mean value (0.44 cm) for the trait capsule width and cluster III and VIII had highest capsule width (0.57cm).

For the trait number of seeds per capsule, the cluster means ranged between 43.70 and 64.61. Genotypes under cluster VI (43.70) recorded the lowest mean while, genotypes of cluster III (64.61) showed the highest mean value.

The results indicated that the selection of genotypes having high values for a particular traits could be made and used in the hybridization programme for improvement of that character.

The cluster III is having the highest mean value for number of capsules per plant, capsule length, capsule width, number of seeds per capsule, seed yield per plant and test weight followed by cluster VI for days to 50 % flowering, days to maturity, capsule length, seed yield per plant and cluster VIII for number of branches per plant, number of capsules per plant, capsule width. The promising genotypes (Table 5) from these clusters with the high mean value for different traits may be directly used for adaptation or may be used as parents in future hybridization to generate superior transgressive segregants.

CONCLUSION:

Divergence studies through D^2 statistics indicated the presence of substantial diversity by forming large number of clusters with a wide range of inter-cluster distances. The 68 genotypes were distributed into eight clusters based on the D^2 values. Among the eight clusters, cluster I was the largest comprising of 30 genotypes followed by cluster II with 22 genotypes and cluster III and V with 6 genotypes and cluster IV,VI,VII and VIII were solitary. The maximum contribution towards genetic divergence was found by days to 50 % flowering (27.30 %) followed by number of capsules per plant (22.78 %), number of seeds per capsule (14.04 %), number of branches per plant (14.04 %), seed yield per plant (10.49 %), capsule width (4.82 %), 1000 seed weight (3.81 %), days to maturity (2.45 %), capsule length (0.08 %) and plant height (0.13 %). The days to 50 % flowering (27.30 %), number of capsules per plant (22.78 %), number of seeds per capsule (14.04 %) together contributed more than 60% towards genetic divergence therefore, the characters should be given importance during selection. Cluster analysis indicates the presence of a large amount of heterogeneity among the genotypes. The highest inter cluster distance (585.57) is between clusters VI and VIII, while lowest (71.13) is between IV and V. The maximum intra cluster distance was recorded for cluster I (70.86) followed by cluster V (69.48). The genotypes viz., JCS 4151 (Cluster VI) and Swetha Thil (Cluster VIII) may be used in hybridization programme to produce useful segregants for yield improvement in recombination breeding programmes. This indicates that genotypes from these clusters can be used directly for adaptation or may be used in hybridization programme.

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Table 1. Details of 68 genotypes of sesame for investigation

S.No.	Genotypes	Source of collection
1	FFAT -147	JNKVV, Jabalpur
2	IC-131546	JNKVV, Jabalpur
3	IC-14120-I	JNKVV, Jabalpur
4	FFAT -141	JNKVV, Jabalpur
5	FFAT -140	JNKVV, Jabalpur
6	IS -113-A	JNKVV, Jabalpur
7	FFAT-135	JNKVV, Jabalpur
8	SI -225	JNKVV, Jabalpur
9	Chandana	RARS, Polasa, Jagtial
10	FFAT-148	JNKVV, Jabalpur
11	FFAT -146	JNKVV, Jabalpur
12	IC-14146-C	JNKVV, Jabalpur
13	IC-131485	JNKVV, Jabalpur
14	FFAT-142	JNKVV, Jabalpur
15	FFAT -10-5	JNKVV, Jabalpur
16	Jagtiala Til-1	RARS, Polasa, Jagtial
17	JCS 3180	RARS, Polasa, Jagtial
18	JCS 3880	RARS, Polasa, Jagtial
19	JCS 3899	RARS, Polasa, Jagtial
20	JCS 2454	RARS, Polasa, Jagtial
21	JCS 3265	RARS, Polasa, Jagtial
22	JCS 3980	RARS, Polasa, Jagtial
23	JCS 3887	RARS, Polasa, Jagtial
24	JCS 3981	RARS, Polasa, Jagtial
25	JCS 3889	RARS, Polasa, Jagtial
26	JCS 2420	RARS, Polasa, Jagtial
27	JCS 3758	RARS, Polasa, Jagtial
28	JCS 2611	RARS, Polasa, Jagtial
29	JCS 3596	RARS, Polasa, Jagtial
30	JCS 3202	RARS, Polasa, Jagtial

