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Estimation of genetic divergence and determining selection criteria in sesame (*Sesamum indicum*)

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Sesame (*Sesamum indicum* L.) is an herbaceous annual plant of the Pedaliaceae family, which is cognized as one of the primordial and pivotal oilseed crop (Mabberley 1997). Sesame enhances and enriches nutritional status as it contain high oil (35–54%) with superior quality of protein (18–25%) and longer storage-life due to presence of lignans, sesamol, tocopherols, sesamolin and their derivatives (Brar and Ahuja 1979). Genetic diversity is a congenital variant among and between populations and it is a ubiquitous characteristic of all species in nature and plays a crucial part in the selection of parents for hybridization. Further, determining the selection criteria is truly based upon character association along with the direct and indirect effects as it is well known that yield is the end product of interaction among various yield components therefore selecting for a high-yielding genotype entails a thorough sageness of the mutual relationship between two variables and to know how the improvement of one character will bring concurrent refinement in other. Therefore, this investigation was carried out to determine these parameters.

The present study was carried out at Agricultural Research Station, Mandor, Jodhpur, Rajasthan during rainy (*kharif*) season 2018 using 28 mutant genotypes of sesame in randomized block design with three replications. All the observations, viz. plant height (cm), number of primary branches/plant, number of capsules/plant, capsule length (cm), seed yield/plant (g), test weight (g), harvest index (%), oil content (%), and protein content (%) were recorded on ten randomly selected plants except for days to 50% flowering and days to maturity which were recorded on whole plot basis.

The mean data of all the observations were utilized to carry out the statistical analysis. An analysis of genetic divergence was made by adopting Mahalanobis's D^2 statistic (Mahalanobis 1936). According to Rao (1952), character means were converted into collections of uncorrelated variables using the pivotal condensation of the common dispersion matrix. The Tocher's method was used to divide genotypes into different clusters. The correlation coefficient was calculated utilizing the procedure suggested by Searle (1961). Using the approach suggested by Wright (1921) and elaborated by Dewey and Lu (1959), path coefficient was estimated.

ANOVA revealed highly significant differences among genotypes for all the studied traits which demonstrated the existence of variation among the genotypes, which can be further exploited in desirable direction for genetic improvement of the crop. The results showed similar trend with earlier reports published by Abate *et al.* (2015), Prithviraj and Parameshwarappa (2017), Singh *et al.* (2018) and Roy *et al.* (2022).

Clustering of genotypes into eight groups on the basis of morphological differences and the greater inter cluster distance than intra cluster also suggested the presence of greater levels of heterogeneity amid the numerous genotypes

Table 1 Pattern of clustering among 28 genotypes of sesame (Tocher's method)

Cluster number	Number of genotypes	Genotypes
I	14	TBS 4, TBS 11, TBS 5, TBS 10, TBS12, TBS7, TBS6, EC 335003, NIC 7921, NIC8478, TBS9, EC303311, GT10, Octalone
II	8	EC 334984B, RT 54, PhuleTil-1, EC 303441B, NIC 205312, EC 138836, RT 103, RT 346,
III	1	RT 127
IV	1	NIC 7909
V	1	TBS 2
VI	1	RT 351
VII	1	PT 49-3
VIII	1	NIC 8167

