



## Genetic Variability and Correlation Studies in Blackgram (*Vigna mungo* L. Hepper)

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### ABSTRACT

The current study was carried out with 12 genotypes of blackgram at Agricultural Research Station, Podalakur, SPSR Nellore, Andhra Pradesh. The high PCV and GCV were recorded for seed yield followed by clusters per plant, pods per plant and branches per plant showing that these traits are significantly count the variation to the total variability. Days to 50% flowering, plant height, clusters per plant, branches per plant, pods per plant, test weight and seed yield recorded high heritability along with high GAM. So, selection of genotypes using these traits would be valuable because they are controlled by additive gene action. Seed yield exhibited a significant positive association with clusters per plant, plant population and 100 SW.

**Keywords:** *Blackgram, Correlation, GAM, GCV, Heritability and PCV*

Blackgram (*Vigna mungo* (L.) Hepper) is an autogamous crop. India is the center of origin for blackgram. Its seeds are nutritious with protein (24-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. The annual production is 27.75 tonnes from 46.33 lakh hectare area in India with the productivity of 599 kg/ha. In Andhra Pradesh, production of blackgram is 4.24 lakh tonnes annually from an area of 4.01 lakh hectares with the productivity of 390 kg/ha (Ministry of Agriculture, 2021-22). The main problems in getting higher yield in blackgram are low genetic variability, low harvest index and lack of appropriate varieties with adjustment to particular agro-climatic situation. The building of variability is complicated through hybridization due to its high self-pollination and flower drop (Deepalakshmi and Anandakumar, 2004). The improvement in any crop species need the understanding of genetic variability for characters of economic value and their heritability and genetic advance are of utmost importance in scheduling upcoming breeding programme for the improvement (Singh *et al.*, 2007). The awareness of correlation analysis is a key to know the relationship between the seed yield and its causative traits to establish strategy for exploitation in breeding. Keeping in view these points, the present investigation was conducted

to assess the genetic variability, heritability, genetic advance and correlation analysis in blackgram.

### MATERIAL AND METHODS

The field experiment was conducted during *rabi* season of 2022-23 at Agricultural Research Station, Podalakur, Andhra Pradesh. The experimental material comprised of 12 lines of blackgram genotypes and the experiment was laid out in a randomized block design with three replications during *rabi* 2022-23. The entries were sown in four rows each of 6 m length with spacing of 30 cm between rows and 10 cm approximately between the plants. For the purpose of cultivating a healthy crop, the suggested packages of practices were followed, and all essential steps were made to safeguard the plants from pests and diseases. The observations were recorded on five selected competitive plants per entry and in each replication for every trait. Days to 50% flowering and days to maturity were recorded on plot basis. The analysis of variance for individual characters was carried out using the mean values of each plot following the method given by Panse and Sukhatme (1998). The coefficients of variations were calculated according to the procedure recommended by Burton (1952). PCV and GCV were grouped as low (< 10%), moderate (10 - 20%) and high (>20%)

according to Sivasubramanian and Madhava menon (1973).

$$PCV = \frac{\sqrt{s_g^2}}{\bar{X}} \cdot 100$$

Where; PCV = Phenotypic coefficient of variation

$\bar{X}$  = Mean value of the trait

$$GCV = \frac{\sqrt{s_g^2}}{\bar{X}} \cdot 100$$

Where; GCV = Genotypic coefficient of variation

$\bar{X}$  = Mean value of the trait

Heritability in percentage was calculated by the procedure suggested by Allard (1960). Robinson (1966) classified heritability as low (< 50%), moderate (50 - 70 %) and high (> 70%).

$$\text{Heritability (h}^2\text{) broad sense} = \frac{\sigma_g^2}{\sigma_p^2} \cdot 100$$

Where,  $\sigma_g^2$  = Genotypic variance

$\sigma_p^2$  = Phenotypic variance

GA and GAM were estimated and categorized as low (< 10%), moderate (10 - 20%) and high (> 20%) according to the technique recommended by Johnson *et al.* (1955).

Where, I = Selection differential (2.06) at five per cent intensity

$\sigma_p$  = Phenotypic standard deviation,  $h^2$  (bs) = Heritability in broad sense

Genetic Advance as per cent of Mean (GAM)

$$= \frac{GA}{\bar{X}} \cdot 100$$

Where, GA = Genetic advance

$\bar{X}$  = General mean

The data collected on different yield contributing characters was analyzed using correlation coefficients standard procedure suggested by Singh and Choudhary (1977).

