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Relative efficiency of different breeding methods for improvement of yield and yield components in chickpea (*Cicer arietinum* L.)

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ABSTRACT

Four breeding methods for generation advancement were evaluated for their efficiency in producing superior genotypes in chickpea. The methods used were pedigree method (PM), single seed descent method (SSD), bulk method (BM) and selected bulk method (SBM) in five crosses. On the basis of per cent increase in highest yielder genotypes over best check mean, SBM produced higher value mean seed yield and its components than PM, SSD and BM over crosses, except in cross (C_3: JG-62 x BG-1073). PM and BM showed equal yield superiority on the basis of per cent increase in mean of selected plants. Estimates of phenotypic variances for seed yield and its components in F_4 showed that SSD method was superior to other methods in maintaining relatively high variances over crosses. Further, seed yield/plant had high positive correlation with harvest index and 100-seed weight under pedigree method (PM) and selected bulk method (SBM) and with harvest index and seeds/pod under single seed descent method (SSD). Thus, these traits could be considered as a selection criteria for higher seed yield/plant in chickpea under each of selection methods. It was concluded that SBM was a preferable method for improvement of yielding ability in chickpea and thus, recommended for chickpea breeding.

Key words: Bulk Method, Chickpea, Pedigree Method, Selected Bulk Method, Single Seed Descent Method

Plant breeders are continuously searching for more effective methods of selection in early breeding generations to obtain superior genotypes from a population with a minimum input of labour and time. Improvement of productivity could be a basic objective of crop improvement programmes conducted by plant breeders. To achieve this goal, the breeders choose breeding methods which facilitate the simultaneous improvement of yield and components traits. The aim of hybridization is to combine desirable genes in single genotypes that are present in two or more genotypes. Breeding methodology employed in self-pollinated crops has, therefore, centred on crossing strains and growing segregating population to homozygosity. Efficient breeding methods are needed to advance segregating populations and to expedite selection of lines with desirable combinations of characters. Pedigree method, bulk method, and single seed descent method are commonly used to manage segregating populations of self-pollinated crops. Breeders of self-pollinated crops usually apply the pedigree method of selection to handle segregating populations. A long felt disadvantage of this method is the limitation it imposes on the number of crosses a breeder can handle. The bulk method was developed to avoid the book keeping (free from pedigree record) required by pedigree method and consists of harvesting all plants in bulk every generation and planting a random sample of seed to propagate the next generation. To minimize the defects of the bulk method and also to reduce the generations, Goulden (1941) proposed the single seed descent method which was later on modified by Grafius (1965) and Brim (1966). This method consists of advancing segregating populations by taking a single seed from each plant to grow the next generation. The population size does not increase with successive generations but there are chances of losing some good genotypes and they cannot be recovered again. In selected bulk method, seed from each of the F_2 to F_5 generation is not bulked, but plants are selected in each generation right from F_2. Seed from only these selected plants is bulked (but no pedigree are maintained) to raise the next generation, rather than raising the generation from a random sample of bulk seed of all plants without any selection. In this manner, constitution of bulked populations is improved by having the progenies of only selected plants. However, which classical method of breeding is most efficient in terms of rate of genetic gain per generation or per unit time still remains unanswered. Therefore, the objective of this study is to compare different breeding methods in terms of isolation of promising genotypes for increasing the yield.

MATERIALS AND METHODS

The present investigation was carried out at the Division of Genetics, Indian Agricultural Research Institute, New Delhi under field conditions during the years 2006-07 to 2008-09. The New Delhi has a sub-tropical semi-arid climate with dry summer and cold winter. The soil is loam to sandy loam. Five crosses and four checks (Pusa 1103, Pusa 362, Pusa 372 and Pusa 1088) of chickpea, involving 8 parents were used in this study. The crosses attempted were: cross 1 (SBD 377 x BG 1103); cross 2 (BG 362 x JG 62); cross 3 (JG 62 x BG 1073); cross 4 (BG 372 x CSG 9505) and cross 5 (BG 362 x BG 1088). These five crosses were selected on the basis of genetic diversity in parents and phenotypic variability in F_2 populations. The plan of generation advancement by these breeding procedures is depicted in Fig. 1. During *Rabi* 2006-07, 500 plants of F_2 generation in each cross were space planted and four selection methods *viz.*, pedigree method (PM), bulk method (BM), selected bulk method (SBM) and single seed descent method (SSD) were performed as follows:

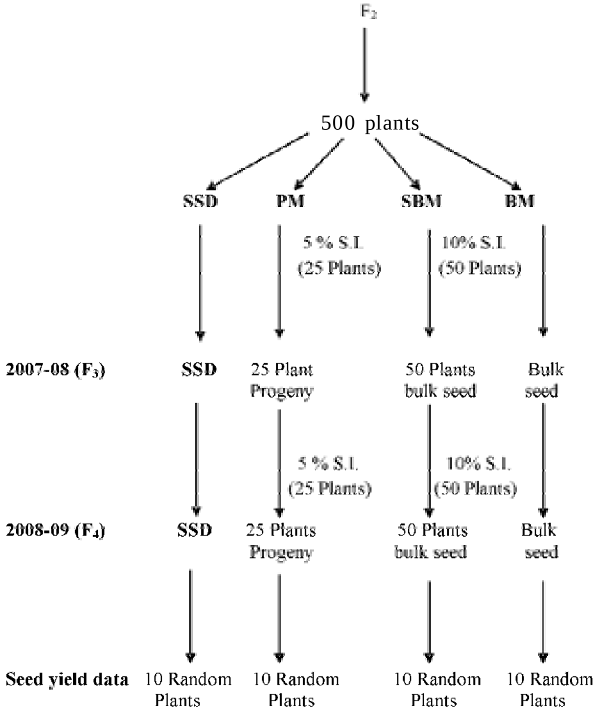

Fig 1. Outlines of generation advancement of each cross for different breeding methods

Pedigree selection method (PM): Out of 500 plants grown in F_2 generation, 25 best plants were selected by exercising 5% selection intensity. 25 plant progenies were grown in F_3 generation in rows having 20 plants each. Again 5% selection intensity was exercised by selecting best 5 families followed by best 5 plants from each progeny. Thus, total of 25 plants were selected from 500 plants. In F_4, 25 plant progenies were again grown in single row of 20 plants each. At maturity, randomly 10 single plants were selected and data were recorded on yield and yield related traits.

Bulk method (BM): The F_3 generation was advanced by bulking the seeds of all plants and a sample was drawn to grow F_4 generation. In F_4 generation, the 10 random single plants were harvested for recording data.

Selected bulk method (SBM): Individual plants in F_2 population were visually scored on the basis of their agronomic suitability as is normally done in pedigree method of selection. Promising plants were marked. Finally 10 % promising plants of the F_2 population in each cross were selected. The seeds of these plants were composited to form the bulk. A random sample of 500 seeds was then extracted to produce the bulk for the next generation. In F_3 generation, the same procedure was followed. In F_4 generation, 10 random single plants were harvested for recording data.

Single seed descent method (SSD): The method followed was exactly similar to single seed descent method of Grafius (1965) and Brim (1966). Single seed from each F_2 plant was collected at maturity and similar procedure was followed in F_3 generation. In F_4 generation, 10 random plants were harvested for recording data.

Statistical design and field observation: The experiment was conducted in a randomized block design (RBD) with three replications. One plot comprised of 4 rows with 30 cm row to row and 10 cm plant to plant distances. In F_4 generation, at harvest time, ten plants were taken randomly from each plot of the 3 replications and observations were recorded for seed yield/plant (SY) (g), biological yield/plant (BY) (g), plant height (PH) (cm), total branches/plant (TB), pods/plant (PP), seeds/pod (SP), 100-seed weight (SW) (g), and harvest index (HI) (%). The mean of selected plants were estimated for comparison of means for each population. The phenotypic variance was estimated on the basis of single plant data.

Criteria for testing efficiency of breeding methods: The efficiency of breeding methods was judged in two ways. First by the per cent increase in yield of the highest yielding plants over mean of the best check and secondly, per cent increase in mean of selected plants over mean of the best check.

