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Diversity Analysis in Sesame (*Sesamum indicum* L.)

J V Ramana, V Satyanarayana Rao, M Lal Ahamed, Y Ashoka Rani and P Anil Kumar
Department of Genetic and Plant Breeding, Agricultural College, Bapatla 522 101, Andhra Pradesh

ABSTRACT

Diversity analysis was carried out using thirty six sesamum genotypes. The genotypes were evaluated for nine characters *viz.,* days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight, oil content and seed yield per plant. In the diversity analysis, it was observed that the per cent contribution towards genetic divergence was maximum by the trait, number of primary branches per plant. The genotypes were grouped into seven clusters using Tocher's method and the distribution into seven clusters was at random with maximum number of genotypes in cluster I (12 genotypes). The maximum intra cluster distance was observed in the cluster IV and the inter cluster distance was the highest between clusters V and VI indicating wide genetic diversity between the clusters and crosses can be attempted between the genotypes of these clusters to obtain desirable transgressive segregants. Higher cluster mean values for number of primary branches per plant, number of seeds per capsule, days to maturity and plant height were observed in cluster V while cluster VI recorded minimum number of days to 50% flowering and the highest seed weight and seed yield per plant indicating the importance of this cluster in breeding programmes to generate early maturity types with increased seed yield through seed weight.

Key words: *Diversity, Sesame, Tochers' method.*

Sesame (*Sesamum indicum* L.) is one of the most important oil seed crops in India, grown next to groundnut, rapeseed and mustard. Sesame oil quality of is excellent with 50-53% of oil and 20-26% of protein content and has medicinal value which imparts a high degree of resistance against oxidative rancidity along with vitamin E and essential amino acid, methionine.

Sesame is cultivated in an area of about 1.94 million hectares in India with a production of about 0.58 million tones (Ministry of Agriculture, 2013-14). In Andhra Pradesh it occupies an area of 0.09 million hectares with a production of about 0.2 million tonnes. The average productivity of sesame in Andhra Pradesh (222.2 kg/ha) is far less as compared to the Indian average of 303 kg/ha (Ministry of Agriculture, 2013-14) which indicates that there is much need to enhance the productivity potential of this crop by evolving high yielding varieties for different agro climatic situations.

The slow improvement in sesame is due to the arbitrary choice of parents and inadequate information about the nature of gene action in governing the traits. A thorough knowledge on genetic diversity, prepotency of parents for producing better recombinants is desirable to isolate high combining lines from germplasm to produce better varieties through recombinant or transgressive breeding programmes. Realising the importance and need, the present study was undertaken to study the diversity among the genotypes.

MATERIAL AND METHODS

The present investigation was carried out during *rabi*, 2010-11 at Agricultural Research Station, Yallamanchili, Andhra Pradesh using thirty six sesamum genotypes for their genetic divergence. The genotypes were evaluated for nine characters *viz.,* days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight, oil content and seed yield per plant. The experiment was laid in randomized block design with three replications. The intra and inter row spacing was 10 cm x 20 cm with 4 rows per genotype per replication. Recommended package of practices were followed to raise a good crop in the field. Observations were recorded on ten randomly selected plants per treatment per replication and were used for statistical analysis. However, days to 50% flowering, days to maturity,

1000-seed weight and oil content were recorded on plot basis. The data collected on different yield contributing characters was analyzed using Mahalanobis' D^2 analysis to determine the genetic divergence among the genotypes (Mahalanobis, 1928).

RESULTS AND DISCUSSION

Genetic divergence played a key role in analyzing the general distance among the genotypes selected as parents. Within a certain limit, hybridization of more diverged parents is expected to enhance the level of heterosis and generate wide range of variability in segregating generations.

Generally, geographical diversity was considered as a measure of genetic diversity when no scientific tools were available. But geographical distribution of genotypes is not the only factor that causes genetic diversity. This may be due to exchange of breeding material over the locations and further selections at different locations which could result in genetic drift. However, this is an inferential criterion and may no be used for discrimination among the populations occupying ecologically marginal habitats (Arunachalam and Ram, 1967). So, selection of parents for hybridization programme should be based on genetic rather than geographical diversity as there is no parallelism between genetic divergence and geographical divergence of genotypes.

The multivariate analysis using Mahalanobis' D^2 provides useful statistical tool for measuring the genetic diversity in a given population with respect to the characters that were considered together. Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discriminations between the populations.

The data collected on nine yield contributing characters from thirty six genotypes of sesamum were subjected to Mahalanobis' D^2 statistic and the magnitude of values suggested that there was considerable variability in the material studied, which led to genetic diversity.

Test with Wilk's criterion '^'

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 **'^'.** The Wilk's criterion thus obtained was used in calculations of 'V' statistic. The statistic was highly significant indicating that genotypes differ significantly when all the characters were considered simultaneously. The value of 'V' statistic was 1169.60 in the present investigation.

