

Heritability Estimates for Grain Yield and Quality Characters in Chickpea (*Cicer arietinum*)

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ABSTRACT

Twenty elite lines of chickpea were planted in the field in a randomized complete block design with three replications. High genotypic and phenotypic co-efficients of variability were observed for days taken to flowering, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, seed yield per plant and protein content. Days taken to flowering, 100-seed weight and protein content were characterized by high broad sense heritability estimates, which indicated the presence of a considerable proportion of total variability due to genetic causes.

Key Words: Heritability; Chickpea; Variability; Genetic advance; Phenotypic variance; Genotypic variance

INTRODUCTION

Chickpea is the most important rabi pulse crop in Pakistan predominantly grown in rainfed areas of the country especially the 'Thal'. As the area under the crop is limited, the efforts are to be focused to increase its per acre yield by developing improved varieties with stable performance. Genetic variability is the first pre-requisite for any crop improvement programme as it provides opportunity to select an ideal plant type. Estimation of heritability is of prime importance as an index of transmission of morphogenetic characters and is thus vital for infusing confidence during selection procedures. Characters with high heritability can easily be fixed with simple selection resulting in quick progress. Singh *et al.* (1992) studied genetic variance for agronomic traits in chickpea. Days to flowering were found to be highly predictable. Jahagirdar *et al.* (1994) studied eight chickpea cultivars and reported high phenotypic and genotypic co-efficient of variation for number of pods per plant. High heritability together with high genetic advance were estimated for 100 seed weight, days to flowering, number of secondary branches, number of pods per plant and number of seeds per pod. Iqbal *et al.* (1994) estimated heritability for various characters in chickpea genotypes and reported low to moderately high estimates for number of pods per plant, yield per plant, number of seeds per pod and 100-seed weight. Mehdi *et al.* (1994) estimated broad sense heritability from F₃ populations of chickpea crosses. Broad sense heritability estimates were higher for number of pods, 100-seed weight and grain yield per plant.

Rao *et al.* (1994) studied 44 varieties of chickpea. Genotypic coefficient of variation was highest for 100-seed weight, secondary branches per plant, pods per plant and seed yield per plant. High heritability was estimated for 100-seed weight and low heritability for pods and secondary branches per plant. Kumar and Krishna (1998) provided information on heritability and genetic advance from 17

chickpea genotypes. Grain yield showed poor heritability; while, 100-seed weight and protein content showed high heritability. Estimates on genetic advance suggested that number of pods per plant was important yield component to select for high yield. High genetic advance was also recorded for 100-seed weight. Nimbalkar (2000) studied 40 genotypes of chickpea for number of days to flowering, number of pods per plant, 100 grain weight and grain yield per plant. The estimates of genetic advance were highest for 100-grain weight. This study was conducted for heritability estimates for grain yield and quality characters in chickpea (*cicer arietinum*)

MATERIALS AND METHODS

The study was conducted in the research area of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. The experimental material comprised 20 elite chickpea genotypes i.e. 818, 1264, 831, 1036, 1138, 1011, 2-444, 926-1, 1159, 943-1, 965, 293, 1276, 1248, 960-1, 1259, 588, 881, C-612 including one check variety (C-44). The genotypes were sown in a triplicated randomized complete block design in a plot size of 4 x 1.2 m. Each entry was planted in three rows keeping plant to plant distances of 30 cm. Uniform cultural and plant protection measures were applied to all entries in the trial. The data were recorded for grain yield, its components and protein content, which were statistically analyzed (Steel & Torrie, 1984)

RESULTS AND DISCUSSION

Mean squares for genotypes (MSG) as shown in Table I were found to be highly significant for days to flowering, number of secondary branches per plant, number of pods per plant, 100-seed weight, seed yield per plant and protein content whereas only significant for number of seeds per pod. Days to flowering exhibited moderately high estimate

Table I. Mean squares and estimates of variability parameters for quantitative traits in chickpea

	Days to flowering	Secondary branches/plant	Pods/plant	Seeds/pod	100 seed weight	Seed yield/plant	Protein content
MSG	24.723**	0.2977* *	108.102**	0.00995*	10.343**	15.186**	5.683**
Mean	117.4	5.017	62.175	1.393	23.397	19.602	22.52
SD	3.232	0.414	7.323	0.080	1.865	2.730	1.379
CV%	2.753	8.249	11.779	5.726	7.970	13.928	6.122
σ^2_g	6.981	0.061	27.934	0.002	3.371	4.034	1.858
GCV	5.947	1.216	44.928	0.127	14.406	20.579	8.252
σ^2_p	10.760	0.176	52.234	0.006	3.5990	7.1180	1.966
PCV	9.165	3.503	84.011	0.460	15.381	36.314	8.731
σ^2_e	3.778	0.115	24.299	0.004	0.228	3.084	0.108
ECV	3.218	2.288	39.082	0.333	0.975	15.736	0.479
h^2_{BS}	64.89%	34.70%	53.48%	27.61%	93.66%	57.67%	94.52%
GA	3.735	0.255	6.783	0.039	3.118	2.653	2.326

*Significant; ** Highly Significant; MSG Mean Squares of Genotypes; SD Standard Deviation; CV% Coefficient of Variability; σ^2_g Genotypic Variance; GCV Genotypic Coefficient of Variability; σ^2_p Phenotypic Variance; PCV% Phenotypic Coefficient of Variability; σ^2_e Environmental Variance; ECV Environmental Coefficient of Variability; h^2_{BS} Broad Sense Heritability; GA Genetic Advance

of heritability (64.89%), which indicated that a reasonable proportion of the total variability was due to genetic causes. The differences between genotypic and phenotypic coefficient of variability showed the environmental influence. The results are in agreement with Jahagirdar (1994) who found high estimate of heritability for this character. Number of secondary branches per plant gave lower estimate of heritability (34.70%), indicating the preponderance of total variability due to environmental factors. The results are in contrast with those of Jahagirdar (1994) who reported high heritability estimates for this character. Number of pods per plant showed moderate estimate of heritability (53.48%), which indicated that total variability was due to genetic causes as well as due to environment. The results are in line with the findings of Iqbal *et al.* (1994) who reported moderate to high heritability estimate. Number of seeds per pod exhibited lower estimates of heritability (27.61%), which indicated that main proportion of total variability was predominantly due to environmental factors. The results are in contrast with Iqbal *et al.* (1994) who reported moderately high heritability estimates. Heritability estimate for 100 seed weight was high (93.66%), indicating the success of selection for this trait. The differences between genotypic and phenotypic coefficient of variability was very small indicating negligible role of environment. The results are in accordance with the findings of Iqbal *et al.* (1994). Seed yield per plant showed moderate heritability (57.67%), which indicated that selection for the trait could be delayed for subsequent generations. The results are in agreement with the findings of Iqbal *et al.* (1994). A high estimate of

broad sense heritability for protein content reflected that selection could be effective for improving the trait. Smaller differences between genotypic and phenotypic coefficient of variability indicated that major proportion of phenotypic variance was due to genetic differences. From the foregoing results it may be concluded that the characters with high heritability i.e. 100-seed weight and protein content with small differences between genotypic and phenotypic coefficient of variability should be selected for constituting desirable genotypes of chickpea.

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