RESULTS AND DISCUSSION

The four breeding methods *viz.*, pedigree method (PM), bulk method (BM), selected bulk method (SBM) and single seed descent (SSD) were applied to populations derived from five crosses from F_2 to F_4 generations and effectiveness of these methods was evaluated in terms of relative means across the crosses. The means and ranges for eight agronomic characters in five F_4 populations advanced by pedigree method, bulk method, selected bulk method and single seed descent method are given in Table 1 and 2.

Based on F_4 means, it was observed that pedigree method (PM) and bulk method (BM) were more effective in increasing population means followed by selected bulk method (SBM) (Table 1). For increasing the generation means for seeds/pod, PM and BM breeding methods were found more effective than SBM and SSD method. In respect of seed weight, it was possible to increase generation means by SSD and BM method. A critical of generation means in F_4 for pods/plant revealed that PM and BM both were equally effective than SBM and SSD methods. In contrast to this, total branches/plant showed highest population means by BM, SBM and PM as compared to SSD method. This evidently indicates that pods/plant, seeds/pod and seed yield are responding to BM and PM for upgrading the population mean.

The lower and higher limits of range for seed yield/plant varied considerably in all the populations advanced by the four methods (Table 2). The populations from SBM method were found to be wider in ranges than those from

Table 1. Range and mean for eight agronomic characters in selected F_4 populations of chickpea