Mahalanobis' D^2 values

The statistical differences (D^2) between pairs of genotypes was obtained as the sum of squares of the differences between the pairs of corresponding uncorrelated values of any two genotypes considered at a time. Thus the possible 780 combinations and the corresponding D^2 values were obtained. The per cent contribution towards genetic divergence by the seed yield per plant and yield contributing characters is presented in Table-1**.** Character wise rank was showed that no single character had a greater contribution to total genetic divergence. The maximum contribution towards the genetic divergence was by the trait, number of primary branches per plant (38.41) followed by 1000 seed weight (29.84) and the contribution of traits, days to 50% flowering (0.63) and days to maturity (0.32) towards the diversity was minimum. Seed oil content contributed maximum as per the studies of Swain and Dikshit (1997) and Thangavelu and Rajasekaran (1983) while Manivannan and Ganesan (2000) reported that plant height followed by number of branches per plant and 1000 - seed weight contributed more towards to total divergence in their studies.

Grouping of genotypes into clusters

The thirty six genotypes were grouped into seven clusters using Tocher's method with the criterion that the intra-cluster average D^2 values (Table -2) and the distribution of genotypes into seven clusters was at random with maximum number of genotypes in cluster I (12 genotypes) followed by the cluster III (10 genotypes), cluster II (6 genotypes) and cluster IV (5 genotypes). Clusters V, VI, and VII were solitary clusters with zero intra-cluster D^2 values. The formation of distinct solitary clusters may be due to the fact that geographical barriers preventing gene flow or intensive natural and human selection for diverse

Table 1. Contribution of different characters towards genetic divergence in sesame.

Character	No. of times ranked first	Per centcontribution
Days to 50% Flowering	4	0.63
Days to Maturity	2	0.32
Plant Height cm	36	5.71
Primary Branches/ plant	242	38.41
Capsules/ plant	45	7.14
Seeds/ capsule	56	8.89
1000 Seed Weight	188	29.84
Oil Content	48	7.62
Seed Yield/ plant	9	1.43

Table 2. Clustering pattern of 36 sesame genotypes by Tocher's method.

Cluster No.	No. of genotypes	Name of genotypes
I	12	YLM 78, YLM 86,YLM 101, YLM 66, YLM 81, YLM 106,YLM 82, YLM 91, YLM 17, YLM 105, YLM 83,YLM 11
II	6	YLM 90, YLM 93, YLM 96, YLM 95, YLM 89, YLM 97
III	10	YLM 102, YLM 104, YLM 100, YLM 108, YLM 79, YLM 85, YLM 103, YLM 84, YLM 87,YLM 88
IV	5	YLM 98, NIRMALA, YLM 80, YLM 99, VZM-5
V	1	YLM 94
VI	1	YLM 107
VII	1	YLM 92

Table 3. Average intra (diagonal) and inter-cluster D^2 and D values (within parenthesis) values among seven clusters in sesame.

Cluster No.	I	II	III	IV	V	VI	VII
I	9.262 (3.0433)	43.071 (6.5628)	24.172 (4.91650)	19.733 (4.4421)	73.992 (8.6018)	63.479 (7.9673)	79.193 (8.8990)
II		8.312 (2.8830)	66.367 (8.1465)	43.049 (6.5611)	17.790 (4.2178)	105.288 (10.2609)	46.708 (6.8343)
III			17.539 (4.1879)	36.516 (6.0428)	93.093 (9.6484)	30.186 (5.4941)	73.763 (8.5885)
IV				19.237 (4.386)	61.106 (7.8170)	66.758 (8.1705)	63.714 (7.9821)
V					0.000 (0.000)	128.311 (11.3274)	43.278 (6.5786)
VI						0.000 (0.000)	62.901 (7.9310)
VII							0.000 (0.000)

Table 4. The nearest and the farthest cluster from each cluster based on D^2 values using Tocher's method in 36 genotypes of sesame.

Cluster No.	Nearest cluster with D^2values	Farthest cluster with D^2 values
I	IV (19.733)	VII (79.193)
II	V (17.790)	VI (105.288)
III	I (24.172)	V (93.093)
IV	I (19.733)	VI (66.758)
V	II (17.790)	III (93.093)
VI	III (30.186)	V (128.311)
VII	V (43.278)	I (79.193)

Table 5. Mean values of seven clusters estimated by Tocher's method for different characters of sesame.

