

Genetic Variability, Heritability and Genetic Advance Study for Seed Yield and Yield Component Traits in a Chickpea Recombinant Inbred Line (RIL) Population

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ABSTRACT

Experimental material consisted 252 intra-specific recombinant inbred line (RIL) population derived from a cross between desi (ICC 283) and kabuli (ICC 8261) type of chickpea, received from ICRISAT, Patancheru, India. Experiment was conducted at Rafi Ahmed Kidwai College of Agriculture, Sehore, Bhopal, India, during rabi 2011-12 and 2012-13. Traits assessed were days to 50% flowering, maturity, plant height, biological yield, seed yield, harvest index and 100-seed weight. Standard statistical analysis was adopted for calculating the genetic variability, heritability and genetic advance. Out of seven characters studied biological yield, seed yield, harvest index and 100-seed weight exhibited high genotypic coefficient of variation and heritability coupled with high genetic advance as percent of mean which revealed that these traits might be under control of additive gene effects and therefore these traits are more reliable for effective selection for developing desirable lines.

Key words: Chickpea, RILs, Yield traits, Genetic variability and Heritability

INTRODUCTION

Chickpea is the second most important pulse crop in the world after dry beans. Crop domestication under the influence of evolutionary forces and human derived selection process has resulted in several desirable traits in crops such as high productivity, short duration, reduced seed dispersal/ dormancy and branching, uniform flowering/ fruiting and seed maturation^{1,2,3,4}. The extent of variability for various

quantitative traits including seed yield available to breeders determine the success that can be achieved through genetic improvement. The observed variability may be grouped under heritable and non-heritable components with the help of suitable parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance.

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Assessment of genetic variability for yield and its contributing traits in recombinant inbred line (RIL) was an important purpose for screening of suitable and diverse RILs. Phenotype of an individual reflects the genotypic constitution and its interaction with the environment. Phenotypic and genotypic coefficient of variations play an important role in understanding the extent and nature of genetic variability present in a population derived from two diverse parents in chickpea. The populations derived from crossing genetically diverse parental sources generate substantial variability that can be harnessed by plant breeders through selection. The present investigation was undertaken using a chickpea RIL population comprising 252 lines developed using two highly diverse genotypes belonging to diverse groups *viz.*, *desi* (ICC 283) and *kabuli* (ICC 8261) to identify desirable lines having better trait combinations that can be used in chickpea improvement.

MATERIAL AND METHODS

The present investigation was carried out at research experimental field of Rafi Ahmed Kidwai College of Agriculture, Sehore (Madhya Pradesh) during *rabi* 2011-12 and 2012-13. Experimental material consisted 252 intra-specific RIL of chickpea and two parents *i.e.* ICC 283 (*Desi*) and ICC 8261 (*Kabuli*) which were received from International Crops Research Institute for the Semi-Arid Tropics, Patancheru (Telangana), India. A set of 252 RILs' population and parents were grown in a randomized block design with two replications during *rabi* 2011-12 and 2012-13. Each entry was sown in 4 m long row with 30 cm row-to-row and 10 cm plant-to-plant spacing. The fertilizer dose of 20:50:0:20 NPKS kg/ha was applied as basal dose. Recommended package of practices were adopted for optimum crop growth and plant protection under both conditions. Data on seven quantitative traits *viz.*, days to 50% flowering, days to physiological maturity, plant height (cm), biological yield per plant (g), seed yield per plant (g), harvest index per plant (%) and hundred seed weight (g) were recorded. The

sample size for experiment was five plants from each line. Standard procedures were adopted for statistical analysis and their interpretation. Statistical analysis included genotypic coefficient of variation (GCV)⁵, phenotypic coefficient of variation (PCV)⁵, broad sense heritability⁶, genetic advance (GA)⁷ and genetic advance as percent of mean (GAM)⁷.

RESULTS AND DISCUSSION

Genotypic and Phenotypic Coefficient of Variation (GCV and PCV)

Information on variability and heritable components is essential to plant breeder for deciding a future breeding procedure. High estimates of GCV and PCV was recorded for seed yield per plant, 100-seed weight, biological yield per plant and harvest index per plant in RILs. Among RILs the variation in yield potential depends upon number of pods, seeds per plant and 100-seed weight. Variation in biological yield per plant depends upon plant growth habit and period of vegetative phase. It is important to mention that variation in maturity period in P₁ (ICC 283) and P₂ (ICC 8261) was 9 days, whereas in RILs it was 107 to 131 days. The range of maturity duration did not vary as was expected. Low variation was also evidenced by low values of PCV and GCV for days to maturity. The range of variation for days to 50% flowering in RILs was quite wide as compared to maturity duration. The range of days to 50% flowering varied from 42 to 93 days in RILs. It was found that the high range of variation in days to 50% flowering was associated with different plant growth habits recorded in RILs. The RILs possessing prostrate plant growth habit started flowering very late as compared to those RILs having spreading, semi-spreading and semi-erect plant growth habit. Prostrate growth habit is predominantly observed in wild species and are not suitable for commercial exploitation in chickpea improvement. The high variation in flowering period provides better scope for selection of late and early flowering RILs.