Breeding methods	Cross	SY (g)		BY (g)		PH (cm)		TB		P/P		S/P		SW (g)		HI (%)	
		Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean
PM	C_1	52.3-35.5	40.3	110.0-80.0	92.5	73.0-68.0	69.7	68.0-53.0	57.8	107.0-79.0	87.0	1.6-1.4	1.5	32.5-22.5	28.5	47.5-40.5	54.1
	C_2	38.5-29.5	33.3	100.0-75.0	84.5	68.0-60.0	63.7	68.0-52.0	57.7	130.0-70.0	89.3	2.0-1.6	1.8	27.5-20.0	23.0	41.9-37.3	39.4
	C_3	25.5-20.0	22.5	70.0-60.0	66.5	65.0-59.0	62.0	63.0-40.0	46.3	75.0-53.0	62.9	1.8-1.6	1.6	25.0-18.5	21.6	36.4-31.2	33.8
	C_4	42.5-30.5	35.8	140.0-70.0	93.5	68.0-66.0	66.9	98.0-50.0	62.8	102.0-63.0	79.7	2.0-1.6	1.7	32.5-22.5	26.8	45.0-30.4	39.3
	C_5	40.6-32.8	37.2	100.0-75.0	86.0	63.0-58.0	59.9	65.0-50.0	56.1	74.0-65.0	67.8	2.0-1.8	1.9	32.5-25.0	28.3	44.8-40.6	43.3
SSD	C_1	34.0-17.0	25.5	90.0-50.0	63.0	73.0-62.0	66.3	55.0-29.0	43.8	74.0-52.0	60.8	1.6-1.4	1.6	35.0-25.5	31.7	46.3-34.0	44.6
	C_2	48.0-13.6	29.0	120.0-60.0	80.2	77.0-58.0	66.8	80.0-34.0	55.9	95.0-42.0	65.6	1.6-1.2	1.4	32.5-22.5	27.3	45.6-21.4	35.0
	C_3	19.2-10.0	14.2	55.0-25.0	42.9	62.0-43.0	51.7	40.0-22.0	30.5	68.0-25.0	44.3	2.0-1.4	1.5	30.0-18.0	24.7	76.8-23.2	35.7
	C_4	52.2-16.8	27.6	140.0-50.0	86.5	75.0-62.0	68.1	65.0-28.0	46.7	130.0-48.0	80.9	1.6-1.4	1.5	27.5-22.5	25.0	37.4-24.2	32.0
	C_5	36.7-13.8	21.4	88.0-50.0	64.2	73.0-49.0	59.4	52.0-28.0	40.1	83.0-50.0	63.8	1.6-1.2	1.3	30.0-20.0	24.5	41.7-27.6	32.9
BM	C_1	46.8-26.7	35.4	130.0-70.0	88.0	72.0-64.0	68.3	76.0-50.0	57.7	130.0-62.0	79.6	1.4-1.2	1.3	32.5-27.5	29.7	48.0-36.0	40.4
	C_2	46.5-28.3	34.0	110.0-70.0	88.0	78.0-68.0	72.2	84.0-58.0	68.8	106.0-66.0	81.2	1.6-1.4	1.6	27.5-25.0	26.3	45.0-31.6	38.7
	C_3	52.8-26.8	41.3	125.0-75.0	90.0	64.0-58.0	61.0	76.0-49.0	59.2	136.0-70.0	98.5	1.6-1.4	1.5	25.0-22.0	23.5	53.2-34.4	45.6
	C_4	42.5-27.3	33.9	110.0-25.0	64.5	64.0-58.0	61.2	83.0-50.0	62.3	144.0-59.0	82.2	2.0-1.8	1.7	27.5-22.5	25.0	32.0-28.6	61.3
	C_5	51.2-25.7	34.9	125.0-55.0	75.5	58.0-50.0	53.3	87.0-45.0	59.3	156.0-50.0	78.3	2.0-1.8	1.9	32.5-25.0	27.5	52.0-41.0	46.5
SBM	C_1	53.4-22.5	35.4	130.0-60.0	84.2	74.0-67.0	69.9	64.0-45.0	53.4	110.0-50.0	66.5	1.8-1.6	1.6	32.5-27.5	28.3	49.2-37.5	42.1
	C_2	53.3-22.4	33.6	125.0-75.0	96.0	74.0-67.0	70.3	66.0-45.0	53.4	85.0-54.0	66.3	1.8-1.6	1.6	27.5-25.0	26.3	42.8-29.6	34.7
	C_3	46.0-29.6	34.6	100.0-75.0	82.0	68.0-58.0	62.3	60.0-50.0	54.8	98.0-64.0	73.0	2.4-1.2	1.4	25.0-22.5	23.0	46.0-38.9	42.1
	C_4	53.2-25.5	32.7	90.0-65.0	76.0	72.0-62.0	65.7	80.0-52.0	62.8	113.0-56.0	74.9	2.0-1.6	1.6	27.5-22.5	24.0	59.1-37.7	42.6
	C_5	52.2-28.2	39.8	120.0-70.0	89.0	67.0-57.0	60.2	80.0-50.0	64.9	137.0-63.0	89.6	2.0-1.8	1.6	32.5-25.0	27.0	49.3-38.9	44.7
Pusa 1103	Check		27.7	-	86.7	-	55.7	-	62.0	-	71.0	-	1.8	-	27.5	-	32.0
Pusa 362	Check		26.1	-	56.7	-	51.0	-	46.7	-	51.3	-	1.2	-	22.5	-	47.7
Pusa 372	Check		25.9	-	55.6	-	50.7	-	46.2	-	50.4	-	1.8	-	20.0	-	47.5
Pusa 1088	Check		23.0	-	73.7	-	71.0	-	35.0	-	70.0	-	1.8	-	30.0	-	31.1

Table 2. Phenotypic variances for eight agronomic characters in selected F_4 populations of chickpea