Cluster No.	Days to 50% Flowering	Days to Maturity	Plant Height	Primary Branches/ Plant	Capsules/ Plant	Seeds/ Capsule	1000 Seed Weight	Oil Content	Seed Yield/ Plant
I	37.333	77.722	96.092	4.233	55.225	**80.465**	**2.388**	48.499	**10.349**
II	36.389	77.389	99.339	4.956	59.922	83.220	2.421	**49.757**	11.844
II	37.167	77.067	98.563	**3.993**	**55.057**	82.843	2.667	48.272	11.858
IV	**37.533**	77.733	**93.907**	4.447	57.833	80.573	2.401	**46.403**	10.963
V	36.000	**78.333**	**108.700**	**5.100**	61.467	**85.567**	2.443	47.290	12.433
VI	**35.333**	77.667	94.233	4.033	55.583	81.000	**3.060**	47.410	**13.417**
VII	36.667	**76.667**	99.833	4.933 I	**61.767**	80.967	2.797	47.217	12.200

Note: Bold figures are minimum and maximum values

and adaptable gene complexes. Swain and Dikshit (1997) through D^2 analysis in forty sesame genotypes for thirteen quantitative characters grouped into fourteen clusters while Manivannan and Ganesan (2000) subjected sixty seven sesame genotypes to D^2 analysis and observed that the genotypes were grouped in ten clusters.

This pattern of grouping has indicated that the diversity need not be necessarily related to geographical diversity and it may be the outcome of several other factors like natural selection, exchange of breeding material, genetic drift and environmental variation. Therefore, selection of varieties for hybridization should be based on genetic diversity rather than geographical diversity. All the earlier studies in sesame clearly indicated the no relationship between the geographical diversity and genetic diversity.

Average intra and inter-cluster values

The average intra and inter cluster D^2 values were estimated and are presented in the Table-3. The proximity and distant among several clusters was indicated in Table-4.

The maximum intra cluster distance was observed in the cluster IV (19.23) followed by cluster III (17.53), cluster I (9.26) and cluster II (8.31). Cluster I with twelve genotypes was the largest and was closest to cluster IV (19.73) and farthest to cluster VII (79.19). There were six genotypes in cluster II and was closest to the cluster V (17.79) and farthest from cluster VI (105.28). Cluster III was the second largest cluster with ten genotypes and was closest to cluster I (24.17) and farthest from cluster V (93.09). Cluster IV comprised of five genotypes and was nearest to cluster I (19.73) and farthest from cluster VI (66.75). Cluster V was solitary with the genotype YLM 94 and was closest to the cluster II (17.79) and farthest from cluster III (93.09). Cluster VI had only one genotype (YLM 107) and was closest to the cluster III (30.18) and farthest to cluster V (128.31). Cluster VII was mono genotypic (YLM 92) and was closest to the cluster V (43.27) and farthest to cluster I (79.19).

The high intra cluster distance in cluster IV indicates the presence of genetic diversity among the genotypes present within this cluster. The genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters measured.

The inter cluster distances were worked out considering nine characters and the inter cluster distance range was from 128.31 (between clusters V and VI) to 17.79 (between clusters II and V) indicating wide genetic diversity between the clusters and crosses can be attempted between the genotypes of these clusters to obtain desirable transgressive segregants.

Choice of the particular cluster and selection of particular genotype from selected cluster are the two important points to be considered before initiating the crossing programme. The hybrids between varieties of different clusters will express high heterosis and throw more useful segregants.

Cluster Mean Values

The cluster mean values for nine characters were presented in Table-5. The character, days to 50% flowering had a range from 35.33 (cluster VI) to 37.53 (cluster IV) indicating the importance of the cluster VI for the development of early maturing types. The trait, days to maturity, showed variability from 76.66 (cluster VII) to 78.33 (cluster V) indicating presence of low variability for this trait in the clusters. The range for plant height was 93.90 (cluster IV) to 108.70 (cluster V) indicating the importance of cluster IV in generating medium height genotypes. Number of primary branches per plant showed the variability from 3.99 (cluster III) to 5.10 (cluster V). Number of capsules per plant recorded 55.05 (cluster III) to 61.76 (cluster VII) cluster mean values indicating the importance of the cluster VII for increased seed yield per plant. The range observed for the trait, number of seeds per capsules, was 80.46 (cluster I) to 85.56 (cluster V) indicating the existence of variability for this trait and exploitation for improvement. 1000 seed weight showed the cluster mean variability from 2.38 (cluster I) to 3.06 (cluster VI) revealing the importance of the cluster VI in breeding programmes for increased seed yield through 1000 seed weight. The cluster mean range for oil content varied from 46.40 (cluster IV) to 49.75 (cluster II) indicating great chances of increasing the oil content by exploiting the cluster II. The cluster mean of seed yield per plant ranged from 10.34 (cluster I) to 13. 41 (cluster VI) indicating greater scope for per se yield improvement by exploiting the cluster VI.

Higher cluster mean values for number of primary branches per plant, number of seeds per capsule, days to maturity and plant height were observed in cluster V while cluster VI recorded minimum number of days to 50% flowering and highest 1000 seed weight and seed yield per plant indicating the importance of this cluster in breeding programmes to generate early maturity types with increased seed yield through seed weight. Cluster II recorded the highest cluster mean for oil content.

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