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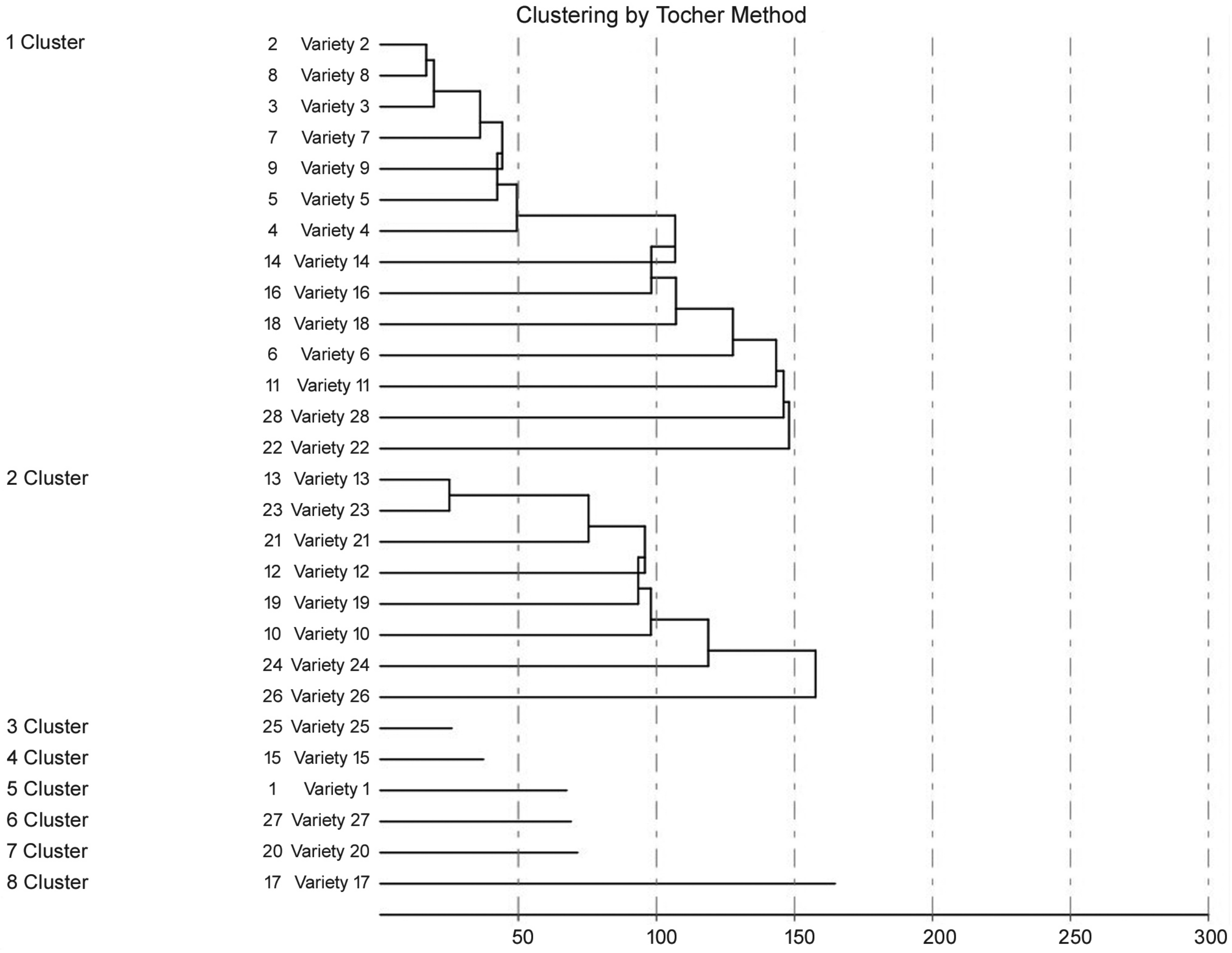

Fig 1 Clustering pattern of 28 genotypes in sesame by (Tocher's method).

(Fig 1). These results are in consonance with the results of Singh *et al.* (2018), Tanwar and Bisen (2018), Paras *et al.* (2022) and Roy *et al.* (2022) (Table 1 and Fig 2). The cluster means for days to 50% flowering and days to maturity was lowest in cluster III while for plant height in Cluster VI. The average mean values of all the characters in the eight clusters revealed that different clusters were superior in respect of different traits. Therefore, the promising genotypes which contains maximum inter cluster distance may be used as parents in the future breeding programme, to obtain superior heterotic segregants. The trait, viz. test weight contributed substantially to genetic differentiation. These results are in agreement with Jadhav and Mohrir (2013) for seed yield/plant.

The trait, test weight (36.24%) furnished most to genetic divergence ensued by number of capsules/plant (20.9%), seed yield/plant (15.08%), oil content (12.17%), harvest index (7.41%), days to 50% flowering (6.08%), protein content (1.85%) and number of primary branches/plant (0.26%). These results were coincided with Gogoi *et al.* (2018). Thus, in conclusion of the research experiment carried out, the promising genotypes which contains

