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Genetic analysis of seed yield characteristics in biparental progenies of blackgram [*Vigna mungo* (L.) Hepper]

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ABSTRACT

The experiment was conducted for the genetic analysis of seed yield determining factors in 625 half-sib progenies developed from a biparental cross beyween two blackgram lines (L-207 × L-400) by using North Carolina Design–II. The mean squares due to females were of higher magnitude in comparison with those due to males and interactions, indicating greater diversity among females. The differences between parents were also highly significant for most of the characters, indicating that the parents differed significantly divergent to create high variables in the F_2 population and thus giving ample scope for selection. The results revealed that additive genetic variances were higher in magnitude than dominance genetic variance for pods per plant, seed yield per plant, clusters per plant, branches per plant, and 100-seed weight. Additive However, traits viz., days to flowering, days to maturity, plant height, seeds per pod, and pod length expressed higher dominance variance than additive variance, indicating that these characters were governed by non-additive gene action. The study demonstrates that both additive (fixable) and non-additive (non-fixable) components of genetic variance were involved in governing the inheritance of most of the quantitative traits. Biparental mating of selected segregants might not only break the undesirable linkages, if any but also allow the accumulation of favorable genes that could be useful for the genetic improvement of traits in blackgram. In the present study, high heritability coupled with high genetic advance as a percent of the mean was recorded for the seed yield per plant, pods per plant, pod length, 100-seed weight and seeds per pod indicating that the additive gene action is involved in the genetic control of these traits. In future breeding programmes, selection can be very effective for the improvement of these traits for enhancing the genetic yield potential in this crop. The results of the genotypic correlation coefficient between the different characteristics revealed that the seed yield per plant had a significant and positive association with the traits viz., pods per plant, clusters per plant, 100-seed weight, seeds per pod and pod length. These results would be quite substantial with the dwarfing genes and intense selection programme for a plant type, which involves several component traits related to productivity.

Key words: Biparental mating, blackgram, correlation, genetic variance, heritability, transgressive segregants

INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper] commonly called as urad bean is an important pulse crop grown in many parts of India and has wide adaptability 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 (Chand and Das, 2024). 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). Considering the population growth and domestic consumption requirement of pulses in our country, black gram, whose genetic potential is yet to be fully exploited (Das et al., 2016), is urgently needed to increase its productivity and the country's total blackgram production by developing high-yielding and widely adopted varieties. However, the bottlenecks in improvement is the lack of variability in different traits and the improvement of one trait affecting the performance of other traits because of genotypic correlations between traits (Das and Baisakh, 2019). Thus the knowledge of the interrelationship of plant characters with seed yield and among themselves is of paramount importance to the breeders, for making improvements in complex characters like seed yield, for which direct selection is not much effective. Therefore, the character association analysis was required to determine the direction of selection and number of characters to be considered in improving the seed yield. To improve the yield potential of cultivated blackgram varieties, it is essential to utilize the available genetic diversity present in the genetic resources and it could be the only possible means to attain sustainable development and nutritional security (Ramya et al., 2013). The success of a breeding programme depends on the extent of heterosis for seed yield and its component characters (Imran et al., 2017). 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). Though, conventional breeding methods were significant and productive in their own right, but imposed restrictions on the chance of recombination because of larger linkage blocks. Information on gene action for seed yield and its component traits in different populations is imperative for planning an effective breeding programme. Many mating designs were proposed by many authors to know the genetics of quantitative characters. Among these, biparental is one of the simplest random mating designs available to effect forced recombination and breaking down undesirable linkages as pointed out by Comstock and Robinson (1952). It provides more reliable estimates concerning both additive and non-additive components. The genetic variance is transmitted, can be utilized for genetic improvement through selection, and provides the estimation of the genetic determination to which a trait is determined by genes. 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). Biparental mating is an effective mating system that breaks larger blocks and provides more chances of recombination for increasing diversity and may be used where the desired variation for traits of interest is lacking (Chand and Das, 2024). Frederickson and Kronstad (1985) stressed that in autogamous crops, intermating among early segregants could open new vistas to new levels of genetic variability by breaking up the genetic recombination within the linkage group. The presence of adequate additive genetic variance for most of the characters is essential for the development of superior pure lines in a self-pollinated crop like blackgram. Therefore, the present investigation was carried out to obtain genetic information for seed yield and its related characters using North Carolina Design-II in blackgram.

