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Inheritance of seed size in chickpea*

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ABSTRACT

Inheritance of seed size in chickpea (*Cicer arietinum*) was studied in two desi × desi crosses, ICCV 10 × ICC 4958 and ICCV 10 × K 850, using generation means of parents, F_1 , F_2 and both the backcrosses. Small-seed size was partially dominant over large-seed size. Generation means analysis showed that the major contribution to genetic variation in these crosses came from additive gene effects, indicating that selection for seed size in early generations should be effective. However, non-additive gene action (dominance and additive × dominance interaction) also affected to a small extent the expression of this character. The estimates of narrow-sense heritability and the expected genetic gain were high. The minimum number of effective factors controlling the seed size varied from 1.33 to 2.19.

Key words: *Cicer arietinum*, Generation means, Genetic gain, Selection.
Abbreviations: KER.

INTRODUCTION

Chickpea (*Cicer aretinum* L.) is an important legume crop throughout the semi-arid regions of the world. There are two distinct types of chickpea: small-seeded desi and large-seeded kabuli. A great amount of genetic variability exists for seed size within each type, some desi types being as large as kabulis, and some kabuli types as small as desis. Seed size is not only one of the most important yield components (SINGH and PARODA, 1986) but also an important criterion for consumer preference (SINGH, 1987). It has also been considered an important factor in germination, seedling vigour, seedling mass, and subsequent plant growth (NARAYANAN *et al.*, 1981; DAHIYA *et al.*, 1985). Therefore, improvement in seed size is an important goal in chickpea breeding programmes. This in turn requires a better understanding of the inheritance pattern and types of gene action governing seed size. Earlier studies involving desi x kabuli crosses showed that small-seed size was dominant over large-seed size in chickpea (ATHWAL and SANDHA, 1967; SMITHSON *et al.*, 1985). NIKNEJAD *et al.* (1971), however, found the reverse to be true. Heritability estimates for seed size were reported to be low (23 to 27%) by SANDHA and CHANDRA (1969) and high (81%) by NIKNEJAD *et al.* (1971). Inheritance of seed size in chickpea was reported to be monogenic (ARGIKAR, 1956), oligogenic (BALASUBRAHMANYAN, 1950; PATIL and D'CRUZE, 1964), and polygenic (ATHWAL and SANDHA, 1967; NIKNEJAD *et al.*, 1971). Further and more definitive studies are therefore required on the genetic nature of seed size in chickpea. In all the reports mentioned above, desi × kabuli crosses were studied. Therefore, we studied the inheritance of seed size involving desi × desi crosses.

MATERIALS AND METHODS

Three desi genotypes were chosen for this study. ICCV 10 has small seeds with a seed mass of 16 g per 100 seeds. The other two genotypes, ICC 4958 (JGC1) and K 850, have large seeds which average 34 g and 32 g per 100 seeds, respectively. ICCV 10 was crossed with ICC 4958 and K 850. The resulting F_1s were self-pollinated and also backcrossed to both parents to obtain F_2 and backcross (B_1 and B_2) generations. Parents (P_1 and P_2), F_1, F_2, and backcross ($F_1 \times P_1$ and $F_1 \times P_2$) generations of the two crosses were evaluated in a randomized complete block design with three replications at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India, in the 1991-92 postrainy season. Plot size varied with the

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generations. Parents and F_1 generations were grown in 2-row plots, F_2s in 10-row plots, and backcrosses in 3- or 4-row plots, depending on the availability of seeds. The rows were 2 m long and 60 cm apart, with plants spaced at 20 cm within a row. Plants were protected from the *Helicoverpa* pod borer by spraying insecticides as and when needed. Standard cultural practices were followed during the crop season. At maturity, a random sample of 100 seeds was taken from each plant. The 100-seed weight was chosen as a measure of seed size.

