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Genetic Variability, Heritability and Genetic Advance in Blackgram (*Vigna mungo* L.)

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ABSTRACT: Blackgram is a self-pollinated crop, hence there is less varition. So in order to obtain high yielding varieties there is a need to know about diversity between parents. To know the diversity between parents, the present study of genetic variability was carried out. The present investigation was carried out in Agricultural Research Station, Madhira Telangana (State) to estimate genetic variability, heritability and genetic advance in blackgram. Analysis of variance was studied for 12 yield and yield attributing traits revealed highly significant differences among the genotypes for all the characters indicating the presence of appreciable amount of genetic variation for all the traits. The genotype MBG-1080 × LBG-17 found to be higher yield per plant followed by TU-94-2 × LBG-17, TBG-104 × TU-40 and remaining genotypes found to be lesser yield. The genotypes, GBG-1 × LBG-20, TU-94-2 × IPU-02-43 and TBG-104 × IPU-02-43 were found to be early maturing in nature. The genotype MBG-1080 × LBG-17 found to be had greater plant height, more number of clusters and pods, higher biological yield and pod yield per plant than the remaining genotypes. Moderate estimates of GCV and PCV were observed for number of clusters per plant, number of seeds per pod and 100 seed weight. Hence simple selection would be beneficial in increasing these traits.100 seed weight had high heritability along with high genetic advance as a percent of mean, indicating additive gene action and thus phenotypic selection would be more effective for improving these characters. For harvest index, number of pods per plant, seed yield per plant, biological yield per plant, plant height, pod yield per plant and high heritability coupled with moderate genetic advance percent of mean and suggested that presence of non additive gene action.

Keywords: GCV, Heritability, PCV, *Vigna mungo*, Variability.

INTRODUCTION

Pulses also known as “grain legumes” which are rich in proteins, fibres and vitamins as well as amino acids. They are most popular in underdeveloped nations, but they are gradually becoming recognized around the world as a good portion of a balanced diet. Pulse crops can continue to be a great alternative for farmers in the developing world with the introduction of new varieties and the promotion of better management practices. One of India's most cherished pulses is Blackgram (*Vigna mungo* L. Hepper), popularly known as urdbean in India, is an important short duration pulse crop and self pollinating diploid (2n = 22) with a small genome size estimated to be 0.56pg/1C (574 Mbp) (Gupta *et al.*, 2006). Blackgram is an excellent source of all nutrients including proteins (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. In terms of dietary protein content, it is second next to soybean. It contains high amounts of thiamine, riboflavin, niacin, vitamin A and C. It has a nitrogen content of 78 to 80 per cent in the form of albumin as well as globulin. The dried seeds are a good source of phosphorus and have a good caloric value (100 g of blackgram has 347 calories).

The lack of high-yielding varieties that can withstand environmental changes to a significant degree is the main problem restricting the production and productivity of pulses. Therefore, it is imperative to create HYV resistant varieties of various pulse crops, such as mung bean, that are resilient to abiotic stresses, particularly drought conditions. Hence the present study was taken up aiming to ascertain the variability heritability and genetic advance among the genotypes for traits related and for framing the effective breeding programme.

MATERIAL AND METHODS

The field experiment was laid out in medium black soil under irrigated conditions at Agricultural Research Station, Madhira during *Rabi* 2021-22. The experiment site is located on latitude 16°92′N and longitude 80°36′S and at an altitude of 38 m from mean sea level. The experimental material consisted of 34 genotypes (Table 1) were grown in "Randomised Block Design" in three replications. Each genotype was sown in 3 rows of 4m length with the spacing of 30 × 10 cm. As per the recommended packaging practices, all cultural operations were followed to raise a good crop.

Table 1: List of genotypes used for experiment.

Sr. No.		Sr. No.	
1.	Tu-94-2	19.	PU-31× LBG-17
2.	TBG-104	20.	PU-31 × LBG-20
3.	PU-31	21.	PU-31 × IPU-02-43
4.	GBG-1	22.	PU-31× TU-40
5.	MBG-1080	23.	GBG-1 × LBG-17
6.	MBG-207	24.	GBG-1 × LBG-20
7.	LBG-17	25.	GBG-1 × IPU-02-43
8.	LBG-20	26.	GBG-1 × TU-40
9.	IPU-02-43	27.	MBG-1080 × LBG-17
10.	TU-40	28.	MBG-1080 × LBG-20
11.	TU-94-2 × LBG-17	29.	MBG-1080 × IPU-02-43
12.	TU-94-2 × LBG-20	30.	MBG-1080 × TU-40
13.	TU-94-2 × IPU-02-43	31.	MBG-207 × LBG-17
14.	TU-94-2 × TU 40	32.	MBG-207 × LBG-20
15.	TBG-104 × LBG-17	33.	MBG-207 × IPU-02-43
16.	TBG-104 × LBG-20	34.	MBG-207 × TU-40
17.	TBG-104 × IPU-02-43		TBG-104 (Check)
18.	TBG-104 × TU-40		