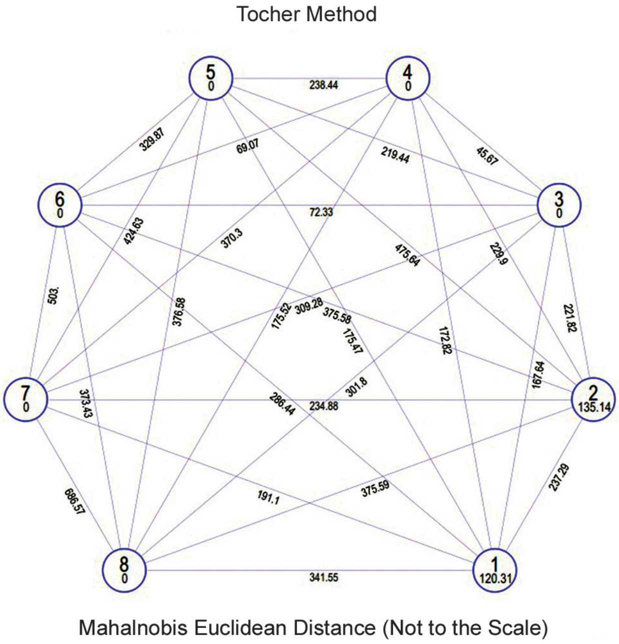

Fig 2 Diagram presenting inter and intra cluster distances.

Table 2 Phenotypic and genotypic correlation coefficients among yield characters in 28 sesame genotypes

Character		Day to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Number of capsules/ plant	Capsule length (cm)	Seed yield/ plant (g)	Test weight (g)	Harvest index (%)	Oil content (%)	Protein content (%)
Day to 50% flowering	G	1.000	0.719**	0.344**	-0.304**	-0.351**	-0.228*	-0.491**	0.675**	-0.568**	-0.342**	0.442**
	P	1.000	0.346**	0.279*	-0.282**	-0.354*	-0.116	-0.478**	0.659**	-0.540**	-0.324**	0.423**
Days to maturity	G		1.000	0.146	0.272*	-0.274*	0.838**	-0.131	0.787**	-0.226*	-0.252*	0.589**
	P		1.000	0.065	0.133	-0.094	0.175	-0.065	0.392**	-0.126	-0.158	0.258*
Plant height (cm)	G			1.000	0.024	0.304**	0.254*	0.118	0.362**	-0.232*	-0.045	0.305**
	P			1.000	0.038	0.255*	0.169	0.105	0.303**	-0.209	-0.028	0.238*
Number of primary branches	G				1.000	0.585**	0.380**	-0.038	-0.159	-0.188	-0.142	0.214
	P				1.000	0.551**	0.225*	-0.024	-0.162	-0.156	-0.143	0.182
Number of capsules/ plant	G					1.000	0.440**	0.407**	-0.077	-0.124	0.091	0.113
	P					1.000	0.199	0.400**	-0.075	-0.117	0.081	0.100
Capsule length (cm)	G						1.000	0.455**	0.418**	0.044	0.409**	0.154
	P						1.000	0.252*	0.189	0.057	0.175	0.061
Seed yield/plant (g)	G							1.000	-0.118	0.644**	0.468**	0.087
	P							1.000	-0.117	0.646**	0.456**	0.076
Test weight (g)	G								1.000	-0.404**	0.014	0.613**
	P								1.000	-0.392**	0.013	0.587**
Harvest index (%)	G									1.000	0.373**	-0.114
	P									1.000	0.352**	-0.103
Oil content (%)	G										1.000	0.056
	P										1.000	0.057
Protein content (%)	G											1.000
	P											1.000

Table 3 Phenotypic and genotypic path coefficients among yield traits in 28 sesame genotypes