Analysis of variance was used to determine whether differences existed among generations for seed size. Generation means were then subjected to the weighted generation means analysis as described by MATHER and JINKS (1982) to estimate different genetic parameters such as mean [m], additive [d], dominance [h], additive × additive [i], additive × dominance [j], and dominance × dominance [l] effects. The weights used in the analysis were the reciprocals of the squared standard errors of each generation mean. The adequacy of the simple additive-dominance model was determined by both individual and joint scaling tests (CAVALLI, 1952). When the simple additive-dominance model proved inadequate, a 6-parameter model was fitted. As suggested by MATHER and JINKS (1977), any genetic effect not significantly different from zero (t test, $P > 0.05$) was eliminated from this model, and the remaining components were estimated again. A chi-square test was also performed on this reduced model to test whether first order (two-loci) epistatic effects adequately accounted for the differences among generation means. The t test was performed to test the significance of different genetic effects. The sequential sums of squares from the reduced model were used to calculate the percentage of variability which could be attributed to additive, dominance, and epistatic effects.

Different components of variance were estimated using population variances. Narrow-sense heritability, $h^2(ns)$, was estimated following Warner's method (1952), and the standard error of heritability estimate was calculated as described by KETALA *et al.* (1976). Expected gain from selection was calculated following ALLARD (1960). The minimum number of effective (segregating) factors controlling seed size was estimated following WRIGHT (1921) and LANDE (1981).

RESULTS AND DISCUSSION

Analysis of variance indicated highly significant differences in seed size among generations of both crosses. An examination of means (Table 1) showed that seed size of ICCV 10 was significantly smaller that that of ICC 4958 and K 850. The seed size of F_1 and F_2 generations of each cross was lower than the mid-parent value, suggesting partial dominance of alleles for small seed-size. All the backcrosses, however, tended to be intermediate between the F_1 and their respective parents. The F_2 generations of both crosses did not segregate into discrete classes of seed size; the frequency distribution of 100-seed mass in F_2 populations of each cross (Figs. 1 and 2) was continuous with no distinct modes. This suggests polygenic inheritance for seed size in chickpea.

The significant chi-square values for the regression residual in the joint scaling (Table 2) and individual scaling tests (A and C) indicated that a simple additive-dominance model was not sufficient to explain the total genetic variability for seed size in the two crosses. The lack of fit of the model indicated the presence of non-allel interactions. The 4-parameter model, which included additive × dominance interaction [j] in addition to [m], [d] and [h], was found adequate to explain the total genetic variation in the ICCV 10 × ICC 4958 cross ($P = 0.69$). However, in the ICCV 10 × K 850 cross, this model did not fit perfectly. Similar models which included one or more of the non-allelic interactions were also tested for this cross, but none was found adequate. This revealed the presence of higher order interactions and/or linkage in this cross. BALASUBRAHMANYAN (1950) and ATHWAL and SANDHA (1967) also found non-allelic interaction in the inheritance of seed size in chickpea.

TABLE 1

Population size (n), mean, variance (σ^2), and range for 100-seed mass (g) in different generations of two chickpea crosses

Generation	ICCV 10 × ICC 4958				ICCV 10 × K 850			
	n	Mean ± S.E.	σ^2	Range	n	Mean ± S.E.	σ^2	Range
P_1	30	16.83 ± 0.19	1.02	15.10 − 18.10	30	16.85 ± 0.19	1.03	15.10 − 18.10
P_2	35	34.18 ± 0.24	1.97	31.40 − 38.30	30	31.99 ± 0.30	2.61	29.80 − 34.60
F_1	35	23.44 ± 0.29	2.96	21.30 − 26.10	42	20.65 ± 0.20	1.63	18.60 − 22.20
F_2	218	24.40 ± 0.35	26.92	14.20 − 38.04	203	23.43 ± 0.36	25.89	13.20 − 35.90
B_1	78	21.50 ± 0.43	14.44	15.80 − 31.20	83	19.40 ± 0.28	6.46	13.90 − 29.70
B_2	71	28.07 ± 0.56	22.20	18.50 − 39.30	90	25.01 ± 0.58	30.05	17.10 − 34.70
Mid-parent value		25.51				24.42		

