



Relative efficiency of bi-parental mating for genetic improvement of seed yield in blackgram [*Vigna mungo* (L.) Hepper]

P. CHAND¹ AND T.R. DAS^{2*}

¹ Regional Agricultural Research Station, Palem, Andhra Pradesh-509215, India.

² Division of Genetics, ICAR- Indian Agricultural Research Institute, New Delhi-110012, India

*trdas.iari@gmail.com

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ABSTRACT

The present investigation was conducted to study the effects of bi-parental mating and pedigree methods on mean performance, genetic variability, transgressive segregants and shifts in correlation coefficients. The analysis of mean squares due to males, females, and interactions (male x female) were significant for almost all the characters. This implied that sufficient genetic variability existed in the parents and F_1 's also, indicating that parents were genetically divergent to create sufficient variability in F_2 populations and provide ample scope for selection. The mean values of bi-parental progenies were higher than the pedigree progenies for all the characters. However, it was lower for days to flowering and maturity, indicating the possibility of getting early segregants. The superior mean and wider ranges of variation in bi-parental progenies may be due to releasing of hidden genetic variability. A positive significant association was observed between seeds per pod and 100-seed weight, and seeds per pod with pod length in the progenies of Chikkuduminumu X L-400, which could have otherwise been negative due to limited source and sink relationship, indicate the breakage of undesirable linkages between these traits. It can be inferred from the study that bi-parental mating in early generation followed by selection would not only effectively accumulated the favorable genes but also maintain variability for more effective selection in blackgram.

Key words: Bi-parental mating, blackgram, correlation coefficient, genetic variability, heritability

INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper] commonly called as urad bean is an important food legumes for South and South East Asia. Being a short duration crop, it is suitable for intercropping with different crops as well as it fits well in crop rotation with cereals, such as wheat or rice (Sakila and Pandiyan, 2018). Its seeds are highly nutritious with an excellent source of easily digestible good quality protein (24-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. The biological value improves greatly, when wheat or

rice is combined with blackgram because of the complementary relationship of the essential amino acids such as arginine, leucine, lysine, isoleucine, valine and phenylalanine, etc. (Mehra et al., 2016). India is the world's largest producer as well as consumer of blackgram. It produces near about 2.77 million tonnes of blackgram annually from 46.3 lakh hectares of area in 2021-22 (Anon., 2023). The bottlenecks in its improvement have been the lack of variability in different traits and improvement of one trait on its own will affect the performance of other traits because of genotypic correlations between traits (Das and Baisakh, 2019). The major

breeding approach for increasing productivity in an autogamous crop is hybridization followed by selection in the segregating generation. However, the success depends on the choice of the parental variety, the nature of gene action, breeding methods and the efficacy of selection in segregating generations (Baisakh et al., 2014). Success of a breeding programme depends on the extent of heterosis for seed yield and its component characters (Imran et al., 2017). Traditional breeding procedures, such as pedigree, bulk, and back crossing methods limit the chances of better recombination because of larger linkage blocks associated with the weakness of creating rapid homozygosity and low genetic variability (Rudra et al., 2009). Due to repeated selection followed by rapid homozygosity, there is a loss in genetic variability and poor recombination. The pedigree method of selection has been the most commonly used breeding procedure but this procedure has certain limitations such as limited parent participation, rapid fixation of genes, low genetic variability, and poor recombination potential. Several comprehensive breeding systems have been proposed to systematically develop and exploit variability in plant populations. Bi-parental mating is an effective mating system for increasing diversity and may be used where desired variation for traits of interest is lacking (Guddadamath et al., 2010; Koli et al., 2018). In early segregating generations of autogamous crops, it has been recommended to (i) generate, retain and exploit greater variability for several cycles of selections, (ii) elevate population mean, and (iii) improve chances of occurrence of potentially useful segregants resulting in to stable and widely adapted genotypes. Conventional breeding methods impose restrictions on the chances of better recombination and cause rapid homozygosity and low genetic variability whereas, bi-parental mating is expected to break larger linkage blocks and provide more chances for recombination than the selfing series (Frederickson and Kronstad, 1985). Bi-parental mating was more efficient in increasing the mean values, variances, genotypic and phenotypic coefficients of variation, heritability and genetic advance in majority of the yield components of blackgram (Chand, 2001). The present investigation

was therefore, initiated to study the effects of bi-parental mating and pedigree method on mean performance, release of hidden genetic variability and shift in correlation coefficients in blackgram by adopting North Carolina Design-II.

