Indian J. Genet., **62**(2): 128-130 (2002)

Genetic variability created through biparental mating in chickpea (*Cicer arietinum* L.)

Nagaraj Kampli, P. M. Salimath and S. T. Kajjidoni

Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad 580 005

(Received: December, 2000; Revised: December, 2001; Accepted: February, 2002)

Abstract

Biparental mating was attempted in the F_2 of ICCV-10 × BG-256 cross of chickpea (*Cicer arietinum* L.). The biparental population (BIP) had better mean performance than the F_3 selfs for all the characters under study. The lower limit of the range was, in general, smaller for almost all the characters in the BIP. The upper limit had also increased in the desired direction for all the characters. Sufficiently high genetic variation was maintained in the BIP population for most of the characters except for secondary branches. BIP also exhibited improved estimates of heritability and genetic advance. The utility of biparental mating in early segregating generations in chickpea is emphasized.

Key words : Chickpea, biparental mating (BIP), variability

Introduction

Genetic variability is the most essential requirement for any successful crop improvement programme. Cultivated chickpea (*Cicer arietinum* L.) is predominantly a self-pollinated crop. It has been argued that one of the reasons for failure to achieve breakthrough in productivity in self-pollinated crops like in legumes including chickpea as compared to the cereals is the lack of sufficient variability. The presence of larger linkage blocks and inverse relations among the correlated characters are most common. Under such circumstances, conventional breeding methods, such as pedigree, bulk and back cross methods again impose restriction on the chance of better recombination are also associated with the weakness of causing rapid homozygosity and low genetic variability [1]. Biparental mating, on the other hand, is expected to break larger linkage blocks and provide more chances for recombination than the selfing series [2]. It is a useful system of mating for generation of increased variability and may appropriately be applied where lack of desired variation is the immediate bottleneck in the breeding programmes.

Though sharply differing views have been expressed on the effectiveness of biparental approach in self-pollinated crops, it has been successfully employed in some self pollinated crops like wheat and safflower. However, no report on the effectiveness of BIP is available in chickpea. The present investigation was therefore, planned to compare the performance of biparental progenies with the selfed generation in releasing genetic variability for yield and other important yield component traits.

Materials and methods

Two genotypes, ICCV-10 and BG-256 were selected on the basis of their peculiar contrasting characteristic productivity related features as well as reaction to wilt. The F_2 generation of the cross between these two parents was thus an ideal material to effect biparental mating and hence about 100 F_2 plants selected on visual basis keeping in view the vigour, plant type and earliness were used for selective intermating. The F_2 plants used in biparental mating were also selfed to yield F_3 progenies. The field experiment was conducted at the Agricultural College, Dharwad during *rabi* 1999-2000. The BIP population and their corresponding F_3 population were sown in 8 rows each in 5m length row. The rows and plants were spaced at 30 cm and 15 cm, respectively. The data were recorded on all the plants in BIP (220 plants) and F_3 (150 plants) for six characters, *viz.*, plant height (cm), primary branches, secondary branches, pods per plant, 100-seed weight (g) and seed yield per plant (g). The mean and ranges in respect to each character were worked out in the biparental as well as F_3 progenies. The phenotypic and genotypic variances were computed considering the variances of non-segregating generations to be an indicative of environmental variance (Ve). Assuming the variation in the segregating population (Vp) to be equal to the sum of Vg and Ve, the parameter Vg was computed by subtracing mean variance of non-segregating generations from the variance of F_2. The phenotypic and genotypic co-efficients of variation [3], heritability in broad sense [4] and genetic advance [5] were computed.

Results and discussion

The comparison of mean and range of expression of different characters (Table 1) between BIP and F_3

indicated that, in general, mean values of BIP were higher than the corresponding mean values in F_3 for all the characters. The mean values of BIP were generally higher than F_3 because as can be seen from Table 1, the upper limit of range values was higher in BIP than the corresponding value in F_3 indicating that the segregants with higher values were available in BIP. This inturn could be due to breakage of linkage and the consequent release of variability. It may also be due to the accumulation of favourable genes since the BIP population was generated by attempting crosses between the segregants selected on the basis of better performance. Under these circumstances, the mean values of BIP are higher than the mean values of F_3 population. It was also of interest to note that the mean performances improved considerably in respect of pods per plant and seed yield per plant. Superior mean performance of BIP appeared to be due to better exploitation of additive and non-additive gene effects. The non-additive gene effects contributing to the expression of character is a function of a interaction of alleles influencing the character. In BIP, which provides a better scope for the reshuffling of the alleles concerned would certainly help in the better exploitation of the non-additive gene effect and hence results in the increase in mean performance. It is also attributed to the creation of more genetic variability by breakage of undesirable linkages which otherwise conceal the genetic variation in the small size F_2 generation [2]. The results of the present investigation are in agreement with the earlier reports on wheat [6, 7].