Breeding method	Cross	Character							
		SY (g)	BY (g)	PH (cm)	TB	P/P	S/P	SW (g)	HI (%)
PM	C_1	28.5	134.7	5.3	26.0	70.0	0.011	15.6	4.5
	C_2	10.3	63.6	4.5	25.6	410.0	0.016	6.7	1.3
	C_3	3.9	16.9	3.8	55.3	53.4	0.004	5.0	2.1
	C_4	16.4	489.2	0.8	231.1	196.0	0.009	11.2	21.2
	C_5	5.9	48.9	3.0	46.1	11.5	0.009	8.4	1.5
SSD	C_1	34.1	195.6	15.1	83.7	59.5	0.011	9.0	20.4
	C_2	147.5	301.5	43.1	243.4	343.4	0.031	7.6	81.0
	C_3	9.6	106.3	40.2	32.7	153.2	0.036	17.8	267.9
	C_4	144.4	1083.6	22.8	110.9	873.4	0.009	5.6	21.1
	C_5	38.4	144.2	57.2	63.9	107.5	0.036	9.4	13.4
BM	C_1	53.3	367.8	6.9	61.6	378.3	0.011	4.8	11.7
	C_2	42.5	206.7	12.2	77.1	191.7	0.007	1.7	16.7
	C_3	101.4	216.7	4.2	77.1	548.9	0.009	1.7	53.4
	C_4	28.0	685.8	4.6	139.8	697.3	0.020	2.8	814.4
	C_5	84.1	480.3	5.8	216.2	1251.6	0.011	5.6	10.8
SBM	C_1	116.7	694.2	5.7	39.2	304.3	0.007	2.8	13.9
	C_2	73.1	298.9	6.9	46.7	122.7	0.007	1.7	13.0
	C_3	28.9	106.7	10.5	6.8	123.1	0.018	1.1	7.5
	C_4	70.3	82.2	12.7	85.3	384.5	0.007	3.1	38.7
	C_5	69.1	293.3	12.0	111.0	624.7	0.011	5.3	11.9

PM = Pedigree method; SSD = Single seed descent method; BM = Bulk method; SBM = Selected bulk method

C_1: SBD 377 X BG 1103, C_2: BG 362 X JG 62, C_3: JG 62 X BG 1073, C_4: BG 372 X CSG 9505, C_5: BG 362 X BG 1088

Table 3a. Yield superiority (in per cent) of F_4 selected plants over checks

Cross	Criteria	Pedigree method	Single seed- descent method	Bulk method	Selected bulk method
C_1	Highest yielder (I)	52.3	34.0	46.9	53.2
	Mean of selected lines (II)	40.29	25.5	35.4	35.4
	Per cent increase of 'I' over best check mean	88.9	27.7	69.3	92.0
	Per cent increase of 'II' over best check mean	47.5	-	27.8	27.8
C_2	Highest yielder (I)	38.5	48.0	46.5	53.3
	Mean of selected lines (II)	33.3	29.0	34.0	33.6
	Per cent increase of 'I' over best check mean	39.0	73.3	67.8	92.41
	Per cent increase of 'II' over best check mean	20.2	4.7	22.7	21.3
C_3	Highest yielder (I)	25.5	19.2	52.8	46.0
	Mean of selected lines (II)	22.5	14.1	41.3	34.6
	Per cent increase of 'I' over best check mean	-	-	90.6	66.0
	Per cent increase of 'II' over best check mean	-	-	49.0	24.9
C_4	Highest yielder (I)	42.5	52.2	51.5	53.2
	Mean of selected lines (II)	35.8	27.6	34.8	32.7
	Per cent increase of 'I' over best check mean	53.4	88.8	85.9	92.0
	Per cent increase of 'II' over best check mean	29.2	-	25.6	18.0
C_5	Highest yielder (I)	40.6	36.7	51.2	52.2
	Mean of selected lines (II)	37.2	21.4	34.9	39.8
	Per cent increase of 'I' over best check mean	46.6	32.5	84.8	88.4
	Per cent increase of 'II' over best check mean	34.3	-	25.9	43.7

Note: - Mean yield of best check is 27.7 g/plant

(I) - Per cent increase in highest yielder over best check mean

(II) - Per cent increase in mean of selected lines over best check mean

C_1: SBD 377 X BG 1103, C_2: BG 362 X JG 62, C_3: JG 62 X BG 1073, C_4: BG 372 X CSG 9505, C_5: BG 362 X BG 1088

Table 3b. Comparative effectiveness of various breeding methods in different crosses of chickpea

Criteria	Cross	Pedigree method	Single seed descent method	Bulk method	Selected bulk method
Per cent increase in highest yielder plant over best check mean	C_1	II	-	-	I
	C_2	-	II	-	I
	C_3	-	-	I	II
	C_4	-	II	-	I
	C_5	-	-	II	I
Per cent increase in mean of selected plants over best check mean	C_1	I	-	II	II
	C_2	-	-	I	II
	C_3	-	-	I	II
	C_4	I	-	II	-
	C_5	II	-	-	I