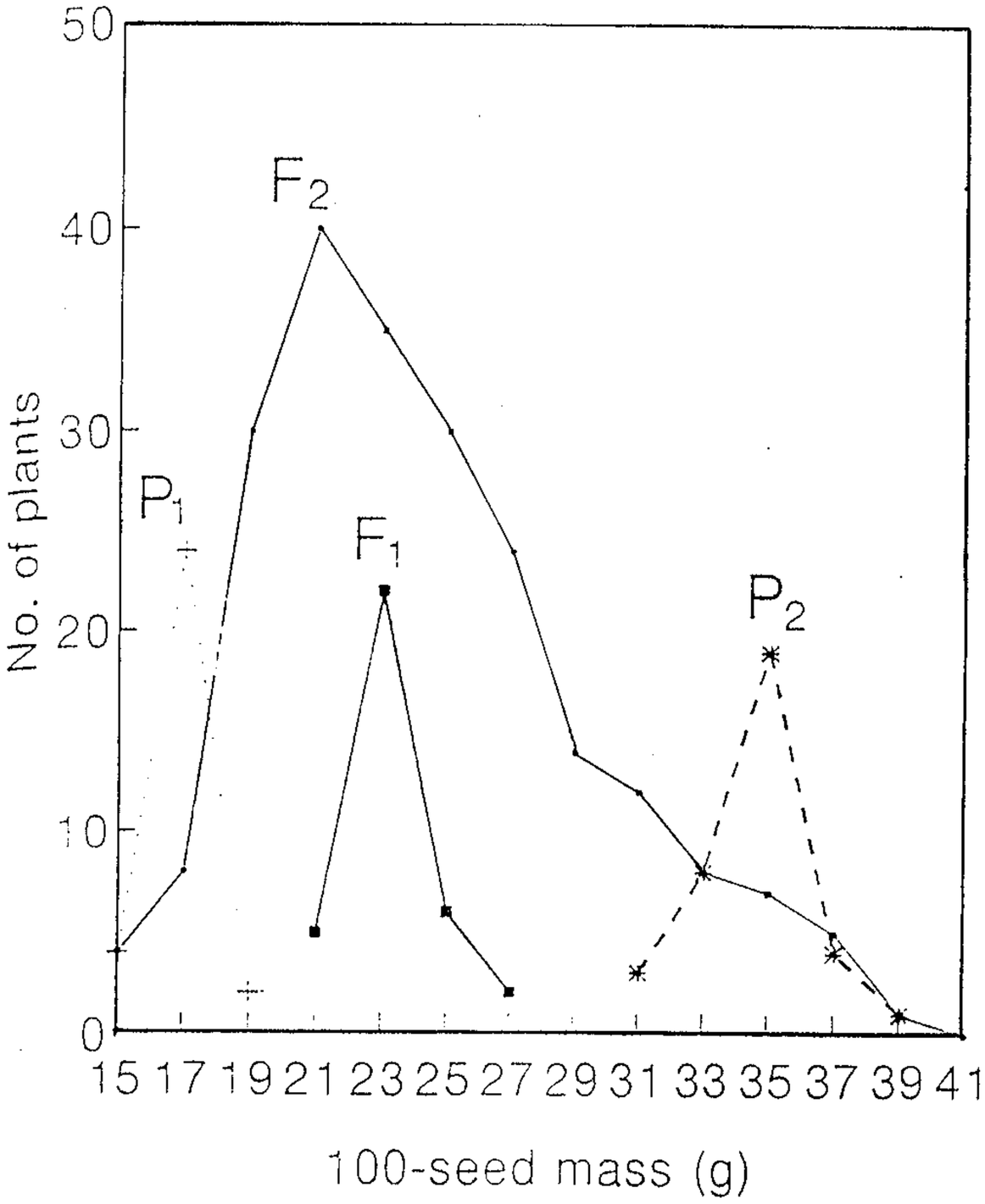

FIGURE 1 - Frequency distributions of seed size for parental, F_1 and F_2 populations of ICCV 10 (P_1) × ICC 4958 (P_2).

