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Estimation of genetic parameters in recombinant inbred population derived from interspecific cross of chickpea (*Cicer arietinum* L.)

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Abstract

A set of 140 recombinant inbred lines (RIL's) population (F_8) derived from interspecific cross *C. arietinum cv* K 850 X *C. reticulatum* (ICCW 8), were studied for the various genetic parameters viz., magnitude of genotypic and phenotypic variation, heritability, genetic advance and correlation coefficients. Maximum variability was observed for yield/plant followed by number of pods/plant and 100-seed weight. Maximum heritability was observed for seed weight (92.5%) followed by seeds/pod (74.5%) and plant height (59.8%). High expected genetic advance coupled with high heritability estimates were observed for yield/ plant, pods/plant and plant height suggesting a possibility of isolation of superior lines for these characters in recombinant inbred population. Yield /plant had significant positive phenotypic and genotypic correlation with 100-seed weight, seeds/pod and pods/plant. Based on mean performance of RILs over control, superior lines were selected for various yield component traits.

Keyword: *Cicer arietinum*, genetic parameters, interspecific cross, RILs

Introduction

Genetic improvement of chickpea by classical breeding involving inter-varietal crosses has met with limited success due to lack of sufficient and satisfactory level of genetic variability within primary gene pool [1]. However, wild species of genus *Cicer* possess many desirable traits *viz.*, resistance to diseases, earliness, tolerance to cold, high protein content, high branches and pods/plant [2]. Several attempts have been made in the past to hybridize chickpea with its wild relatives [2-6]. However, still there lies a wide gap between the availability of desirable genes in wild species and their utilization in chickpea improvement [7].

The utilization of wild species of *Cicer* is often restricted by the incompatibility barriers between wild and cultivated species [8]. Among wild *Cicer* species, *C. reticulatum* is only species known to be easily crossable with *Cicer arietinum.* However, there are only a few reports of successful gene transfer for agronomic traits from *C. reticulatum* in to cultivated chickpea. Hence, molecular marker-mediated introgression of QTLs may hasten the process of gene transfer. This requires development of mapping population with high level of polymorphism and its accurate phenotyping [9] as variability in populations developed through intra-varietal crosses of chickpea is very limited [10],

An attempt was made to cross *C. reticulatum* with elite chickpea genotypes with objectives of developing immortal mapping population (RILs), its phenotyping and introgression of quantitative trait loci (QTLs).

Materials and methods

A crossing program was initiated in the year 1994-95 with five chickpea genotypes (K-850, PDG-84-10, Gaurav, Pusa 408 and KPG 59) and *Cicer reticulatum* (ICCW 8). The true F_1s along with their parents were characterized for different morphological attributes and pollen fertility. F_1s was selfed to produce F_2 in one of the cross *C. arietinum cv* K 850 x *C. reticulatum* (ICCW 8) and advanced up to F_8 generation to develop a set of recombinant inbred populations using modified single pod descent method [11]. These 140 Recombinant Inbred Lines (RILs) were evaluated during year 2003-04 in Augmented Block Design in 14 blocks, where each block had 10 RILs along with 2 controls (K-850 and PDG 84-10). Two rows of 2 meters length constituted one RIL. Row-to-row and plant-to-plant distance were 60 cm and 10 cm, respectively. The observations were recorded on five randomly taken plants for seven quantitative traits

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*Corresponding author's e-mail: narendrasingh@scientist.com *viz*., days to flowering, plant height, branches/plant, pods/plant, seeds/pod, 100-seed weight and yield /plant.

Selection was practiced in RILs population based on their mean values over the control. RILs having higher mean value for a specific trait over respective control values were considered promising. The estimation of magnitude of variability (variance and coefficient of variation), heritability, genetic advance and correlation coefficients were done using the standard statistical procedures.

Results and discussion

Out of five genotypes of chickpea used for hybridization with *Cicer reticulatum*, success was obtained only with K 850 in both directions (using as male as well as female parent). The success in getting pod set following hybridization was more when wild species was used as male (3.3%) than female (1.8%) parent. The hybridization of wild species with other genotypes (PDG 84-10, Gaurav, Pusa 408 and KPG 59) did not result in any pod set (Table 1). The effect of maternal genotypes on development of interspecific hybrids has been well documented [12].

F_1 of the cross K850 X ICCW8 (*Cicer reticulatum*) was found intermediate between wild and cultivated parents for growth habit, seedling height, flowering, maturity and seed color (Table 2). However, pollen fertility in F_1 showed drastic reduction (58%) as compared to either of the parents. These features clearly indicated the hybrid nature of F_1 plants. The reduction in fertility level of F_1 plants obtained through interspecific hybridization is natural and it happens due to genetic distance between two species. Similar reports indicating intermediate morphological features and reduction in fertility level of interspecific hybrids (F_1) of chickpea is not uncommon [6].