C_1: SBD 377 X BG 1103, C_2: BG 362 X JG 62, C_3: JG 62 X BG 1073, C_4: BG 372 X CSG 9505, C_5: BG 362 X BG 1088

Table 4. Phenotypic correlation coefficient among eight agronomic characters in F_4 populations of chickpea

Character- combination	Pedigree method	Single Seed- Descent method	Selected bulk method	Bulk method
Plant height-Total branches	0.126	0.572**	0.036	0.138
do Seed yield/ plant	0.400**	0.630**	0.092	-0.017
do Biological yield	0.459**	0.609**	0.291*	0.240
do Harvest index	-0.068	0.082	-0.171	-0.396**
do Pods/plant	0.196	0.440**	-0.110	0.018
do Seeds/pod	-0.220	0.361**	0.080	-0.213
do 100-seed weight	0.245	0.108	0.191	0.080
Total branches-Yield/plant	0.441**	0.620**	0.459**	0.607**
do Biological yield	0.663**	0.781**	0.424**	0.777**
do Harvest index	-0.203	-0.102	0.078	-0.497**
do Pods/plant	0.563**	0.723**	0.683**	0.791**
do Seeds/pod	0.167	0.268*	0.184	-0.051
do 100-seed weight	0.184	0.033	0.048	0.152
Seed yield-Biological yield	0.675**	0.693**	0.599**	0.774**
do Harvest index	0.439**	0.439**	0.462**	-0.029
do Pods/plant	0.407**	0.615**	0.635**	0.827**
do Seeds/pod	-0.037	0.427**	0.126	-0.217
do 100-Seed Weight	0.550**	0.015	0.260*	0.067
Biological yield-Harvest index	-0.338**	-0.268*	-0.407**	-0.622**
do Pods/Plant	0.576**	0.878**	0.501**	0.825**
do Seeds/pod	0.062	0.332**	0.182	-0.121
do 100-seed weight	0.337*	-0.089	0.307**	0.125
Harvest index-Pods/plant	-0.199	-0.164	0.151	-0.300*
do Seeds/pod	-0.104	0.109	-0.066	-0.127
do 100-seed weight	0.252	0.113	-0.034	-0.025
Pods/plant - Seeds/pod	0.057	0.296*	0.242	-0.117
do 100-seed weight	0.060	0.033	-0.011	0.049
Seeds/pod - 100- seed weight	0.131	0.005	0.216	-0.258*

*,** Significant at P=0.05 and P=0.01 respectively

other three methods. The study of phenotypic variances (Table 3) showed that SSD method was superior to other methods in maintaining relatively higher variances over crosses for plant height. No single method was superior to others for maintaining higher variances for grain yield. For variances in respect of 100-seed weight, PM and SSD was superior to other two methods. However, for seeds/pod, SSD method was superior in maintaining higher variances in the population. For pods/plant, no single method was found superior to others for maintaining higher variances over breeding methods. However, for biological yield, SBM and SSD methods were equally effective as compared to other two methods for maintaining higher variances. Rahman and Bahl (1985) also found that SSD method was superior to other methods in maintaining relatively higher variances over crosses for most of the characters. Ahmed *et al.* (2008) found that pedigree selection method (PSM) was best method for faba bean breeding for higher yield as compared to the other two methods. Adnan *et al.* (2010) also reported that bulk population method showed superiority over pedigree for grain yield, panicle length, panicles/plant, tillers/plant and harvest index in F_3 generation in rice. Teerawat and Charassri (2010) found that the pedigree selection (PS) and SSD selection methods, pod yield and yield components in two yardlong bean populations were not significantly different.