Character		Days to 50% flowering	Days to maturity	Plant height (cm)	Numbers of primary branches	Numbers of capsules/ plant	Capsule length (cm)	Test weight (g)	Harvest index (%)	Oil content (%)	Protein content (%)	Seed yield/ plant (g)
Days to 50% flowering	G	-0.299	0.131	-0.000	0.315	-0.192	-0.156	-0.562	-0.090	0.052	0.312	-0.491**
	P	-0.132	0.031	0.022	0.083	-0.192	-0.010	0.043	-0.332	-0.033	0.043	-0.478**
Days to maturity	G	-0.215	0.182	-0.000	-0.282	-0.150	0.572	-0.655	-0.035	0.038	0.415	-0.131
	P	-0.045	0.091	0.005	-0.039	-0.051	0.016	0.026	-0.077	-0.016	0.026	-0.065
Plant height (cm)	G	-0.103	0.026	-0.002	-0.025	0.166	0.173	-0.301	-0.036	0.007	0.214	0.118
	P	-0.037	0.005	0.080	-0.011	0.139	0.015	0.020	-0.128	-0.002	0.024	0.105
Number of primary branches	G	0.091	0.049	-0.000	-1.035	0.321	0.259	0.132	-0.029	0.021	0.150	-0.038
	P	0.037	0.012	0.003	-0.294	0.299	0.020	-0.010	-0.096	-0.014	0.018	-0.024
Numbers of capsules/ plant	G	0.105	-0.050	-0.000	-0.607	0.548	0.300	0.064	-0.019	-0.014	0.080	0.407**
	P	0.047	-0.008	0.020	-0.162	0.543	0.018	-0.005	-0.072	0.008	0.010	0.400**
Capsule length (cm)	G	0.068	0.153	-0.000	-0.394	0.241	0.682	-0.348	0.007	-0.062	0.108	0.455**
	P	0.015	0.015	0.013	-0.066	0.108	0.092	0.012	0.035	0.018	0.006	0.252*
Test weight (g)	G	-0.202	0.143	-0.000	0.164	-0.042	0.285	-0.832	-0.064	-0.002	0.432	-0.118
	P	-0.087	0.035	0.024	0.047	-0.041	0.017	0.066	-0.241	0.001	0.059	-0.117
Harvest index (%)	G	0.170	-0.041	0.000	0.194	-0.068	0.030	0.336	0.158	-0.057	-0.080	0.644**
	P	0.071	-0.011	-0.016	0.046	-0.064	0.005	-0.026	0.615	0.036	-0.010	0.646**
Oil content (%)	G	0.102	-0.046	0.001	0.147	0.050	0.279	-0.012	0.059	-0.153	0.039	0.468**
	P	0.043	-0.014	-0.002	0.042	0.044	0.016	0.001	0.216	0.103	0.005	0.456**
Protein content (%)	G	-0.132	0.107	-0.007	-0.221	0.062	0.105	-0.510	-0.018	-0.008	0.704	-0.087
	P	-0.056	0.023	0.019	-0.053	0.054	0.005	0.038	-0.063	0.005	0.101	0.076

maximum inter cluster distance (PT 49-3, NIC 8167 and RT 351, PT 49-3) and higher cluster mean (RT 127 and NIC 7909) values from the above clusters were identified may be used directly according to the objective of the hybridization programme for adaptation or may be utilized as parent in the future breeding programme, to obtain superior heterotic segregants.

Further, the estimates of genotypic correlation coefficients were higher than the phenotypic correlation coefficients. The trait seed yield/plant had positive significant genotypic and phenotypic correlation with harvest index followed by oil content, capsule length and number of capsules/plant hence selection for these traits may be effective to increase seed yield (Table 2). The results are in accordance with reports of Sabiel *et al.* (2015), Abhijatha *et al.* (2017), Kindeya *et al.* (2017), Patil and Abate (2018) and Singh *et al.* (2022). The association analysis exhibited that number of capsules per plant, capsule length, harvest index and oil content were the important characters and may be selected to increase the seed yield. Results in the experiment also exhibited that by making selection for a particular trait, simultaneous improvement in the associated trait(s) may be achieved.

The path coefficient result demonstrated that direct selection for the characters like capsule length, number of capsules/plant, days to maturity and harvest index may be carried out as these traits had direct and positive effect on seed yield/plant yield but it had negative correlation based on genotypic level due to indirect negative effect through days to 50% flowering, number of primary branches per plant, plant height, test weight and oil content (Table 3). The trait, days to maturity had direct positive effect on seed yield but it had negative non-significant correlation due to negative indirect effect of days to 50% flowering, number of primary branches, number of capsules/plant and harvest index. Besides this, number of primary branches/plant and test weight had negative direct effect as well as negative correlation with seed yield per plant. The findings seem to correspond with the reports of Ramprasad *et al.* (2019), Bharathi *et al.* (2021) and Sahu *et al.* (2022).

SUMMARY

Twenty eight mutant lines of sesame were evaluated in randomized block design at Agricultural Research Station, Mandor, Jodhpur, Rajasthan, during *kharif*, 2018. ANOVA stated the existence of significant difference for all the characters studied. The percentage contribution towards genetic divergence was found highest for test weight followed by number of capsules/plant and seed yield/plant. Character association study indicated that simultaneous selection for the traits like harvest index, oil content, capsule length and number of capsules and direct selection for protein content, capsules/plant, length of capsule, days to maturity and harvest index will be advantageous for aiding yield improvement. Out of ten independent characters studied in path coefficient three traits, viz. number of capsules/plant, capsule length and harvest index expressed maximum direct as well as indirect contributions through other characters on seed yield. Hence, these characters may be considered as important quantitative traits in sesame improvement programme and direct selection for these traits will be useful.

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