MATERIALS AND METHODS

Experimental materials and data collection

The experimental material consisted of parents and 625 half-sib progenies of blackgram derived from a divergent cross L-207 × L-400. The F_1s were developed at the Regional Agricultural Research Station, Palem. The F1 was raised to produce a large F_2 population and twenty-five chosen parents (males and females) from the F_2 population were intermated following North Carolina Design-II resulted in 625 half-sib progenies. The 625 biparental progenies; 25

male parents; 25 female parents and 125 selected advanced (F_3) plants were studied in randomized block design with three replications with 2 rows of 4 m length and spacing of 30 cm × 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 from each parent and F1's randomly selected from each progeny in each replication 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). Other two traits viz., days to 50% flowering and days to maturity were observed on a plot basis.

Analysis of data for genetic parameters

The mean data of all the characters were subjected to analysis of variance in randomized block design. After ascertaining significant differences among the BIPs, the data was used to estimate the components of genetic variance appropriate to North Carolina Design-II using the statistical model of Comstock and Robinson (1952). The great utility of BIPs is in getting precise estimates of additive (σ^2_A) and dominance (σ^2_D) components of genetic variance and average level of dominance.

$\sigma^2_D = 4\,\sigma^2_m$

$\sigma^2_A = 4\,\sigma^2_m$

$\sigma^2_m = Cov(HSm)$

$\sigma^2_f = Cov(HSf)$

$\sigma^2_{mf} = [Cov(FS)\text{-}Cov(HSm)\text{-}Cov(HSf)] = 1/4\,\sigma^2_D$

σ^2_m : Variance due to males,

σ^2_f : Variance due to females,

σ^2_{mf}: Variance due to males x Females,

Cov(FS) = covariance of full-sibs,

Cov(HSm) : Covariance of half-sibs with common male,

Cov(HSf) : Covariance of half-sibs with common female.

The average degree of dominance (d) of genes controlling quantitative traits can be estimated in a population with two equally frequent alleles using a ratio of additive and dominance genetic variances.

$$d = \sqrt{\frac{2\sigma_A^2}{\sigma_D^2}}$$

If the value of the average degree of dominance is 0= then there is no dominance; if it is > 0 but < 1, then there is partial dominance; if it is 1, then there is complete dominance, and if it is >1, then there is over dominance types of gene action. The dominance ratio (σ^2_D / σ^2_A) indicating prevalence or otherwise of dominance alleles in the population is < 1 this indicates that, dominant alleles are slightly less frequent than recessive alleles.

The components of variance were used for the estimation of coefficients of variations (PCV, GCV) as described by Panse and Sukhatme (1967) as follows:

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

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

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

X = Grand mean

σ^2 p = Phenotypic variance

σ^2 g = Genotypic variance

Heritability in broad sense (h^2) was estimated as the ratio of genetic variance to the phenotypic variance as reported by Burton (1952) as follows:

It was categorized according to Robinson et al. (1949) into three classes: 0-30% (Low), 31-60% (Medium) and more than 60% (High).

Genetic advance (GA) and Genetic advance as percent of mean (GAM) were estimated as suggested by Johnson et al. (1955) by the following formula and GAM was categorized into three classes: less than 10% (Low), 10-20% (Moderate) and more than 20% (High).

$$GA = k.h.\sigma\ g = k.h^2.\sigma\ p$$

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

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

The mutual relationship between various characters determining the component characters on which selection can be relied upon for genetic improvement of seed yield can be estimated by correlation analysis (Chand and Das, 2024). At the genetic level, positive correlation occurs due to the coupling phase of linkage and negative correlation arises due to the repulsion phase of linkage of gene controlling two different traits. 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 estimate the genetic correlation. Another basic use of genetic correlation is a prediction of genetic gain. The genotypic correlations (r_g) were computed according to Al-Jibouri et al. (1958) by the following formula:

$$r_g = \frac{\sigma_{g(xy)}}{\left(\sigma^2_{g(x)}.\sigma^2_{g(y)}\right)^{½}}$$

Where, is the genotypic co-variance between x and y and

$\sigma^2_{g(x)}$ and $\sigma^2_{g(y)}$ are the genotypic 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:

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

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

RESULTS AND DISCUSSION

Analysis of variance

In the present study, the analysis of variance revealed highly significant differences among progenies for all the characters showing sufficient genetic differences at p = 0.01 or 0.05 level of significance (Table 1). The mean squares due to females were of higher magnitude in comparison with those due to males and interactions, indicating greater diversity among females. The differences between parents were highly significant for most of the characters, indicating that the parents differed significantly for these characters. Similarly, the sum of squares for F_1s (inter-mated progenies) was also highly significant for all the characters under study, suggesting that parents used in the cross were genetically divergent to create high variables in the F_2 population thus giving ample scope for selection.