31	JCS 3287	RARS, Polasa, Jagtial
32	JCS 4001	RARS, Polasa, Jagtial
33	JCS 3603	RARS, Polasa, Jagtial
34	JCS 3890	RARS, Polasa, Jagtial
35	JCS 4049	RARS, Polasa, Jagtial
36	JCS 3122	RARS, Polasa, Jagtial
37	JCS 4036	RARS, Polasa, Jagtial
38	JCS 3997	RARS, Polasa, Jagtial
39	JCS 3985	RARS, Polasa, Jagtial
40	JCS 3976	RARS, Polasa, Jagtial
41	JCS 3987	RARS, Polasa, Jagtial
42	JCS 3999	RARS, Polasa, Jagtial
43	JCS 4053	RARS, Polasa, Jagtial
44	JCS 3879	RARS, Polasa, Jagtial
45	JCS 3886	RARS, Polasa, Jagtial
46	JCS 4045	RARS, Polasa, Jagtial
47	JCS 4057	RARS, Polasa, Jagtial
48	JCS 4104	RARS, Polasa, Jagtial
49	JCS 4096	RARS, Polasa, Jagtial
50	JCS -4105	RARS, Polasa, Jagtial
51	JCS 4120	RARS, Polasa, Jagtial
52	JCS 4151	RARS, Polasa, Jagtial
53	JCS 4113	RARS, Polasa, Jagtial
54	JCS 4115	RARS, Polasa, Jagtial
55	JCS 4154	RARS, Polasa, Jagtial
56	DS-28	JNKVV, Jabalpur
57	DS-10	JNKVV, Jabalpur
58	DS-21	JNKVV, Jabalpur
59	JCS 3593	RARS, Polasa, Jagtial
60	JCS 3762	RARS, Polasa, Jagtial
61	GT-10	JNKVV, Jabalpur
62	JCS 3599	RARS, Polasa, Jagtial
63	Rajeshwari	RARS, Polasa, Jagtial
64	Swetha thil	RARS, Polasa, Jagtial
65	YLM 17	RARS, Yelamanchali
66	YLM 11	RARS, Yelamanchali
67	YLM 66	RARS, Yelamanchali
68	TKG 22	JNKVV, Jabalpur

Table 2. Relative contribution (%) of yield and yield contibuting traits towards divergence

Character	Times ranked 1st	Contribution %
Days to 50% flowering	622	27.30
Days to maturity	56	2.45
Plant height (cm)	3	0.13
Number of branches per plant	519	14.04
Number of capsules per plant	320	22.78
Test weight (g)	87	3.81
Seed yield per plant (g)	239	10.49
Capsule length (cm)	2	0.08
Capsule width (cm)	110	4.82
Number of seeds per capsule	320	14.04

Fig 1. Relative contribution (%) of yield and yield contibuting traits in sesame genotypes towards divergence

