

## GENETIC STUDY IN F<sub>3</sub> AND F<sub>4</sub> GENERATIONS OF CHICKPEA

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### ABSTRACT

The segregating populations of six crosses were studied in F<sub>3</sub> and F<sub>4</sub> generations. By using intraclass correlation and regression (F<sub>4</sub>-F<sub>3</sub>) methods, heritability and genetic correlations involving five quantitative characters were worked out. The intraclass correlation method revealed consistent estimates of heritability in F<sub>3</sub> and F<sub>4</sub> generations. Grain weight showed the highest heritability as against yield per plant which was the least heritable trait. The estimates obtained from regression method deviated from those obtained from intraclass correlation method. The genetic correlations in F<sub>4</sub> revealed much stronger association among characters as compared to those seen in F<sub>3</sub> generation. Seed yield per plant showed positive association with pods per plant and seeds per pod, and negative association with grain weight.

Key words: Heritability, genetic correlation, chickpea.

Estimation of narrow sense heritability and genetic correlation is essential for predicting the response to selection, correlated response and efficiency of indirect selection over direct selection, etc. Since these parameters are properties of the population, they should be estimated separately for each segregating population to ensure a systematic genetic improvement. This becomes particularly essential in a genetically underexploited crop like chickpea. The present study aims at estimating the narrow sense heritability and genetic correlation by using the observations in F<sub>3</sub> and F<sub>4</sub> generations.

### MATERIALS AND METHODS

The population used here consisted of 150 F<sub>3</sub> rows and 150 F<sub>4</sub> rows derived from these F<sub>3</sub> rows, grown simultaneously. In winter 1986, F<sub>3</sub> and F<sub>4</sub> generations of these 150 families were grown in randomized block design with three replications. Each family in F<sub>3</sub> and F<sub>4</sub> was grown in four rows of 4 m length in each replication at 30 x 10 cm spacing. Twenty five plants in each family chosen randomly from the middle two rows were used to record

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observations on five quantitative characters and the data thus obtained were subjected to following analyses.

*Estimation of heritability.* (a) Intraclass correlation method (t method): The estimates of  $\hat{h}^2$  values were computed using the formulae given by Cahaner and Hillet [1]. (b) F<sub>4</sub>-F<sub>3</sub> regression method: The regression of F<sub>4</sub> family means on corresponding F<sub>3</sub> values was used to estimate b<sub>F<sub>4</sub>-F<sub>3</sub></sub> values [2] and from these  $\hat{h}^2$  values estimates were computed.

*Estimation of genetic correlation.* Genetic correlations between traits were calculated by using the method suggested by Cahaner and Hillet [1].

## RESULTS AND DISCUSSION

The mean values for the six traits either remained equal in the two generations or showed an improvement in F<sub>4</sub> over F<sub>3</sub> values (Table 1). The increase in mean was further accompanied by increase in variability for pods/plant, seeds/pod, and seed yield. The

Table 1. Mean and coefficient of variability for quantitative characters in F<sub>3</sub> and F<sub>4</sub> generations of chickpea

Genera- tion	Plant height		Pods per plant		Seeds per pod		100-Seed weight		Seed yield	
	mean (cm)	cv	mean	cv	mean	cv	mean (g)	cv	mean (g)	cv
F <sub>3</sub>	31.2	12.2	26.1	49.3	1.2	16.6	15.8	25.0	4.6	54.0
F <sub>4</sub>	35.5	11.3	43.1	66.6	1.3	21.9	15.7	21.6	7.4	62.3

heritability values in F<sub>3</sub> and F<sub>4</sub>, calculated on the basis of the intraclass correlation (Table 2) method, revealed seed weight to be a highly heritable trait, while seeds/pod was moderately heritable, followed by plant height, pods/plant, and seed yield in decreasing order. Heritability estimates obtained in the two generations for these characters were comparable. However, heritability values estimated by the regression method differed from the above estimates. Though seed weight again registered the highest heritability value, plant height showed the lowest. Genetic correlations among the five characters differed in magnitude and direction (Table 3).