Table 1. Mean and range of expression in respect of six quantitative traits in intermated (BIP) and selfed (F_3) populations of chickpea

Character	Range		Mean	
	F_3	BIP	F_3	BIP
Plant height (cm)	28-50	20-57	34.53 ± 0.35	40.58 ± 0.40
Primary branches	2-7	2-9	3.57 ± 0.10	4.23 ± 0.10
Secondary branches	6-38	4-44	16.88 ± 0.54	18.44 ± 0.47
Pods per plant	30-261	20-365	95.57 ± 3.91	106.64±3.59
100-seed weight (g)	14.1-24.0	14.0-28.6	18.45 ± 0.16	18.86 ± 0.17
Seed yield per plant (g)	6.0-52.3	4.6-77.9	20.95 ± 0.88	24.37 ± 0.84

The range of expression of characters in biparental progenies were wider. It is noteworthy that especially the upper limit of range was higher in BIP for all characters. At the same time, the lower limit was smaller compared to that of F_3 progenies suggesting that intermating has helped in releasing more variability than mere selfing. The higher variability in the BIP population could have resulted from the additional opportunity for genetic recombination. The general shifts in the values of range of expression of characters by biparental approach was also reported in wheat and safflower [7, 8].

The estimates of variability, heritability and genetic advance for various characters in BIP and corresponding F_3 progenies are presented in Table 2. The BIP had greater variance, GCV, PCV, heritability and genetic advance (% of mean) in respect of all the characters. The characters which showed wider range were also characterised by higher magnitudes of GCV and PCV. Generally, BIP population had higher GCV and PCV for all the characters except for secondary branches. Higher GCV and PCV in the BIP as compared to F_3 were also reported in wheat [9]. Among the characters, GCV and PCV were high for seed yield per plant (37.81 and 50.87, respectively) and pods per plant (41.84 and 49.95, respectively) in BIP. This suggests that, there is more scope for selecting better segregants in BIP population on the basis of pods per plant and seed yield per plant.

Table 2. Estimates of genetic variability parameters in respect of six quantitative traits in F_3 and BIP populations of chickpea

Character	Population	GCV (%)	PCV (%)	h^2 (bs) (%)	GA (% of mean)
Plant height (cm)	F_3	10.32	11.96	74.42	18.33
	BIP	13.80	14.73	87.78	26.64
Primary branches	F_3	25.16	33.90	55.09	38.38
	BIP	28.27	34.16	68.49	48.20
Sec. branches	F_3	32.53	38.63	70.92	56.43
	BIP	32.26	37.06	75.81	57.86
Pods per plant	F_3	37.91	48.62	60.79	60.88
	BIP	41.84	49.95	70.17	72.20
100-seed wt (g)	F_3	8.03	10.49	58.56	12.62
	BIP	11.62	13.36	75.58	20.81
Seed yield/plant(g)	F_3	30.06	49.70	36.58	37.47
	BIP	37.81	50.87	55.25	57.90

In case of BIP, the heritability was higher in respect of yield and its component characters than in F_3s. Improvement of heritability from moderate to high level was observed even for primary branches and 100-seed weight in BIP. This suggested that the variation due to environment played a relatively limited role in influencing the inheritance of these characters and thus the expected response to selection is higher in BIP. High heritability in case of BIP over F_3 has also been reported in wheat [6, 9]. Like for heritability, BIP also

showed relatively high expected genetic advance (as per cent mean) estimates for all characters as compared to selfed progenies. Among the characters, pods per plant and seed yield per plant showed higher genetic advance. This suggested that, the gain from selection based on these two traits would be higher in BIP than in their corresponding selfed progenies. This is further supported by the wider range of expression and that too in the desirable direction in BIP as mentioned earlier.

The comparison of biparental mating and selfing shows that whatever additional variability realised with biparental mating in the early segregating generations has been the consequence of release of concealed variability in the segregating generations which is probably brought about by rare recombination between the tightly linked genes. In addition to this, it is also expected to help in maintaining a greater variability for selection to be effective for longer period. Chickpea is a self-pollinated crop where lack of variability has been implicated as one of the important causes for lack of desired progress in breeding. Hence, the present report on the use of biparental mating in an early segregating generation like F_2 of an appropriate cross, could be of much use in widening variability and consequently in making considerable gains in improving productivity.

References

1. **Clegg M. T., Allard R. W. and Kahlar A. L.** 1972. Is the gene unit of selection? Evidence from two experimental plant populations. Proc. Acad. Sci. (USA)., **69**: 2474-2478.
2. **Gill K. S., Bains S. S., Singh G and Bains K. S.** 1973. Partial diallel test crossing for yield and its components in *Triticum aestivum* L. Proc. 4th Intern. Wheat Genet. Symp. Missouri, Columbia 29-33.
3. **Burton G. S. and Devane E.J.** 1953. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. Agron. J., **45**: 478-481.
4. **Hanson G. H., Robison H. F. and Comstock R. E.** 1956. Biometrical studies of yield in segregating populations of Koren hespedeza. Agron. J., **48**: 267-282.
5. **Robinson H. F., Comstock R. E. and Harvey P. H.** 1949. Estimates of heritability and degree of dominance in corn. Agron. J., **41**: 353-359.
6. **Yunus M. and Paroda R. S.** 1983. Extent of genetic variability created through biparental mating in wheat. Indian J. Genet., **43**: 76-81.
7. **Nematullah and Jha P. B.** 1993. Effect of biparental mating in wheat. Crop Improv. **20**: 173-178.
8. **Parameshwarappa K. G., Kulkarni M. S., Gulganji G. G., Kubsad V. S. and Mallapur C. P.** 1997. An assessment of genetic variability created through biparental mating in safflower (*Carthamus tinctorius* L.) IVth Intern. Safflower conference, BARI (Italy) 2-7 June 238-239.
9. **Nanda G. S., Singh G and Gill K. S.** 1990. Efficiency of intermating in F_2 generation of an intervarietal cross in bread wheat. Indian J. Genet., **50**: 364-368.