Early flowering and late maturity facilitate long reproductive period and long seed setting period, hence early flowering with late maturity is considered as desirable for yield improvement in chickpea. Duration of reproductive period is also important criteria for realizing high yields⁸. It is reported that 50-55 days reproductive period is optimum for good seed setting. Therefore, early flowering coupled with optimum duration of reproductive period is important for increasing higher yields. In this investigation high GCV and PCV was recorded for seed yield per plant, biological yield per plant, harvest index per plant and 100-seed weight, whereas days to 50% flowering, days to maturity and plant height showed moderate to low variability. The proportion of heritable variation evidenced by the magnitude of GCV and PCV values was relatively high in respect of seed weight compared to that of pods per plant and seed yield per plant⁹. Narrow PCV was recorded by^{10,11} in chickpea germplasm. Sidramappa¹² also reported GCV and PCV in RILs' population of chickpea derived from a cross between ICCV 2 x JG 62, they reported GCV and PCV for days to 50% flowering were slightly lower as compared to present investigation. They also reported the PCV values which were slightly higher than GCV values for plant height, number of branches/plant, days to first flowering, days to 50% flowering, days to pod initiation, days to physiological maturity, duration of reproductive phase, number of pods/plant, 100-seed weight and seed yield/plant indicating very low influence of environment in the expression of these traits. The proportion of heritable variation is evidenced by the magnitude of GCV and PCV values. The PCV and GCV values were relatively high for seed weight as compared to pods per plant and seed yield per plant⁹. Sharma¹³ observed high GCV for seed yield, 100-seed weight, plant population per m², number of secondary branches per plant, number of pods per plant, number of grains per plant, plant height and days to flowering. High GCV for these traits

suggested a good scope of chickpea crop improvement.

Heritability

Heritability is the heritable portion of phenotypic variance. It is a useful index of the transmission of characters from parents to their offspring¹⁴. Heritability is a measure of the contribution of the genotypes to the total variation. It provides the relationship between the genotypic and phenotypic variance and indicates the degree to show that to what extent the characters of the individuals are inherited to the offspring. When the heritability estimates of qualitative and quantitative traits are high (*i.e.* more than 60%), the phenotypic appearance would provide a close measure of genotypic value and selection on the basis of phenotypic performance alone may be effective. If the heritability is low (*i.e.* less than 30%), the environmental influence are high in the expression of these traits which ultimately necessitates progeny testing for assessing the true breeding value of characters. Selection based on particular character will be effective when its heritability estimate is high. Burton⁵ suggested that GCV together with heritability estimates would give the best picture of the extent of advance to be expected by selection. In the present investigation, high estimates of heritability in broad sense were observed for days to 50% flowering, days to maturity, plant height, biological yield per plant, seed yield per plant, harvest index per plant and 100-seed weight studied. This result indicates that these characters were highly heritable and hence were less affected by the environment. The plant breeder therefore may use these characters for selection on the basis of phenotypic expression in the individual RIL. Mathur and Mathur¹⁵ estimated high heritability for plant height, days to flowering, days to maturity, pods per plant, grain yield per plant and thousand grain weight in chickpea. Sidramappa¹² observed high heritability along with high variation for pods per plant, seed yield per plant, 100-seed weight, days to 50% flowering, days to pod initiation and plant height compared to other traits. The findings of present study are in accordance with the results of¹⁶ as their

findings also showed high heritability with high variation for pods per plant, seed yield per plant, 100-seed weight, days to 50% flowering, days to pod initiation and plant height. Chauhan¹⁰ reported genetic variability was highest for pods per plant, flower initiation and number of primary and secondary branches per plant.