## RESULTS AND DISCUSSION

The results showed that the genotypic variation for all traits was significant and indicating

the occurrence of morphological differences among the blackgram genotypes for all the traits (Table 1). Results from the Table 2 showed that the PCV was slightly higher than GCV for all the traits, representing that presence of environment role on the expression of all studied traits. High values of PCV and GCV were obtained for seed yield followed by clusters per plant, pods per plant and branches per plant revealing huge differences for these traits. These results were supported by Mehra *et al.* (2016), Sushmitharaj *et al.* (2018) and Priya *et al.* (2021). Moderate values of PCV and GCV were noticed for days to 50% flowering, plant height, number of seeds per pod and 100 seed weight indicating module variability for these traits whereas small values of PCV and GCV noticed for days to maturity and plant population.

In the present investigation, the heritability values ranged from 66.78% to 93.92% (Table 2). High heritability coupled with high GAM was noted for the characters *viz.*, days to 50% flowering, plant height, clusters per plant, branches per plant, pods per plant, 100 SW and seed yield. Similar findings are previously recorded by Mehra *et al.* (2016), Sushmitharaj *et al.* (2018) and Priya *et al.* (2021) for plant height; Rolaniya *et al.* (2017), Sushmitharaj *et al.* (2018) and Priya *et al.* (2021) for number of clusters per plant; Priya *et al.* (2021) for 100 seed weight and Mehra *et al.* (2016) and Sushmitharaj *et al.* (2018) for seed yield. Seed yield is highly complicated trait of the plant in which breeder is interested. The simple correlation coefficients between various traits are given in Table 3 and Figure 1. A significant positive association was recorded between seed yield with clusters per plant, plant population and 100 seed weight. Similar findings of association were reported by Mehra *et al.* (2016) for 100 seed weight and Sushmitharaj *et al.* (2018) for clusters per plant with seed yield in blackgram.

Thus, the study revealed that the traits like seed yield, number of clusters per plant, number of pods per plant and number of branches per plant were managed by additive gene effects thus selection based on these traits is fairly successful. The association studies indicated that the number of clusters per plant, plant population and 100 seed weight were seems to be important yield attributing characters and selection of genotypes based on these characters will be useful in further improvement in these blackgram genotypes.

**Table 1: Analysis of variance for seed yield and its contributing traits in blackgram**

Source of Variation	Df	Mean sum of squares									
		Days to 50% flowering	Days to maturity	Plant height (cm)	Clusters per plant	Branches per plant	Pods per plant	Plant population (Lakhs)	Seeds per pod	100 SW (g)	Seed yield (Kg ha <sup>-1</sup> )
Genotypes	11	22.816**	15.394*	9.628**	1.810*	3.751**	5.002*	0.052**	0.303*	0.203**	37012.739**
Replications	2	5.444	24.083*	13.661**	0.608	0.708	1.021	0.011	0.093	0.029	725.3
Error	22	3.626	6.568	1.992	0.7	1.136	1.815	0.01	0.125	0.033	2343.012

\* Significantly different at 5% probability level

\*\*Significantly different at 1% probability level

**Table 2: Estimates of genetic parameters for seed yield and seed yield component traits in blackgram**

Character	Mean	Range	PCV	GCV	H (bs) %	Exp. GAM
Days to 50% flowering	43.00	39.00 – 54.00	11.73	10.86	85.62	20.70
Days to maturity	80.00	73.00 – 86.00	5.58	4.56	66.78	7.67
Plant height	21.67	17.60 – 26.80	15.27	13.81	81.81	25.74
Clusters per plant	5.00	3.20 – 7.00	30.14	25.08	69.25	42.99
Branches per plant	8.16	5.40 – 11.80	26.01	22.50	74.81	40.09
Pods per plant	8.71	6.20 – 12.60	28.61	24.07	70.78	41.71
Plant population (Lakhs/ha)	3.14	2.92 – 3.36	7.71	7.00	82.64	13.12
Seeds per pod	5.78	4.80 – 6.60	10.75	8.84	67.70	14.99
100 SW (g)	4.02	3.50 – 4.60	11.80	10.89	85.28	20.73
Seed yield (kg ha <sup>-1</sup> )	482.39	315.27 – 656.94	40.71	39.45	93.92	78.77

GCV = Genotypic coefficient of variation

H<sub>(bs)</sub> = Heritability (broad sense)