Variance component and gene action

An overall understanding of the gene action for different characters is possible by making a comparison of variances due to additive/ or dominance. The breeding method might be decided based on the relative importance of additive and dominance variances (Barker, 1978). A higher magnitude of additive genetic variance indicates the predominance of additive gene action and that of dominance variance indicates the non-additive gene action. The choice of breeding method primarily depends upon the nature and magnitude of gene action. In predominantly self-pollinated crops, additive genetic variance plays a pivotal role. In cases where nonadditive genetic variance is predominant, a breeder has to look in for transgressive segregants to fix up such characters and further utilization in the crop improvement for the reason that nonadditive genetic variance cannot be totally ignored. The relative magnitudes of the component parts of genetic variance are required to determine the genetic properties of the population particularly the degree of resemblance among relatives and to study the inheritance pattern of a metric trait. The genetics of a metric trait is the study of the relative magnitude of the components of its variance attributed to various causes. The higher the additive genetic variance, the higher will be the genetic progress. The genetic variance attributed to the non-additive genetic variance is not fixed and hence cannot be predicted for the next generation because the function of the gene's combination in an individual is unpredictable. The selection for genetic improvement based on this part of the genetic variance is not effective. Therefore, it is not desirable to plan for genetic improvement through selection based on the amount of non-additive variance. However, the non-additive genetic variance can also be exploited by heterosis breeding methods.

In the present study, the biparental progenies exhibited significant variance due to females for days to flowering, plant height, clusters per plant, pods per plant, and seed yield per plant, whereas the significant variance due to males was observed for pods per plant only Table 2. The estimates of variance due to interaction (males and females) were highly significant for days to flowering, plant height and pods per plant. A perusal of variance estimates in the present investigation revealed that additive genetic variance was higher in magnitude than dominance genetic variance for pods per plant, seed yield per plant, clusters per plant, branches per plant, and 100-seed weight. The existence of additive variance is a prerequisite for improvement through selection because this is the only variance that responds to selection. Additive variance is a measure of additive gene action and thus gene action is the chief cause of resemblance between relatives and progress by selection is directly proportional to the degree of resemblance between the parent and progeny. Thus, additive gene action is a measure of the breeding value of a genotype. Hence for the above traits which showed preponderance of additive gene action, reliance should be placed on pure line selection and progeny selection. This is in agreement with the findings of Manickavelu et al. (2006). Further, these traits could be improved by pedigree breeding method while going for hybridization and selection. The remaining traits viz., days to flowering, days to maturity, plant height, seeds per pod, and pod length expressed higher dominance variance than additive variance, indicating that these characteristics were governed by non-additive gene action. Since the dominance variance is the chief cause of heterosis, these traits could be improved by heterosis breeding. But in blackgram being a self-pollinated crop, heterosis breeding is not widely adopted, unlike recombination breeding. Therefore, to get better genotypes by way of recombination breeding, hybridization followed by selection at a later generation is suggested for exploiting dominance gene action. However, both additive and dominance genetic variance were significant for days to flowering, days to maturity, plant height, clusters per plant, pods per plant and seed yield per plant. The importance of both additive and non-additive gene effects has also been emphasized for seed yield and its components (Natrajan et al., 1990; Samantaray et al., 2018). The dominance ratio of the total number of dominant to recessive genes revealed, that dominant genes were excess than the recessive for all the characters except days to flowering, days to maturity, and seeds per pod which conforms to the report of Chand (2001) in this crop. The average degree of dominance was more than one for days to flowering, plant height, branches per plant, clusters per plant, pods per plant and seeds per plant, 100 seed weight and seed yield per plant, indicating the existence of over dominance for these characters. Partial dominance was observed for days to maturity and pod length as the degree of dominance was less than one. Similar results have also been reported by Luthra et al. (1979).

Estimation of genetic parameters

The success of any breeding programme depends largely on the extent of the genetic variability present in the base population. Substantial genetic variability was released for many traits in bi-parental progenies developed from the F_2 population in blackgram. Such a release of latent variability is attributed mainly to the breakdown of undesirable linkages (Chand and Das, 2024). The mean performance, coefficient of variation, heritability (bs) and genetic advance as a percent of the mean were computed and presented in Table 3. The mean performance showed variation for most of the characteristics under study. The high genetic variations (GCV and PCV) were observed for seed yield per plant, pods per plant, clusters per plant, pod length and seeds per plant. Whereas, moderate values of GCV and PCV were observed for the 100-seed weight branches per plant and plant height. Similar findings had also been reported for these traits by Ayyappan et al. (2022). The low estimates of GCV and PCV were observed for the traits viz., days to maturity and days to flowering.