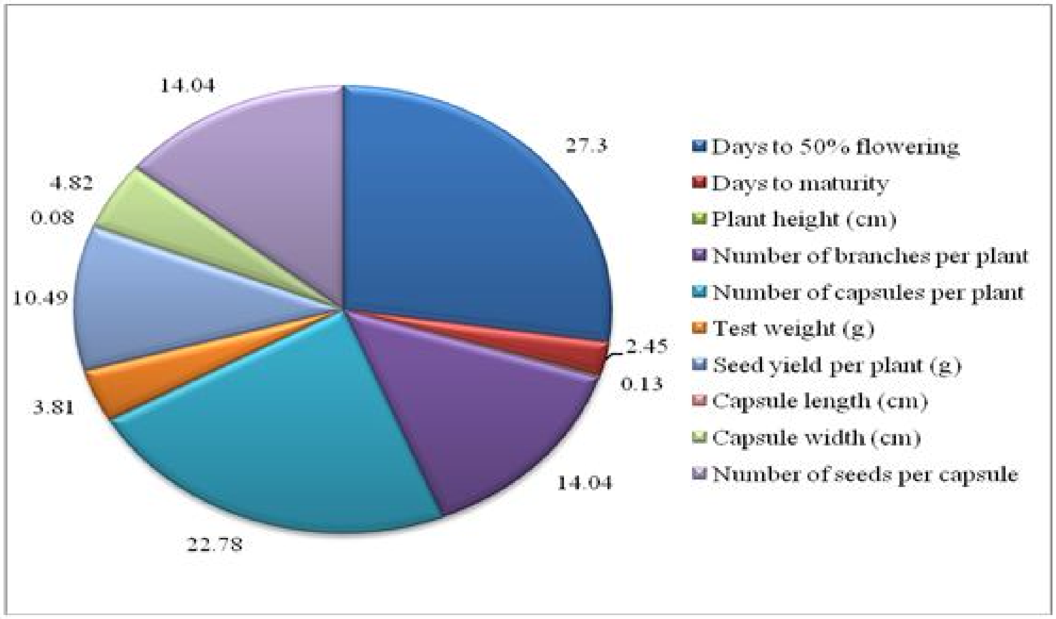

Figure 2 Clustering pattern of sesame genotypes based on Tocher's method

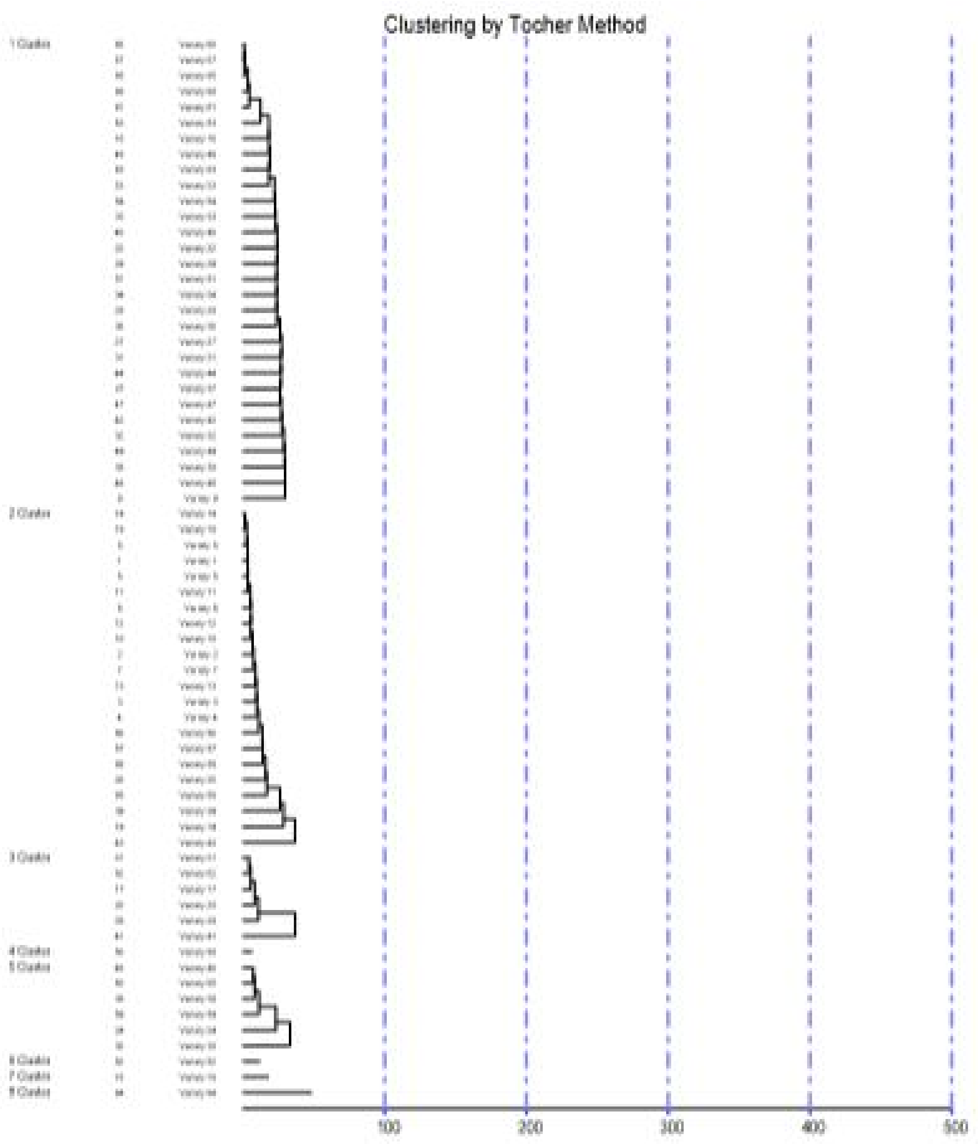

Table 3. Clustering pattern of sesame genotypes based on D^2 values

Clusters	No. of genotypes	Name of Genotypes
Cluster 1	30	Jagitala Til-1, JCS 4120 , JCS 4113 , JCS 4115, JCS 3887, JCS 3886, JCS 3889, JCS 3596, JCS 3980, JCS -3758, JCS 3180, JCS 4001, JCS 3603, JCS 3890, JCS 4049, JCS 3122, JCS 4036, JCS 3976, JCS 3999, JCS 3879, JCS 4057, JCS 4104, JCS 4096, Rajeshwari,YLM 17, YLM 11, YLM 66, GT 10, TKG 22 and Chandana.
Cluster 2	22	SI -225, FFAT -147, IC-131546, IC-14120-I, FFAT -141, FFAT -140, IS -113-A, FFAT-135, FFAT-148, FFAT -146, IC-14146-C, IC-131485, FFAT-142, FFAT -10-5, DS-28, DS-10, DS-21, JCS 4154, JCS 4053, JCS 3985, JCS 2420 and JCS 3899.
Cluster 3	6	JCS 2454, JCS 3265, JCS 2611, JCS 3287, JCS 3987, and JCS 3599.
Cluster 4	1	JCS 4105
Cluster 5	6	JCS 3762, JCS 3593, JCS 4045, JCS 3202, JCS 3997, and JCS 3981.
Cluster 6	1	JCS 4151
Cluster 7	1	JCS 3880
Cluster 8	1	Swetha thil

Table 4. Average intra (diagonal) and inter cluster distances of sesame genotypes

Clusters	**Cluster 1**	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**	**Cluster 7**	**Cluster 8**
Cluster 1	**70.86**	116.74	127.07	89.93	126.43	106.84	130.48	**325.13**
Cluster 2		**44.26**	195.34	131.65	140.15	214.58	105.54	238.78
Cluster 3			**58.06**	199.70	183.92	194.02	161.65	241.02
Cluster 4				**0.00**	71.13	141.58	179.30	**330.23**