MATERIALS AND METHODS

Experimental materials and data collection

The experiment consisted of 625 bi-parental progenies developed in F_2 generation of the cross viz., Chikkudumunumu \times L-400. The F_2 population was raised and 25 each male and female competitive plants were randomly selected from F_2 base population and intermated following North Carolina Design (NCD)-II, thus 625 half sib progenies were developed. The parents were selected based on their phenotypic diversity of plant types. In pedigree method, exercised 10% selection on the same F_2 population, 150 phenotypically superior plants were selected to raise the individual plant progenies in F_3 generation. The 625 bi-parental progenies; 25 male parents; 25 female parents and 125 selected advanced (F_3) plants were studied in randomized block design with three replication with 2 rows of 4 m length and spacing of 30 cm \times 10 cm at Regional Agricultural Research Station, Palem, Andhra Pradesh, India. The package and practices for raising good crop was followed as per recommendation. The observation was recorded on ten randomly selected plants for eight quantitative traits viz. plant height (cm), branches per plant, clusters per plant, pods per plant, seeds per pod, pod length (cm), 100-seed weight (g), and seed yield per plant (g). Days to 50 per cent flowering and days to maturity were observed on plot basis. Percentage of transgressive segregants in F_2 and F_3 generation was obtained by the defining extreme progeny as significant transgressive segregants (i.e. the lines exceeded their better parental mean and L.S.D. at 5% probability). Analysis and comparison were made based on the value of individual plants. The transgressive segregants were calculated in favorable direction only.

Analysis of data for genetic parameters

The data were analyzed using statistical model of North Carolina Design-II (Comstock

and Robinson, 1952) on the basis of mean values. Components of variance (σ^2_p , σ^2_g , σ^2_e) were used for the estimation of coefficients of variation (PCV, GCV) as described by Panse and Sukhatme (1967) as follows:

$$PCV = \frac{(\sqrt{\sigma^2_p}) \times 100}{X}$$

$$GCV = \frac{(\sqrt{\sigma^2_g}) \times 100}{X}$$

$$\sigma^2_g = P - (G \times E) - E \text{ and } \sigma^2_p = \sigma^2_g + E$$

Where;

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

X = Grand mean

G × E = Genotype × environment interaction effect

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Broad sense heritability (h^2) was estimated as a ratio of additive and dominance variance to the total variance (Allard, 1960). Heritability (broad-sense) is the proportion of a population's phenotypic variance that is attributable to genetic differences. Heritability was classified as low (< 20 %), medium (20 - 50 %), and high (> 50 %). Genetic advance (GA) suggested by Johnson et al. (1955) were estimated using following formula.

$$GA = k.h.\sigma_g = k.h^2.\sigma_p$$

$$GA \text{ (as \% of mean)} = GA/\text{Mean} \times 100$$

Where,

k = Standardized selection differential for specified selection intensity (k=2.06 at 5% selection intensity)

h = Square root of heritability coefficient

σ_g = Square root of genotypic variance

σ_p = Square root of phenotypic variance

Correlation analysis

In plant breeding, it measures the mutual relationship between various characters and determines the component characters on

which selection can be relied upon for genetic improvement of yield. At genetic level, positive correlation occurs due to coupling phase of linkage and negative correlation arises due to repulsion phase of linkage of gene controlling two different traits. Both types of these correlations may be because of pleiotropy, i.e. developmental correlation. Genetic correlation expresses the extent to which two measurements reflect what the same character is genetically. The offspring - parent relationship can also be used to estimating the genetic correlation. No correlation indicates that genes concerned are located far apart on the same chromosomes or they are located on different chromosomes. Another basic use of r_g is prediction of genetic gain.