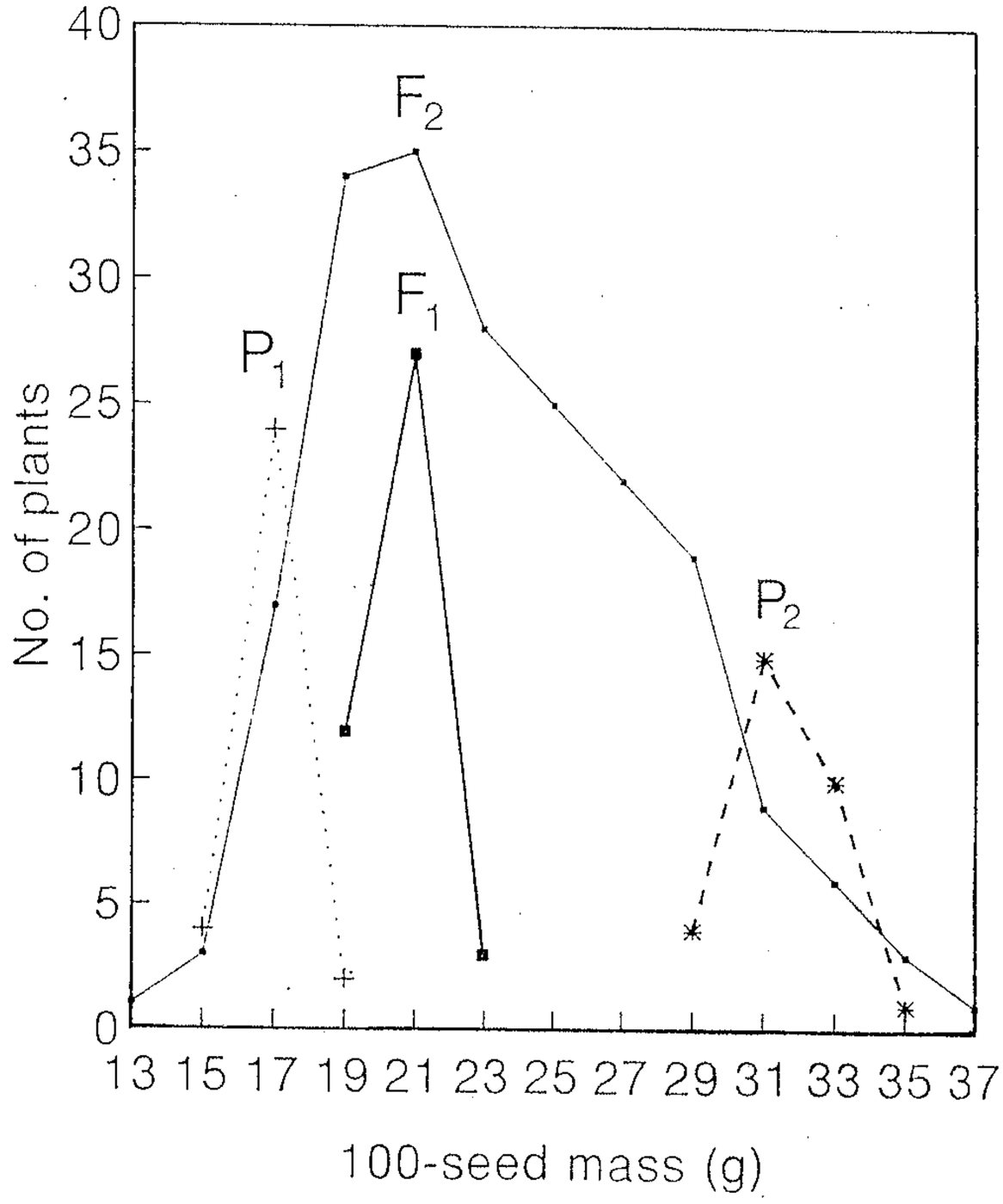

FIGURE 2 - Frequency distributions of seed size parental, F_1 and F_2 populations of ICCV 10 (P_1) × K 850 (P_2).

Additive gene effects [d] were highly significant, whereas dominance gene effects [h] were significant but low in magnitude relative to [d], indicating the preponderance of additive gene effect in the inheritance of the trait. Dominance effects were negative, suggesting a net dominance for small seed size. Additive × additive [i] and dominance × dominance [l] interaction effects were non-significant in both crosses. The positive and significant additive × dominance [j] interaction