Cluster 5					**69.48**	266.28	220.16	238.52
Cluster 6						**0.00**	158.13	**585.57**
Cluster 7							**0.00**	256.99
Cluster 8								**0.00**

Table 5. Cluster means for yield and yield contibuting traits using Tocher's method

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches	Number of capsules per plant	1000 seed weight (g)	Seed yield per plant (g)	Capsule length (cm)	Capsule width (cm)	Number of seeds per capsules
Cluster 1	48.65	89.83	91.82	2.67	46.57	3.09	7.87	2.26	0.54	61.23
Cluster 2	50.98	91.05	78.85	2.74	23.62	2.86	4.21	2.25	0.53	47.18
Cluster 3	46.42	88.17	98.15	4.23	57.75	3.83	10.37	2.28	0.57	64.61
Cluster 4	55.50	95.50	93.50	2.20	47.50	3.41	7.36	2.20	0.45	61.00
Cluster 5	57.33	96.67	100.80	2.80	43.12	3.29	8.98	2.17	0.55	63.05
Cluster 6	42.50	85.50	92.50	2.20	50.00	3.18	8.96	2.35	0.44	55.50
Cluster 7	43.50	92.50	94.50	3.15	44.50	3.20	4.55	2.35	0.49	43.70
Cluster 8	57.50	97.00	105.50	5.00	52.50	3.21	3.07	2.25	0.57	59.00

Table 6. Promising genotypes having outstanding cluster mean values for yield and contributing traits.

Cluster	Character	Genotype
III	Number of capsules per plant, capsule length,capsule width, number of seeds per capsule, seed yield per plant and test weight.	JCS 2454, JCS 2611
VII	Days to 50% flowering, days to maturity, capsule length and seed yield per plant	JCS 4151
VIII	Plant height, number of branches per plant and capsule width.	Swetha thil

These genotypes can be exploited successfully in evolving high yielding varieties.