The perusal of data (Table 3) revealed very high variability for most of the quantitative traits *viz*., yield/plant (21.3-210.7g), plant height (31.0-69.3), branches/plant (3.3-8.7) and seeds/pod (1.1-1.9). Besides, highest estimates of phenotypic and genotypic coefficients of variation were obtained for yield/plant (67.4 & 42.5) followed by pods/plant (63.1 & 43.8). Other characters exhibited moderate variability (PCV & GCV), 100-seed weight (24.3 & 23.4) and branches/plant (34.1 & 19.8). However, seeds/pod (23.4 & 11.5) and plant height (19.3 & 14.9) exhibited low phenotypic and genotypic coefficient of variability. Similar trend of release of higher magnitude of genetic variability for different quantitative traits in F_2 of inerspecific crosses involving *C. reticulatum* has also been reported [6]. The higher estimates of genotypic coefficient of variation for yield/plant and pods/

Table 1. Details of crosses attempted between *Cicer reticulatum* (ICCW 8) x *Cicer arietinum* genotypes

S.N.	Details of crosses	No. of pollinations	No. of pods set	No. of seeds set	Pod set (%)
1.	K 850 x *Cicer reticulatum*	1557	51	98	3.3
2.	*Cicer reticulatum* x K 850	2010	36	69	1.8
3.	Gaurav x *Cicer reticulatum*	1650	0	0	0
4.	Pusa 408 x *Cicer reticulatum*	1568	0	0	0
5.	PDG 84-10 x *Cicer reticulatum*	1830	0	0	0
6.	KPG 59 x *Cicer reticulatum*	1763	0	0	0

Table 2. Characterization of F_1s of cross *Cicer arietinum* cv K 850 x *Cicer reticulatum* (ICCW8)

S. No.	Characters	*Cicer arietinum* cv K850	*Cicer reticulatum* (ICCW 8)	F_1
1.	Growth habit	Erect	Prostrate	Semi-spreading
2.	Seedling height	48-68 cm	5-7 cm	15-20cm
3.	Flowering	36-48 d	90-110 d	46-67 d
4.	Maturity	50-125 d	90-110 d	56-110 d
5.	Pollen fertility*	98%	96%	58%
6.	Seed color	Yellowish brown	Dark brown	Dark brown

*Average

plant indicated that these traits can be improved tremendously through selection in recombinant inbred population.

The heritability estimates ranged from 33.8 to 92.5 % for branches /plant and 100-seed weight, respectively. However, heritability values for grain yield/plant (42.5%) was found comparatively low as compared to other yield component traits *viz*., 100-seed weight (92.5%), seeds/ pod (74.5%), plant height (59.8%) and pods/plant (48.2%) as expected. Hence, increase in yield may be obtained through selection of component traits *viz*., 100-seed weight, seeds/pod and plant height with high values of heritability coupled with high GCV. Whereas, higher heritability (%) values for 100-seed weight and seeds / pod indicates low influence of environment [13]. High heritability for 100-seed weight and seeds/pod has also been reported in inter-varietal crosses of chickpea by several workers [14-16]. However, no such information is available for interspecific crosses of chickpea. High estimates of genetic advance (percentage of mean) were obtained for grain yield/plant (49.3%) followed by pods/ plant (45.8%) but extremely low for 100-seed weight (7.4%) and plant height (11.6%). The characters like pods/plant having high heritability and genetic advance can be used as parameter for indirect selection for enhancing grain yield. These results are in agreement with the findings of other workers in inter-varietal crosses of chickpea [16, 17]. Significant positive genotypic and phenotypic correlations of grain yield was observed with pods/plant (0.81 & 0.78), branches /plant (0.44 & 0.28), seeds/pod (0.57 & 0.30) and 100-seed weight (0.42 & 0.39) (Table 4). This clearly indicated further that increase in yield should be obtained by indirect selection for component traits. The high correlation of grain yield with pods/plant, branches /plant, seeds/pod, 100-seed weight and plant height have also been reported by several workers in inter-varietal crosses of chickpea [13, 16].

Significant and positive genotypic and phenotypic correlation of pods/plant with 100-seed weight (0.41 & 0.39) was also obtained. Besides, branches/plant was found to be positively (genotypic and phenotypic) correlated with pods/plant (0.34 & 0.25) and seeds/ pod (0.48 & 0.23). Further, seeds/pod was found positively (genotypic) correlated with pods/plant (0.28). Similar findings on correlation among yield and component traits were also reported in inter-varietal crosses of chickpea by other workers [14]. Hence, the trend of correlation between different metric traits in derivatives of inter-specific crosses is not different from those of inter-varietal crosses.