TABLE 2

Estimates of genetic effects for 100-seed mass (g) in two crosses of chickpea

Cross	Genetic parameter	Simple additive-dominance model	Six-parameter model	Reduced model	% Genotype S.S.
ICCV 10 × ICC 4958	m	25.52** ± 0.15	23.94** ± 2.00	25.52** ± 0.15	
	d	8.58** ± 0.15	8.67** ± 0.15	8.68** ± 0.15	98.5
	h	−1.94** ± 0.31	2.32 ± 5.11	−2.02** ± 0.31	1.1
	i	—	1.56 ± 1.99	—	—
	j	—	4.20** ± 1.44	4.49** ± 1.40	0.3
	l	—	−2.82 ± 3.22	—	—
	χ^2 cal	11.061*		0.77	
ICCV 10 × K 850	m	24.48** ± 0.17	29.32** ± 1.93	24.46** ± 0.17	
	d	7.46** ± 0.17	7.57** ± 0.17	7.59** ± 0.17	89.5
	h	−3.66** ± 0.26	14.90** ± 4.83	−3.75** ± 0.26	9.8
	i	—	−4.90 ± 1.92	—	—
	j	—	3.91** ± 1.33	3.00** ± 1.08	0.4
	l	—	−6.33 ± 2.98	—	—
	χ^2 cal	14.87**		7.136*	

*, ** Significant at 5% and 1% levels of probability.

TABLE 3

Estimates of variance components, heritability, and minimum number of effective factors (N) for 100-seed mass (g) in two crosses of chickpea

Estimates	Formula	ICCV 10 × ICC 4958	ICCV 10 × K 850
Genetic Variance (V_G)	$V_{F2} - V_E$	24.694	24.163
Additive variance (V_A)	$2V_{F2} - V_{BC1} - V_{BC2}$	17.208	15.265
Dominance variance (V_D)	$V_{BC1} + V_{BC2} - V_{F2} - V_E$	7.486	8.898
Environmental variance (V_E)	$0.25V_{P1} + 0.25V_{P2} + 0.5V_{F1}$	2.229	1.727
Heritability (ns)	V_A / V_{F2}	0.639 ± 0.044	0.590 ± 0.051
Expected genetic gain	$K \cdot \sigma_p \cdot h^2$ (n.s.)	6.83	6.18
Minimum number of effective factors			
Lande (1981)	$D^2/8V_A$	2.19	1.88
Wright (1921)	$[0.25(0.75 - h + h^2)D^2]/(V_{F2} - V_{F1})$	1.62	1.33

V_{P1}, V_{P2}, V_{F1}, V_{F2}, V_{BC1}, and V_{BC2} represent the variances of parents, F_1, F_2 and backcross to P_1 and P_2, respectively; K = selection differential; σ_p = phenotypic standard deviation; $D = (P_1 - P_2)$; $h = (F_1 - P_1)/D$.

effect indicated that genes with positive effects showed overall dominance.

Genetic variance cannot be partitioned precisely into additive and dominance components in the presence of epistasis. Therefore, relative contributions of [d], [h], and [j] to the total genetic variation were calculated by using sequential sums of squares (Table 2). In the ICCV 10 × ICC 4958 cross, the additive gene effects accounted for a major proportion (98.5%) of the total sum of squares. Dominance and additive × dominance effects were small. In the ICCV 10 × K 850 cross, 89.5% of the total genetic variation among generations was due to additive gene action. Non-additive (dominance and epistasis) effects accounted for only a small proportion of the total sum of squares. This suggested that most of the observed variation could be explained by simple additive and dominance effects and that variance components, heritability, and genetic advance could reliably be estimated. The estimates of additive (V_A) and dominance (V_D) variances were significant and V_A was larger than V_D in both crosses (Table 3). Estimates of heritability and genetic advance enable breeders to predict the genetic gain under selection. Narrow-sense heritability was high (0.59 ± 0.051 to 0.64 ± 0.04) for this trait. This is in agreement with an earlier report of NIKNEJAD *et al.* (1971). Therefore, good progress in improving the seed size in the segregating populations can be expected through conventional methods of breeding and selection based on additive genetic variance. The expected genetic gain (Table 3) shows the possible gain from selection as percent increase in the F_3 over the F_2 mean when the most desirable 5% ($K = 2.06$) of the F_2 plants are selected. Estimates of both heritability and genetic advance show that selection in the F_2 would lead to a substantial improvement in seed size.

