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SELECTION RESPONSE AS ASSESSED THROUGH INTER-GENERATION CORRELATION AND REGRESSION IN SESAME

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ABSTRACT

The correlation and regression coefficient between F_3 means and corresponding parental F_2 values were positive and significant in crosses SVPR1 x TMV3, SVPR 1 x Co 1 and TMV 3 x SVPR 1 at + SD level, in crosses SVPR 1 x TMV 3 and SVPR 1 x Co 1 at - SD level indicated that the selection for single plant yield at these levels should be effective in the respective crosses.

KEY WORDS : Sesame, correlation, regression

Recombination breeding has been recognised a successful method to develop new sesame *sesamum indicum* (L.) varieties. This involves a systematic pedigree selection initiated in the F_2 population which exhibits a wide array of variations among the segregating generations. According to Allard (1960), high mean with high variability for a character in the F_2 population constituted the ideal source for exercising selection. Selection made in F_2 as a single plant yield is insufficient since single plant yield is the result of cumulative effect of both genotype and environment. Selection will be effective if only the performance of F_3 is more dependable on that of F_2 performance. Hence, it is necessary to evaluate as to how far the F_2 values have a bearing on F_3 generation mean and whether such parameter can be relied upon for selection. Its real genetic potentiality can be ascertained only in progeny performances of the individual selection since the mean of the progeny is more reliable estimate than the individual values of the selected plants. One way of ascertaining influence of environment on different characters, is the parent-progeny regression (Lush, 1940). In the present study, the inter generation correlation between F_2 and F_3 mean values and regression of F_3 on F_2 for the three levels of selection namely $\bar{x}$ level, $\bar{x}$+ SD and

$\bar{x}$ - SD level for single plant yield and other unselected traints were discussed.

MATERIALS AND METHODS

The materials for the present study consisted of F_2 and F_3 generations for four cross combinations of sesame *viz.*, SVPR 1 x TNAU 22 (Cross 1), SVPR 1 x TMV 3 (Cross 2), SVPR 1 x Co 1 (Cross 3) and TMV 3 x SVPR 1 (Cross 4). Three hundred F_2 plants per cross per replications were raised in randomised block design with three replications at the Agricultural College and Research Institute, Madurai. From each cross combinations, 30 F_2 plants consisting 10 plants each on $\bar{x}$ level, $\bar{x}$ + SD level and $\bar{x}$ - SD level and seed from each plant were sown for family study. Altogether, 120 families were raised as F_3 generations. Observations were recorded on 75 plants in each cross combination and 20 plants per family per replication in F_2 and F_3 generation respectively. The estimates of parent-progeny regression analysis was calculated (Lush, 1940). The significance of regression co-efficient was tested by using 't' test (Singh and Chaudhary, 1985).

RESULTS AND DISCUSSION

Single plant yield, an important criterion for selection showed significant positive correlation

Table 1. Inter-correlation and regression between F_2 and F_3 generations for three levels of selection

Character	Selection level	Cross 1		Cross 2		Cross 3		Cross 4	
		r	b	r	b	r	b	r	b
Plant	$\bar{x}$	0.9760**	1.1851**	0.9472**	0.9653**	0.9693**	0.9380**	0.8969**	0.8318**
height	$\bar{x}+SD$	0.7838**	1.0086**	0.9258**	0.9872**	0.8893**	0.5594**	0.8601**	0.6823**
	$\bar{x}-SD$	0.9870**	1.0440**	0.9593**	1.0090**	0.9660**	0.9966**	0.9833**	1.0942**
Primary	$\bar{x}$	0.9211**	0.9504**	0.8524**	1.0045**	0.9260**	1.1550**	0.9138**	1.0470**
branch	$\bar{x}+SD$	0.3706	0.4319	0.5234	0.4754	0.6952**	0.5246**	0.6903**	0.7019**
number	$\bar{x}-SD$	0.9473**	0.9029**	0.6927**	0.7188**	0.8833**	0.8802**	0.7777	0.8658**
Secondary	$\bar{x}$	0.7595**	0.7563**	0.5881	0.6336	0.4752	0.4143	0.9528*	0.8556**
branch	$\bar{x}+SD$	0.7767**	0.8303**	0.8872**	0.7011**	0.8068**	0.7679**	-0.1443	-0.2156
number	$\bar{x}-SD$	0.6304	0.6469	0.8919**	1.0294**	0.7958**	0.7687**	0.9561**	1.0138**
Capsule	$\bar{x}$	0.1172	0.1127	0.7841**	1.2588**	0.4865	0.4496	0.9601**	1.1851**
number	$\bar{x}+SD$	0.6927**	0.8527**	0.4593	0.7846**	0.8256**	0.9178**	0.8641**	1.0312**
	$\bar{x}-SD$	-0.1460	-0.0381	0.8547**	1.0617**	0.5173	0.4924	0.6208	1.3059**
Seed	$\bar{x}$	0.9573**	0.9432**	0.9606**	1.0367**	0.8276**	0.9605**	0.9570**	0.7631**
number	$\bar{x}+SD$	0.5228	0.0350**	0.9120**	0.9817**	0.5583	0.8569**	0.9339**	1.0255**
	$\bar{x}-SD$	0.9654**	1.1395**	0.7449**	0.6370*	0.8872**	0.9406**	0.9494**	0.7952**
1000 seed	$\bar{x}$	0.8500**	1.0163**	0.8849**	1.1593**	0.9837**	1.1408**	0.8890**	1.2506**
weight	$\bar{x}+SD$	0.9574**	0.9228**	0.4195	0.2709	0.8855**	1.5653**	0.9447**	0.9678**
	$\bar{x}-SD$	0.9731**	1.0849**	0.8936**	0.8651**	0.7511*	0.7873**	0.9662**	1.0040**
Oil	$\bar{x}$	0.7589**	0.7405**	0.9148**	0.9263**	0.8705**	0.8162**	0.8759**	0.8981**
content	$\bar{x}+SD$	0.9346**	1.0348**	0.9153**	0.7397**	0.8019**	0.8453**	0.9397**	0.9833**
	$\bar{x}-SD$	0.9701**	1.1142**	0.8403**	0.9753**	0.9856**	0.9585**	0.8986**	0.9029**
Plant	$\bar{x}$	-0.2278	-0.1256	0.4526	0.5887**	-0.2979	-0.1762	0.2840	0.1695
yield	$\bar{x}+SD$	0.3707	0.3767	0.7826**	0.9351**	0.7670**	0.7635**	0.9443**	0.5376**
	$\bar{x}-SD$	0.2145	0.1252	0.7974**	0.4208	0.9077**	0.7071**	-0.3624	-0.3713