The ANOVA of Augmented Block Design indicated significant block effects which were eliminated while comparing the mean values of RILs. Besides, treatment effect (eliminating block effect as well as ignoring block effects) was also found significant (AVOVA table not given). The superior lines (RILs) for each character over control based on mean values (tested statistically) were identified. It was noted that some of the promising RILs from the cross *C. arietinum* X *C. reticulatum* also showed many undesirable traits *viz*., pod shattering, prostrate growth habit, hard seed coat, undesirable seed surface and seed color. Generally the correlation between phenotypes of selected plants and their progenies was very poor making selection for desirable characters difficult. Besides, segregation in several characters *viz*., growth habit, flower and seed color, seed size and seed shape continued to occur even in F_6/F_7 generations despite of tremendous variability generated in early generations (F_2/F_3) of interspecific crosses [18].

Table 3. General mean, range, variance, coefficient of variation, heritability and genetic advance for different characters in recombinant inbred lines (RILs) population

Character	General mean	Range	Variance		Coefficient of variation (%)		Heritability (%)	Genetic advance(%)
			Geno-typic	Pheno-typic	Geno-typic	Pheno-typic		
Plant height	48.64±0.49	31.0-69.3	52.3	87.9	14.90	19.27	59.8	11.6
Branches/plant	5.53±0.13	3.3-8.7	1.2	3.6	19.82	34.11	33.8	1.3
Pods/plant	73.01±0.89	20.0-197.7	1024.0	2124.4	43.83	63.13	48.2	45.8
Seeds/pod	1.29±0.21	1.1-1.9	0.07	0.09	11.49	23.38	74.5	0.5
100-seed wt.	15.94±0.87	10.3-31.3	13.9	15.1	23.4	24.30	92.5	7.4
Yield/plant	83.58±0.86	21.3-210.7	1350.0	3176.5	67.43	42.50	42.5	49.3

Table 4. Genotypic and phenotypic correlation coefficients in recombinant inbred population derived from cross *Cicer arietinum* cv K850 *x C. reticulatum* (ICCW8)

Characters[@]	1	2	3	4	5	6
Plant height (1)						
Genotypic	-	–0.15	0.03	-0.09	0.08	0.04
Phenotypic		0.02	0.02	0.01	0.09	0.05
Branches/plant (2)						
Genotypic		-	0.34**	0.48**	0.21**	0.44**
Phenotypic			0.25 *	0.23**	0.14	0.28**
Pods/plant (3)						
Genotypic			-	0.28**	0.41**	0.81**
Phenotypic				0.13	0.39**	0.78**
Seeds/pod (4)						
Genotypic				-	0.02	0.57**
Phenotypic					0.01	0.30**
100 seed wt. (5)						
Genotypic					-	0.42**
Phenotypic						0.39**
Yield/plant (6)						
Genotypic						-
Phenotypic						

* Significant at 5 %, ** Significant at 1 %, [@]Characters in parenthesis

The RILs derived from interspecific cross were evaluated for various agronomic traits in F_8 generation. On the basis of superiority of traits (higher mean of RILs over control), promising lines were selected. Maximum numbers of lines were found to be promising for pods / plant (34) followed by branches /plant (32), plant height (30), yield /plant (12) and days to flower (12) over checks (Table 5). This is indicative of translation of expressed variability in recombinant inbred population in terms of isolation of superior lines for various agronomic traits.

The results obtained in the present investigation clearly indicated possibility of improvement of chickpea through wide hybridization. Superior lines isolated through selection in recombinant inbred population having high yielding traits may be used as donors in chickpea improvement program or may be directly tested for their superiority under AICRP trails for the specific regional requirements and the cropping systems. Besides, the RIL populations derived from interspecific crosses can also be used for molecular mapping of QTL's for yield component traits which will eventually provide

Table 5. Promising lines isolated for various characters from F_8 generation of cross *Cicer arietinum* x *C. reticulatum*

S.No.	Characters	Mean of check I (PDG 84-10)	Mean of check II (K 850)	No. of superior lines over check I (PDG 84-10) & check II (K850)
1.	Days to flower (d) (earliness)	45.8	61.2	12
2.	Plant height (cm) (dwarfness)	38	55	30
3.	No. of branches/plant	6.5	5.2	32
4.	No. of pods/plant	81.3	86.5	34
5.	No. of seeds/pod	2.2	1.8	00
6.	100-seed weight (g)	18.2	22.6	01
7.	Yield/plant (g)	88.4	110.2	12

better understanding of the genetics of quantitative traits to formulate appropriate breeding strategies.

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