With the assumption of no dominance, no linkage and no epistasis, it is possible to estimate the minimum number of effective factors involved in the inheritance using population variances. The estimates of the minimum number of effective factors controlling seed size in chickpea ranged to 1.33 to 2.19 (Table 3). These estimates are, however, most likely biased downward by epistatic effects. The first formula is less affected by the presence of dominance and likely to provide more reliable estimates of the minimum number of effective factors.

A preponderance of additive effects coupled with high heritability and genetic advance obtained in this study for seed size indicate that selection for seed size should be highly effective. Since selection for seed size was reported to be the best method for improving seed yield in chickpea (BISEN *et al.*, 1985; KUMAR and BAHL, 1992), indirect selection for yield via seed size would also be very effective.

REFERENCES

ALLARD, R.W., 1960. Principles of plant breeding. John Wiley & Sons, New York.

ARGIKAR, G.P., 1956. Some qualitative and quantitative observation on the genetic improvement of green seeded strains of *Cicer arietinum*. *Indian J. Genet.*, **16:** 52-56.

ATHWAL, D.S. and SANDHA, G.S., 1967. Inheritance of seed size and seed number per pod in *Cicer*. *Indian J. Genet.*, **27:** 21-33.

BALASUBRAHMANYAN, R., 1950. Association of seed size and colour in gram. *Curr. Sci.*, **19:** 246-247.

BISEN, M.S., SINGH, S.P. and RAO, S.K., 1985. Selection gains in chickpea. *Egypt J. of Genet. and Cytol.*, **1:** 51-58.

CAVALLI, L.L., 1952. An analysis of linkage in quantitative inheritance. In: E.C.R. REEVE, and C.H. WADDINGTON eds., Qualitative Genetics, HMSO, London, pp. 135-144.

DAHIYA, B.S., SOLANKI, I.S. and KUMAR, R., 1985. Germination rate and its genetics in chickpea. *International Chickpea Newletters*, **13:** 6-8.

KETALA, H., EDWARDS, L.H. and SMITH, E.L., 1976. Inheritance of eight agronomic characters in a winter wheat cross. *Crop. Sci.*, **16:** 19-22.

KUMAR, J. and BAHL, P.N., 1992. Direct and indirect selection for yield in chickpea. *Euphytica*, **60:** 197-199.

LANDE, R., 1981. The minimum number of genes contributing to quantitative variation between and within populations. *Genetics*, **99:** 541-553.

MATHER, K. and JINKS, J.L., 1977. Introduction to biometrical genetics. Cornell University Press, Ithaca, NY.

MATHER, K. and JINKS, J.L., 1982. Biometrical genetics. Chapman and Hall, London.

NARAYANAN, A., SAXENA, N.P. and SHELDRAKE, A.R., 1981. Varietal differences in seed size and seedling growth of pigeon pea and chickpea. *Indian J. Agric. Sci.*, **51:** 289-393.

NIKNEJAD, M., KHOSH-KHUI, M. and GHORASHY, S.R., 1971. Inheritance of seed size in chickpea (*Cicer arietinum*). *Crop. Sci.*, **11:** 768-769.

PATIL, J.A. and D'CRUZE, R., 1964. Inheritance of seed size in gram (*Cicer arietinum*). *Poona Agric. Coll. Mag.*, **54:** 21-22.

SANDHA, G.S. and CHANDRA, S., 1969. Heritability of some quantitative characters in two crosses of bengalgram. *Indian J. Genet.*, **29:** 216-219.

SINGH, K.B., 1987. Chickpea Breeding. In: M.C. SAXENA and K.B. SINGH eds., *The chickpea,* CAB International, Wallingford, pp. 127-162.

SINGH, O. and PARODA, R.S., 1986. Association analysis of grain yield and its components in chickpea following hybridization and a combination of hybridization and mutagenesis. *Indian J. Agric. Sci.*, **56:** 139-141.

SMITHSON, J.B., THOMPSON, J.A. and SUMMERFIELD, R.J., 1985. Chickpea (*Cicer arietinum*). In: R.J. SUMMERFIELD and E.H. ROBERTS eds., *Grain Legumes Crops*, Collins, London, pp. 312-390.

WARNER, J.N., 1952. A method for estimating heritability. *Agron. J.*, **44:** 427-430.

WRIGHT, S., 1921. System of mating. *Genetics*, **6:** 111-178.