For seed yield and its components, the selected bulk method (SBM) of breeding was found best in four crosses (C_1: SBD 377 x BG 1103, C_2: BG 362 x JG 62, C_4: BG 372 x CSG 9505, C_5: BG 362 x BG 1088) followed by bulk method (BM) in cross 3 (JG 62 x BG 1073) on the basis of per cent increase of highest yielder over the best check (PUSA 1103) mean (Table 3 a, b). While, on the other hand, the pedigree method (PM) was found best in two crosses (C_1: SBD 377 X BG 1103 & C_4: BG 372 x CSG 9505) followed by bulk method in two crosses (C_2: BG 362 x JG 62 & JG 62 x BG 1073) and selected bulk method (SBM) in one cross (C_5: BG 362 x BG 1088) on the basis of per cent increase of mean of selected plants. On the basis of per cent increase in yield of best selected plant over best check mean, SBM resulted higher means for seed yield and its components than other three breeding methods over crosses except in cross (C_3: JG 62 x BG 1073). It was concluded that SBM is the most preferred method for improvement of yielding ability in chickpea and is recommended most suitable for chickpea breeding.

Moderate to strong positive association of seed yield with total biomass and pods/plant was obtained in all the four breeding methods (PM, SSD, BM and SBM) (Table 4). Singh *et al.* (1976), Katiyar *et al.* (1977) and Singh and Shrivastava (1977) also reported the positive correlation between pods/plant and seed yield. Khan and Chaudhary (1975) also observed that yield was positively correlated with plant height in F_3 populations of chickpea.

While comparing the relative performance of different breeding methods, it was found that more and more superior high-yielding segregants were obtained when population was advanced through selected bulk method (SBM) of breeding. Similar results were also reported by Singh *et al.* (2004). The study of phenotypic variances showed superiority of SSD method over other methods in maintaining relatively higher variances across crosses for most of the characters. Further, correlation analysis revealed that seed yield had significant phenotypic relationship with pods/plant, seeds/pod and biological yield. Therefore, it can be concluded that selected bulk method (SBM) is superior and most effective followed by bulk method (BM) of breeding in chickpea improvement programme for better seed yield, the selection for pods/plant, seeds/pod and biological yield should be exercised in segregating generations.

REFERENCES

Adnan K, Katsuhiko K and Shashidhar HE. 2010. Comparative efficiency of pedigree modified bulk and single seed descent breeding methods of selection for developing high-yielding lines in rice (*Oryza sativa* L.) under aerobic condition. Electronic Journal of Plant Breeding **2:** 184-193.

Ahmed MSH, Abd-El-Haleem SHM, Bakheit MA, and Mohamed SMS.2008. Comparison of three selection methods for yield and components of three faba bean (*Vicia faba* L.) Crosses. World Journal of Agricultural Sciences **4:** 635-639.

Brim CA. 1966. A modified pedigree method of selection in soybeans. Crop Science **6:** 220.

Goulden CH. 1941. Problem in plant selection. Proc. Seventh Int. Genetical Congress (1939). Edinburg. Pp 132-133.

Grafius JE. 1965. Short cuts in plant breeding. Crop Science **5:** 377.

Katiyar RP, Prasad J, Singh AB and Ram L. 1977. Association analysis of grain yield and its components in segregating populations of chickpea. Indian Journal of Agricultural Sciences **47:** 325-327.

Khan MA and Chaudhary MA. 1975. Inter-relationship between yield and other plant characters in gram (*Cicer arietinum* L.). Journal of Agricultural Research (Pakistan) **13:** 589-592.

Rahman MA and Bahl PN. 1985. Comparison of single seed descent, mass selection and random bulk methods in chickpea. Indian Journal of Genetics **45:** 186-195.

Singh H, Dahiya BS and Sandhu TS. 1976. Correlations and path coefficient analysis in gram (*Cicer arietinum* L.). Journal of Research, Punjab Agricultural University, Ludhiana **13:** 1-7.

Singh RP and Srivastava MP. 1977. Heritability and correlation of some quantitative characters in pigeonpea [*Cajanus cajan* (L.) Millsp.] Mysore Journal of Agricultural Sciences **11:** 315-317.

Singh KB, Bejiga G and Malhotra RS. 2004. Associations of some characters with seed yield in chickpea collections. Euphytica **49:** 83-88.

Teerawat S and Charassri N. 2010. The efficiency of pedigree and single seed descent selections for yield improvement at generation 4 (F_4) of two yardlong bean populations. Kasetsart Journal (Natural Science) **44:** 343–352.