Cross 1 = SVPR 1 x TNAU 22 ; Cross 2 = SVPR 1 x TMV 3 ; Cross 3 = SVPR 1 x Co 1 ; Cross 4 = TMV 3 x SVPR 1
** Significant at 1% level ; * Significant at 5% level

4 for $\bar{x}+$ SD level and in the crosses 2 and 3 for $\bar{x}-$ SD level. Among the levels, $\bar{x}+$ SD level was the best for selection rather than $\bar{x} -$ SD level and $\bar{x}$ level, since cross 4 had negative non-significant correlation and regression at $\bar{x} -$ SD level (Table 1).

A non-significant positive correlation and regression was observed for cross 1 at $\bar{x}+$ SD level and $\bar{x}-$ SD levels, for crosses 2 and 4 at $\bar{x}$ indicating equal chances of selecting high yielding genotypes at these levels. Such positive correlation and regression between F_2 and F_3 generation at more than one level of selection indicates that it is possible to exercise selection effectively in a wide population. Similar results were also reported by wilfred Manuel *et al.* (1977) for three levels of selection in F_2 to F_4 generation in rice.

The parent progeny regression was non-significant and negative for crosses 1 and 3 at $\bar{x}$ level and cross 4 at $\bar{x}-$ SD level. It may be due to the fact that the single plants in heterogenous F_2 population were unable to express their potentiality due to competition by genetically different neighbours. In such crosses rejection in F_2 based on yield should not be resorted to perhaps in addition to single plant yield, plant type and other traits have to be included for advancing the single plants.

In the unselected characters at $\bar{x}+$ SD level, significant positive correlation and regression were recorded in all crosses for plant height and oil content, in crosses 3 and 4 for primary branch number and crosses 1, 3 and 4 for capsule number and 1000 seed weight. However, at $\bar{x}$ level of selection showed significant positive correlation and regression in all crosses for plant height, primary branch number, seed number, 1000 seed weight and oil content, in crosses 2 and 4 capsule number and crosses 1, 3 and 4 for secondary branch number. At the $\bar{x} -$ SD level of selection significant correlation and regression in all crosses for plant height, primary branch number, seed number, 1000 seed weight and oil content, in crosses 2 and 4 for capsule number and crosses 1, 3 and 4 for secondary branch number. At the $\bar{x}-$ SD level of selection significant correlation and regression was observed in all crosses for plant height, prima

branch number, seed number, 1000 seed weight and oil content, in cross 2 for capsule number and in crosses 2, 3 and 4 for secondary branch number. These results indicated that selection would be more effective, when exercised at these levels for the respective traits.

However, the observed inter-generation correlation adn regression were negative in cross 4 for secondary branches at $\bar{x}$ + SD level, in cross 1 at $\bar{x}$ - SD level for capsule number and in crosses 1 and 3 for single plant yield at level. This indicated that F_2 performance was not an indicator of better F_3 performance possibly due to non-additive gene action or environmental influence (Meredith and Bridge. 1973).

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GENETIC DIVERGENCE IN CHICKPEA

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ABSTRACT

Fifty genotypes of chickpea (*Cicer arietinum* L.) were grouped into 11 clusters using Mahalanobis's D^2 statistic. Maximum distance was observed between the cluster VIII and XI. Plant height, number of secondary branches/plant, seeds/plant, 100 seed weight and seed yield/plant had shown more divergence among the clusters.

KEY WORDS : Chickpea, genetic divergence

Study of genetic diversity helps in selection of diverse parents for their use in hybridisation, as heterosis is known to depend on the extent of genetic diversity between parents. Mahalanobis's generalized distance (D^2) is used in the present investigation to ascertain the magnitude of genetic divergence and group the 50 varieties of chickpea.

MATERIALS AND METHODS

Fifty genotypes of chickpea (*Cicer arietinum* L.) were grown in randomised block design with three replications, during *rabi*, 1993-94. Each genotype was grown in two rows of 3 m length with inter and intra row spacings of 30 and 10 cm, respectively. Observations were recorded on five random competitive plants for the characters : plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of seeds per pod, number of seeds per plant, 100 seed weight (g) and seed yield per plant (g). Genetic divergence was studied using Mahalanobis's D^2 statistics as described by Rao (1952).

RESULTS AND DISCUSSION

Analysis of variance indicated highly significant differences among the genotypes for all the characters under study indicating the existence of a considerable variability among the genotypes.

The D^2 values between pairs of genotypes ranged from 10.7 (intracluster D^2 of IV) to 250.86 (pair VIII & XI). The group constellations were obtained on the basis of D^2 values using the method suggested by Rao (1952). Fifty genotypes were grouped into 11 clusters of which cluster I is the largest having 28 genotypes followed by 4 each in the clusters II, III, IV and V and remaining 6 clusters had only one genotype each (Table 1).