The genetic correlations among characters showed large differences in the two generations. The correlations between the characters were observed to be higher (positive or negative) in F<sub>4</sub> as compared to F<sub>3</sub> generation. The negative associations, particularly of seed weight with seeds/pod, pods/plant, and seed yield/plant were consistent in the two generations and the magnitude of negative association enhanced in F<sub>4</sub>. The components having positive association with seed yield were pods/plant and seeds/pod. In contrast, plant height was responsible for decrease in yield.

Table 2. Heritability estimates using intraclass correlation (*t*) and regression (*b*<sub>F<sub>3</sub>-F<sub>4</sub></sub>) methods for quantitative characters in chickpea

Character	Generation	Variance		<i>t</i>	Heritability	
		between family	within family		<i>t</i> method	<i>b</i> method
Plant height	F <sub>3</sub>	0.75	13.90	0.05	0.08	0.00
	F <sub>4</sub>	1.69	14.83	0.10	0.18	
Pods/plant	F <sub>3</sub>	4.28	163.35	0.03	0.04	0.20
	F <sub>4</sub>	47.39	694.61	0.06	0.11	
Seeds/pod	F <sub>3</sub>	0.01	0.03	0.27	0.41	0.06
	F <sub>4</sub>	0.01	0.05	0.14	0.24	
Seed weight	F <sub>3</sub>	10.28	7.02	0.59	0.89	0.33
	F <sub>4</sub>	5.85	6.55	0.47	0.82	
Seed yield	F <sub>3</sub>	0.17	6.01	0.03	0.04	0.28
	F <sub>4</sub>	0.18	6.28	0.03	0.04	

In the present study, since F<sub>3</sub> and F<sub>4</sub> populations were grown together, a comparison of the two populations was possible with respect of mean and variability parameters. There was a slight improvement in the population mean in respect of yield and important yield attributes. The selection of normal looking plants at random for advancing the generation accounts for the general improvement in the population. Consistent estimates of heritability were obtained from the intraclass correlation method. Among different characters, grain weight was highly heritable. This is in accordance with most of the earlier reports in chickpea [3]. As compared with intraclass correlation method, the regression method resulted in very inconsistent estimates of heritability. It appears that the use of regression method is more appropriate for open-pollinated populations, where every individual mates with a random sample of individuals to give rise to its progeny. In self-pollinated crops, where the F<sub>3</sub> and F<sub>4</sub> rows are grown from selected seeds, the effect of selfing particularly on dominance

Table 3. Genetic correlations between different pairs of characters in F<sub>3</sub> and F<sub>4</sub> generations of chickpea

Character	Plant height	Pods per plant	Seeds per pod	100-seed weight	Seed yield per plant
Plant height	—	0.01	0.22	-0.03	-0.19
Pods/plant	-0.45	—	-0.22	-0.27	0.63
Seeds/pod	-0.66	0.46	—	-0.59	0.00
100-seed weight	0.53	-0.79	-0.76	—	-0.39
Seed yield/plant	-0.76	0.80	0.82	-0.75	—

Values above diagonal — F<sub>3</sub> generation; below the diagonal — F<sub>4</sub> generation.

(heterozygotes) makes it less efficient in estimating narrow sense heritability. Cahaner and Hillet [1] also indicated that heritability estimated based on regression method contains greater proportion of nonadditive variance in the numerator and hence it is less reliable. The genetic correlations, calculated separately for F<sub>3</sub> and F<sub>4</sub> generations, revealed that yield had strong positive association with pods/plant, seeds/pod, but a strong negative association with seed weight (size) and plant height. These results are in agreement with earlier observations on association of yield with pods/plant [4-6] grain weight [7] and plant height [8]. It was interesting to note that the magnitude of correlations among different traits increased in F<sub>4</sub> generation. Possibly the associations among different traits becomes stronger in F<sub>4</sub> as against F<sub>3</sub> generations due to the fixation (through selfing) of recombination and segregation in earlier generations.

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