The different correlations i.e. genotypic correlations (r_g) and phenotypic correlations (r_p) were computed according to Al-Jibouri et al. (1958) by following formula:

$$r_g = \frac{\sigma_{g(xy)}}{(\sigma_{g(x)}^2 \cdot \sigma_{g(y)}^2)^{1/2}}$$

Where, $\sigma_{g(xy)}$ is the genotypic co-variance between x and y and $\sigma_{g(x)}^2$ and $\sigma_{g(y)}^2$ are the genotypic variance of the characters X and Y, respectively.

$$r_p = \frac{\sigma_{p(xy)}}{(\sigma_{p(x)}^2 \cdot \sigma_{p(y)}^2)^{1/2}}$$

r_p = Where, $\sigma_{p(xy)}$ is the phenotypic co-variance between x and y and $\sigma_{p(x)}^2$ and $\sigma_{p(y)}^2$ are the phenotypic variance of the characters X and Y, respectively.

Significance of correlation coefficient was tested by t-test with (n-2) d.f. by the formula:

$$t = \frac{r}{\left[\frac{1-r^2}{n-2} \right]^{1/2}}$$

Where, 'r' is the correlation coefficient and 'n' is the number of cultures.

RESULTS AND DISCUSSION

Release of variability

Substantial genetic variability was released for many traits in bi-parental progenies developed from F₂ population in blackgram. Such a release of latent variability is attributed mainly to the breakdown of undesirable linkages. A comparison of mean values, phenotypic and genotypic coefficients of variation, heritability and genetic advance were higher in bi-parental progenies than those of pedigree progenies for all the characters except clusters per plant (Table 1). The estimates of PCV were higher in the pedigree progenies than bi-parental population (BIP) for clusters per

plant indicated the predominance of coupling phase linkage for this trait in the parents. The enhanced variability for all traits in the bi-parental progenies could be attributed to the accumulation of favorable genes spread over the population and maintained sufficiently high genetic variation for all traits (Chand and Rao, 2001). With the help of GCV alone, it may not be feasible to determine the amount of heritable variation and the relative degree to which a character is transmitted from parent to offspring is indicated by the estimate of heritability. Heritability estimates along with genetic advance are normally helpful in predicting the genetic gain under selection than heritability estimates alone.

Table 1. Genetic parameters for different seed yield characters in bi-parental and pedigree progenies of blackgram cross

Characters	Progenies	Mean	Range	GCV	PCV	Heritability	Genetic advance (% of mean)
DF	B	42.66	37.00 - 45.00	4.56	5.10	79.81	8.39
	P	42.37	38.00 - 46.00	3.51	4.11	72.94	6.17
DM	B	71.33	68.00 - 75.00	2.89	3.43	71.05	5.02
	P	72.33	69.00 - 77.00	1.82	2.43	56.15	2.80
PH	B	27.33	16.00 - 36.00	4.52	5.71	62.59	7.37
	P	25.22	15.00 - 30.00	7.04	9.83	51.29	10.39
BP	B	4.66	2.00 - 6.00	7.66	9.43	65.92	12.81
	P	3.66	2.00 - 5.00	6.26	8.23	58.30	9.89
CP	B	20.33	9.00 - 28.00	2.90	3.74	63.59	4.91
	P	20.33	10.00 - 25.00	1.99	4.32	73.87	3.53
PP	B	96.33	49.84 - 130.00	14.35	15.53	85.35	27.31
	P	75.66	40.00 - 85.00	12.34	13.35	85.31	23.48
SP	B	8.53	5.00 - 10.00	9.89	11.69	71.64	17.25
	P	5.13	4.00 - 8.00	8.79	10.93	64.64	14.52
PL	B	6.26	4.00 - 7.00	13.57	15.19	79.78	24.97
	P	4.60	3.00 - 5.50	11.55	13.27	75.80	20.70
TW	B	5.60	4.00 - 6.00	6.40	7.29	77.07	11.59
	P	4.50	4.00 - 5.40	4.10	5.29	60.21	6.55
SYP	B	31.91	11.00 - 51.00	9.12	10.26	78.98	16.69
	P	25.67	10.00 - 30.00	7.10	8.21	74.75	12.63