High heritability was recorded for the seed yield per plant followed by pods per plant, pod length, 100-seed weight, seeds per pod, clusters per plant and branches per plant whereas, the moderate values of heritability were recorded for days to 50% flowering, plant height and days to maturity. Highest genetic advance as a percentage of mean was recorded for the pods per plant followed by seed yield plant, pod length, clusters per plant and seeds per pod, while, moderate genetic advance as percent of mean was recorded for the traits viz., branches per plant and 100-seedweight. The low genetic advance as a percent of the mean exhibited by plant height followed by the days to 50% flowering and days to maturity. High heritability coupled with high genetic advance as the percent of mean was recorded for the seed yield per plant, pods per plant, pod length, 100-seed weight and seeds per pod indicating that the additive gene action is involved in the genetic control of these traits. In the future breeding programme, selection can be very effective for the improvement of these traits for enhancing the genetic seed yield potential in blackgram while days to 50% flowering, days to maturity and plant height with low genetic advance indicated selection is less effective due to non-additive gene action. The present results are in agreement with the findings of earlier workers (Baisakh et al., 2014 ; Srividya et al., 2005).

Nature and magnitude of genetic association

Seed yield is a polygenic controlled complex character and is greatly influenced by many interrelated component traits, which are also mostly polygenic and the direct selection for seed yield is often not very effective (Das and Baisakh, 2019). Thus the correlation between seed yield and other component traits would be of key consideration for all crop breeders. Sardar and Behera (2017) emphasized the importance of indirect selection for seed yield through component traits governed by genes with additive effect and strong correlation with yield. This necessitates a thorough knowledge of the nature of the relationship prevalent between contributory characters and seed yield and the extent of genetic variability (Mahanthesha et al., 2017). Correlation would give a better insight into the cause-and-effect relationship between different pairs of characters (Venkatesan et al., 2004). Correlations between yield and other characteristics are useful in selecting the desired plant type in designing an effective breeding program for the improvement of seed yield. The estimates of correlation coefficients mostly indicate the inter-relationships of the characters and are useful for breeders in selecting genotypes possessing groups of desired traits (Prusti and Das, 2020). Selection based on the detailed knowledge of the magnitude and direction of association between seed yield and its attributes is very important to identify the key characters, which can be exploited in crop improvement through a suitable breeding programme. At the genetic level, positive correlation occurs due to the coupling phase of linkage and negative correlation arises due to the 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. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the components characters on which selection can be based for genetic improvement of seed yield. 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 a correlated response for several other characters resulting in a changed pattern of variability (Waddington and Robertson, 1966). Therefore, the genotypic correlation coefficient between the different characteristics was analyzed and presented in Table 4. The results revealed that the seed yield per plant had a significant and positive association with the traits viz., pods per

Table 1. Analysis of variance for N.C.D.-II for various characters in biparental progenies of blackgram

Source of variation	d.f.	DFF	DM	PH	BPP	CPP	PPP	SPP	PL	TW	SYPP
Treatments	624	149.181*	56.017*	45.139*	3.494**	21.967*	255.722*	0.98**	0.812	2.732**	28.109**
Females	24	232.125	62.517	165.063**	9.954**	81.977**	435.258**	2.385**	3.715**	5.592**	86.661**
Males	24	167.723	60.267	61.848	3.561**	22.841**	343.366**	1.151**	3.035**	3.252**	32.051**
Males & Females	576	149.789*	35.964*	59.665*	0.385**	10.476*	236.638**	0.403*	0.631*	0.376*	10.002**
Error	1250	145.413	34.467	52.611	0.075	8.591	230.416	0.251	0.437	0.120	7.067

*, ** Significant at 5% and 1% levels respectively

DFF: Days to 50% flowering, DM: Days to maturity, PH =plant height (cm), BPP =branches per plant, CPP=clusters per plant, PPP=pods per plant, SPP=seeds per pod, PL=pod length (cm), TW=100-seed weight (g), and SYPP= seed yield per plant (g).