Genetic Advance

The genetic gain that can be expected by selection for a character was estimated by genetic advance. A relative comparison of heritability estimates and expected genetic advance will give an idea about the nature of gene action governing a particular character. A comparison of these two estimates made in this study revealed that seed yield per plant, biological yield per plant, harvest index per plant and 100-seed weight had high heritability estimates coupled with high genetic advance as percentage of mean suggesting that these characters are under the control of additive gene action and potential possibilities exist for the improvement of these traits through simple selection. Moderate genetic advance as percentage of mean for days to 50% flowering and plant height was due to low genetic variability for these traits. Present research findings also showed agreement with the outcome cited by various scientists. The high genetic advance expressed in percent of mean was recorded in the present study for seed yield per plant followed by 100-seed weight, biological yield per plant and harvest index per plant are in agreement of the findings of¹². Moderate genetic advance was observed for days to 50% flowering and plant height. These

findings of moderate genetic advance for days to 50% flowering were also obtained by^{12,17}. Ali^{18, 12} reported that seed yield per plant, number of pods per plant and 100-seed weight had high heritability estimates coupled with high genetic advance. High heritability coupled with low genetic advance for 100-seed weight was also reported by^{19,20}, and for seed yield per plant reported by^{21,22,23}. Plant height had high heritability was also reported by^{24,10}. High heritability coupled with high genetic advance was observed for biological yield per plant, seed yield per plant, harvest index and 100-seed weight in this investigation that indicated that additive gene played a major role for inheritance of these traits and these traits were least influenced by environmental effects. Low genetic advance was recorded for days to maturity. High heritability was associated with low genetic advance for days to maturity that indicated presence of dominant gene for the control to maturity duration. Qureshi²⁵ reported high heritability with low genetic advance of days to 50% flowering, days to maturity and 100-seed weight indicated the influence of dominant and epistatic genes for these traits and high heritability for biological yield coupled with high genetic advance suggest that additive gene effects are important in determining these characters. Sharma¹³ recorded high heritability for 100-seed weight, days to flowering, days to maturity, plant height, which indicated heritable portion of the variability. High heritability was associated with high genetic advance as percent of mean for plant height, days to flowering and 100-seed weight^{10,26}.

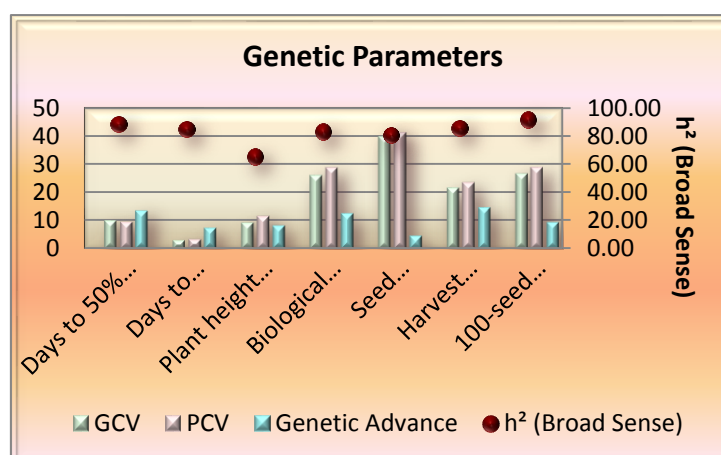


Fig. 1: Different values of genetic parameters in RILs & parents

Table 1: GCV, PCV, h² and Genetic advance as percentage of mean for yield and yield attributes in RILs and parents

Traits Genetic parameters	Days to 50% flowering	Days to maturity	Plant height (cm)	Biological yield/ plant (g)	Seed yield/ plant (g)	Harvest index/ plant (%)	100-seed weight (g)
Genotypic coefficient of variation (GCV) (%)	10.2 (M)	3.1 (L)	9.4 (L)	26.3 (H)	40.0(H)	21.8 (H)	26.9 (H)
Phenotypic coefficient of variation (PCV) (%)	9.6 (L)	3.4 (L)	11.6 (M)	28.8 (H)	41.1(H)	23.5 (H)	28.9 (H)
Heritability (h ²) (%)	88.3 (H)	84.7 (H)	65.3 (H)	83.1 (H)	80.6(H)	85.6 (H)	91.5 (H)
Genetic advance (GA) (%)	13.3	7.3	8.1	12.3	4.6	14.4	9.3
Genetic advance as percentage of mean (GAM)	18.6 (M)	5.9 (L)	15.6 (M)	49.4 (H)	68.3(H)	41.6 (H)	53.3 (H)
Range	Min.	42	107	28.20	7.91	2.14	11.65
	Max.	93	131	54.15	39.69	17.49	48.60

CONCLUSION

Out of seven characters studied biological yield per plant, seed yield per plant, harvest index and 100-seed weight exhibited high GCV and heritability coupled with high genetic advance as percent of mean which revealed that these traits might be under control of additive gene effects and therefore these traits are more reliable for effective selection for developing desirable lines.

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