DF= Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); BP= No. of branches per plant; CP= No. of clusters per plant; PP= No. of Pods per plant; SP = No. of seeds per plant; PL = Pod length (cm); TW = 100-seed weight (g); SYP = Seed yield per plant; B=Bi-parental; P= Pedigree

Hence, both heritability and genetic advance were determined to get a clear picture of the scope of improvement in various characters through selection. The heritability was higher in BIP for yield and its component characters than in F_3 which suggested that the variation due to environment showed relatively limited role in influencing the inheritance of these characters and thus the expected response to selection is higher in BIP. Like heritability, BIP also showed relatively high expected genetic advance (as per cent of mean) estimates for all the characters as compared to pedigree progenies. Higher genetic advance observed for pods per plant, seeds per pod, pod length and seed yield per plant, indicating that the gain from selection based on these traits would be higher in BIP than in their corresponding selfed progenies.

The observed higher means and larger magnitude of genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as percent of mean might be attributed to selection, release of hidden genetic variability, and breaking of undesirable linkage and accumulation of favorable genes. The estimates of heritability derived from BIPs are considered to be realistic as BIPs are comparatively free from linkage disequilibrium (Kanwar and Korla, 2004). In the present study, very high heritability estimates for some of the traits are outcome of high additive variance. Hence, selection in early segregating generations based on accumulation of additive genes may be productive for getting superior inbreds which could be used in hybrid breeding programs (Hendawy, 2008; Hassan et al., 2013).

For most of the characters, this mating system (NCD-II) proved to be superior for creating the desirable variability. This makes possible the emergence of those segregants, which would have been rarely obtained in the selfing series. The higher variability in the intermated population could also result from the additional opportunities for genetic recombination.

Transgressive segregants

Breeding for yield generally aims at isolating gene combination (recombinants), which possesses new characters or new intensity of

trait. These segregants are superior to either of parents or also to the existing local best cultivars. Bi-parental mating resulted in the highest number of transgressive segregants for all the characters than pedigree method (Fig.1). Transgressive segregants are produced by accumulation of favorable genes affecting yield and other characters. No transgressive segregants for 100-seed weight were observed in pedigree method, suggesting that the parents had similar constitution of the genes for this trait. The ineffectiveness of pedigree method in producing transgressive segregation for yield and its components may be attributed to the genetic drift, which is an important factor in determining probability of increase of desirable alleles with a single family. Most of the transgressants for yield showed transgressive segregation for pods per plants and clusters per plant indicating that these traits are a major yield contributing component in this cross. However, some lines also showed transgressive segregants for seeds per pod and 100-seed weight but in low frequency. Transgressive segregants in F_2 may arise due to dominance and dominance interactions in addition to additive x additive interaction which is fixable or due to recombination of genes with positive effects and responsible for the production of transgressive segregants in the F_3 generation. The findings therefore, also revealed that the parents differed for many genes and introgression of genes from exotic germplasm lines created large amount of genetic variability for yield and its components in some of the crosses suggesting the scope to use these crosses/material. Similar results were also reported by Vandodariya et al. (2020) and Sateesh et al. (2022) in blackgram. The crosses which gave high frequency of transgressive segregants for yield per plant, pods per plant in both the methods may be preferred over the other crosses in an ongoing breeding program. Combining distantly related parents possessing desirable traits in the required intensity but controlled by different set of genes, tends to ensure release of transgressive segregants. Chance of recombination of productivity genes might be expected to enhance the yield level of such segregants.