PCV = Phenotypic coefficient of variation

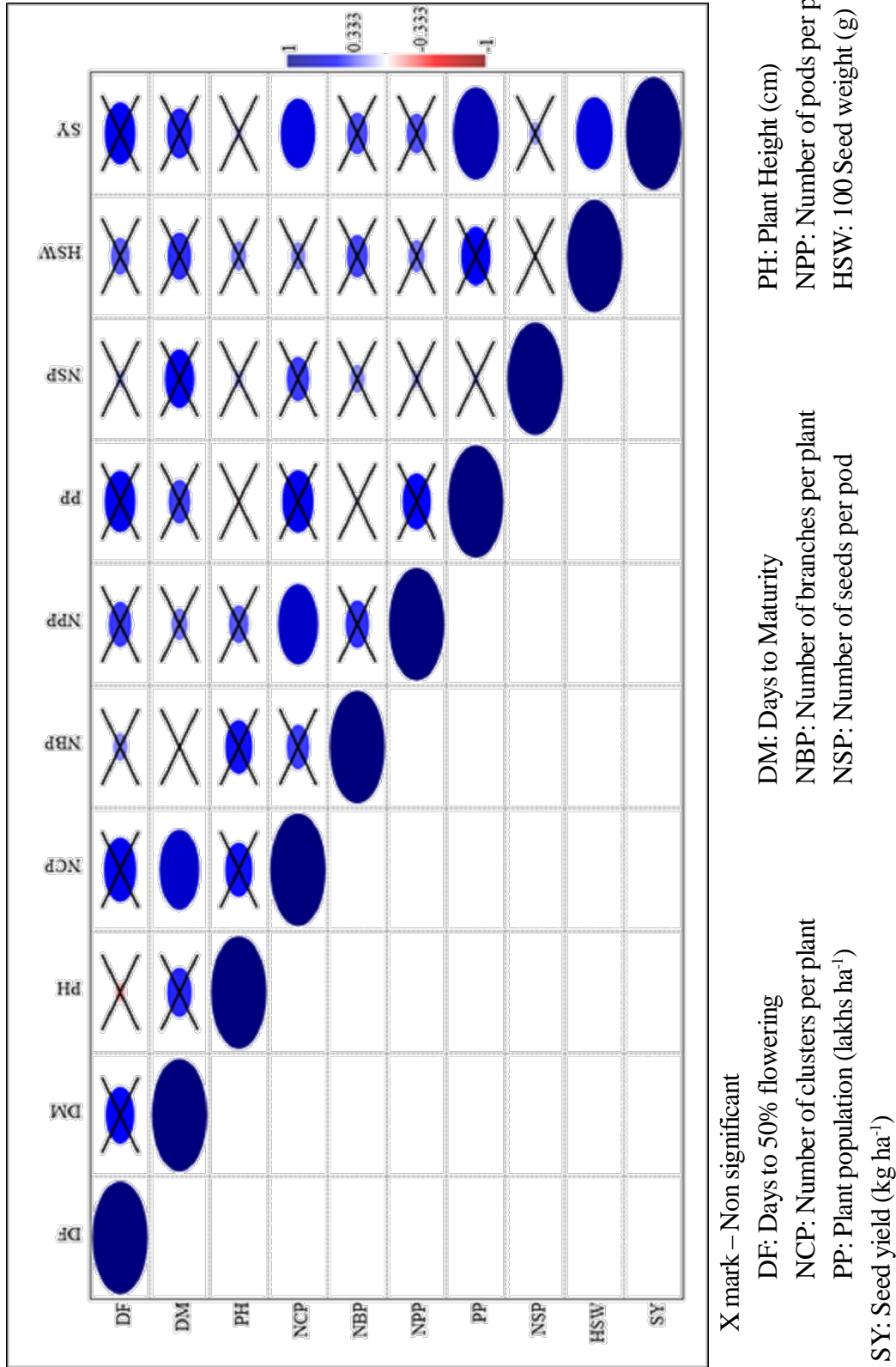
Exp. GAM = Expected genetic advance as per cent of mean

Table 3: Correlation coefficients among different characters of black gram

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Clusters per plant	Branches per plant	Pods per plant	Plant population (Lakhs)	Seeds per pod	SW (g)	Seed yield (kg ha <sup>-1</sup> )
Days to 50% flowering	1	0.497	-0.16	0.567	0.232	0.389	0.541	0.152	0.318	0.542
Days to maturity		1	0.428	0.706*	0.065	0.269	0.377	0.513	0.412	0.438
Plant height (cm)			1	0.474	0.468	0.328	-0.095	0.153	0.249	0.136
Clusters per plant				1	0.383	0.711*	0.552	0.384	0.235	0.616*
Branches per plant					1	0.409	0.088	0.237	0.367	0.358
Pods per plant						1	0.493	0.156	0.273	0.341
Plant population (Lakhs/ha)							1	0.135	0.516	0.814**
Seeds per pod								1	0.076	0.196
100 SW (g)									1	0.642*
Seed yield (kg ha <sup>-1</sup> )										1

\* - Significantly different at 5% probability level

\*\* - Significantly different at 1% probability level



**Figure 1: Correlation coefficients among different characters of black gram**

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