Table 2. Estimation of variance components and degree of dominance for different characters in biparental progenies of blackgram

Characters	Variance due to			Genetic variance		Dominance Ratio	Average degree of dominance
	Females	Males	Males × Females	Additive (σ_A^2)	Dominance (σ_D^2)		
DFF	1.372**	0.298	1.457**	5.488**	5.834**	3.592	2.680
DM	0.442	0.495	0.499	1.770*	1.996*	0.092	0.429
PH	1.756*	0.036	2.351**	7.026**	9.404**	47.258	9.721
BPP	0.159	0.052	0.103	0.637	0.412	2.013	2.006
CPP	1.191*	0.206	0.628	4.766**	2.513*	40784	3.093
PPP	3.310**	1.778*	2.073*	13.241**	8.295**	0.861	1.312
SPP	0.033	0.012	0.050	0.132	0.203	1.640	1.811
PL	0.051	0.040	0.064	0.205	0.259	0.281	0.750
TW	0.086	0.047	0.085	0.347	0.340	0.814	1.276
SYPP	1.327**	0.367	0.978	5.310**	3.913**	2.612	2.285

*, ** Significant at 5% and 1% levels respectively

Table 3. Genetic parameters for different characters in biparental progenies of blackgram

Characters	Mean	Range		Coefficient of Variation (%)		Heritability (h^2bs)	Genetic advance as % of mean (GAM)
		Minimum	Maximum	GCV	PCV		
DFF	40.68	35.50	47.60	4.06	4.20	59.71	07.38
DM	70.35	68.60	75.20	2.68	3.43	57.25	06.35
PH	23.05	16.50	36.30	5.52	5.71	59.48	08.46
BPP	5.66	3.30	7.60	8.56	9.43	62.87	15.53
CPP	18.33	10.40	26.50	14.90	15.74	66.74	22.74
PPP	92.33	50.50	110.20	15.25	16.54	88.45	28.63
SPP	6.53	4.40	9.50	11.68	12.77	70.60	21.23
PL	5.25	4.60	6.50	12.54	14.12	78.66	26.88
TW	4.80	4.10	6.70	6.50	8.29	76.33	13.49
SYPP	30.80	20.40	54.60	17.23	18.16	89.54	27.76

Table 4. Genotypic correlation coefficients among the seed yield components in blackgram

Characters	DM	PH	BPP	CPP	PPP	SPP	PL	TW	SYPP
DFF	0.85**	-0.11	-0.05	-0.44	0.18	0.30	0.69**	0.59**	0.26
DM	-	0.17	0.30	0.22	0.28	0.65**	0.49*	0.62**	0.34
PH		-	-0.33	0.60**	0.65**	0.56**	0.53**	0.05	0.42*
BPP			-	0.41*	0.45*	0.12	0.01	0.88**	0.52**
CPP				-	0.66**	0.76**	0.81**	0.12	0.81**
PPP					-	0.67**	0.34	0.06	0.86**
SPP						-	0.31	0.37	0.62**
PL							-	-0.31	0.51**
TW								-	0.73**
SYPP									-

plant, clusters per plant, 100-seed weight, seeds per pod and pod length, and branches per plant. Days to 50% flowering had a positive and significant association with the days to maturity, pod length and 100-seed weight. Clusters per plant is strongly correlated with pods per plant, seeds per pod and pod length. The present findings are in close agreement with the earlier results of Kumar et al. (2014). These results would be quite substantial with the dwarfing genes and intense selection programme for a plant type, which involves several component traits related to productivity.

CONCLUSION

In the present study, non-allelic interactions along with additive and dominant components played a pertinent role in the determination of various characters in blackgram. In general, the involvement of both additive and non-additive gene effects for most of the characters suggested that it would be desirable to adopt biparental mating followed by a population improvement method involving the conventional breeding approach of selection of superior recombinants and their inter-mating for the development of elite homozygous recombinants having high quality and high yielding potentiality. Thus, population improvement approaches involving intermating of selected plants in an advance generation like biparental mating and diallel selective mating design that take care of both additive and non-additive gene actions are more promising for the improvement of various characters studied. High heritability coupled with high genetic advance as a percent of mean was recorded for the seed yield per plant, pods per plant, pod length, 100-seed weight and seeds per pod indicating that the additive gene action is involved in the genetic control of these traits. In a future breeding programme, selection can be very effective for the improvement of these traits for enhancing the genetic yield potential in blackgram. The seed yield per plant had a significant and positive association with the traits viz., pods per plant, clusters per plant, 100-seed weight, seeds per pod, pod length, and branches per plant. Thus, these traits could be for the development of new types in blackgram towards the enhancement of genetic yield potential.

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