Fig. 1. Desirable transgressive segregants in blackgram for seed yield and its component characters

Shifts in nature and magnitude of genetic association

The aim of correlation studies is primarily to know about the suitability of various characters for indirect selection because selection for one character results in correlated response for several other characters resulting into changed pattern of variability. A significant effect of bi-parental mating was reflected in a change in the nature of genetic correlations. A comparison of genotypic correlation among the characters between the bi-parental and pedigree progenies indicated several new correlations in terms of magnitude and direction in this cross (Table 2). For example, in bi-parental progenies of CKM XL-400, significant positive association was observed between seeds per pod and 100-seed weight, and pod number and pod length, which could have otherwise been negative due to limited source and sink

relationship, indicates the breakage of undesirable linkage between these traits. This is in agreement with the findings of Destro et al. (2003) in soybean and Ahmed et al. (2008) in fababean. Such changes in magnitude and direction may occur due to genes reshuffling and breakage of linkage due to bi-parental intermating in the early segregating generations. These associations particularly in desirable direction will be useful for selection in desirable traits for blackgram improvement. Some desirable recombinants with high pod number, more seeds per pod and number of branches was realized from the present study. The association of high heritability with high genetic advance was observed for days to flowering, days to maturity, branches per plant, clusters per plant, pods per plant, and seed yield. This indicated the presence of additive gene effects and consequently a high genetic gain (Fig. 2) from phenotypic selection will be effective. The changes in correlations from one breeding method to other may be due to differential changes of gene and genotypic frequency associated with different procedures of generation advancement in different breeding methods. Bi-parental 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. Blackgram 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 bi-parental 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 in blackgram.

Table 2. Genotypic correlations in bi-parental and pedigree progenies in black gram

Characters	Progenies	PP	SP	PL	TW	SYP
CP	B	0.933	0.087	0.337	0.032	0.532
	P	-0.341	0.031	0.099	0.004	0.127
PP	B	-	0.083	0.104	0.024	0.784
	P	-	-0.024	0.074	0.011	0.433
SP	B	-	-	0.623	0.540	0.412
	P	-	-	0.322	-0.147	0.213
PL	B	-	-	-	0.540	0.048
	P	-	-	-	0.133	0.013
TW	B	-	-	-	-	0.251
	P	-	-	-	-	0.097

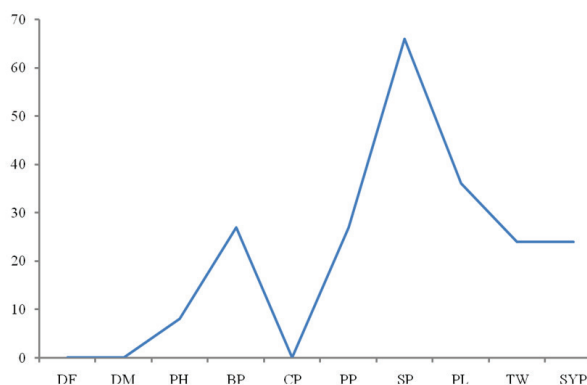


Fig. 2. Genetic gain for seed yield and component characters in bi-parental over pedigree progenies of blackgram

CONCLUSION

On the basis of the estimates of the genetic parameters in the present study, it is concluded that the selection of diversified parents based on their plant type characters, raising of a large F_2 population, carrying out selection and intermating of selected plants from F_2 itself for utilizing both the additive and non-additive gene effects and minimizing the undesirable linkages and repeating the process of intermating if necessary in the succeeding generations and further selection may be adopted for identifying desirable plant types in segregating generations. The bi-parental mating approach in the blackgram may substantially supplement the conventional breeding procedure by way of improving the mean performance and creating more genetic variability because of accumulation of favorable genes and breaking of undesirable linkage and improving the efficiency of selection.

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