Observations on quantitative features were recorded from five randomly selected competitive plants in each genotype from each replication. On a plot basis, days to 50% flowering and days to maturity were recorded. The observations like Plant height, Number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, pod yield per plant, biological yield per plant, 100 seed weight, harvest index and yield per plant recorded from five randomly selected plants. From statistical analysis, mean value of each character was taken. Analysis of variance was estimated by following the standard procedures. The PCV and GCV were calculated as per the method suggested by Burton (1952), whereas heritability and expected genetic advance were estimated according to Johnson *et al.* (1955); Allard (1960). Heritability in broad sense (h^2b) was calculated as per Burton and Devane (1953).

RESULTS AND DISCUSSION

To determine the effectiveness of selection in any crop improvement programme, knowledge of genetic variability is essential. Its existence is essential for broad adaptability and biotic and abiotic stress resistance. The analysis of variance carried out for 12 yield and yield component traits revealed highly significant (at 0.01%) differences among the genotypes for the characters *viz.*, days to 50% flowering, days to maturity, plant height, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, pod yield per plant, biological yield per plant, harvest index and yield per plant (Table 2). These results indicated the presence of considerable amount of genetic variation for all the 12 traits in the experimental material.

The genotype MBG-1080 × LBG-17 found to be higher yield per plant followed by TU-94-2 × LBG-17, TBG-104 × TU-40 and remaining genotypes found to be lesser yield. In case of early flowering, the genotypes, GBG-1 × LBG-20, TU-94-2 × IPU-02-43 and TBG-104 × IPU-02-43 were found. The genotypes, GBG-1 × LBG-20, TU-94-2 × IPU-02-43 and TBG-104 × IPU-02-43 were found to be early maturing in nature. In case of plant height, MBG-1080 × LBG-17, MBG-207 × LBG-17 and MBG-1080 × TU-40 found to be had long stature. For number of clusters per plant the genotypes, MBG-1080 × LBG-17, TU-94-2 and MBG-1080 were found to be higher than the other genotypes. The genotypes MBG-1080 × LBG-17, MBG-1080 × TU-40 and GBG-1 × TU-40 found to be had more number of pods per plant. For greater pod length, MBG-207, TU-94-2 and LBG-20 genotypes found to be desirable. For number of seeds per pod, PU-31, TU-94-2 and TU-94-2 × IPU-02-43 found to be desirable. For 100 seed weight, TU-94-2 × LBG-20, GBG-1 × TU-40 and TBG-104 genotypes found to be desirable. The genotypes MBG-1080 × LBG-17, TU-94-2 × LBG-17 and TBG-104 × TU-40 found to be had highest pod yield per plant than the other genotypes. The genotypes GBG-1 × LBG-20, MBG-1080 × LBG-17 and PU-31 × TU-40 recorded maximum biological yield. The genotypes TU-94-2 × LBG-17, LBG-17 and TBG-104 × TU-40 recorded higher harvest index than the other genotypes. The results of mean performance were given in Table 3.

Table 2: Analysis of variance (ANOVA) for all the 12 yield and its attributing traits.

Sr. No.	Trait	Mean sum of squares		
		Replication (df = 2)	Treatment (df = 34)	Error (df = 68)
1.	Days to 50% flowering	0.343	6.222**	1.588
2.	Days to maturity	1.114	7.192**	1.438
3.	Plantheight(cm)	2.523	23.725**	2.589
4.	Number of clusters per plant	0.543	4.822**	1.141
5.	Number of pods per plant	4.229	33.105**	3.631
6.	Podlength (cm)	0.002	0.195**	0.03
7.	Numberof seeds per pod	0.124	1.108**	0.369
8.	100 seed weight (g)	0.012	0.676**	0.026
9.	Pod yield per plant	0.145	2.094**	0.171
10.	Biological yield per plant (g)	1.144	10.932**	0.379
11.	Harvest index	2.736	20.456**	1.436
12.	Seed yield per plant(g)	0.226	1.413**	0.078

Table 3: Mean performance of 34 genotypes of blackgram for twelve different yield and yield attributing traits.

Genotype	DFF	DM	PH	NCP	NPP	PL	NSP	TW	PYPP	BYPP	HI	YPP
TU-94-2 × LBG-17	41.0	73.3	36.1	10.7	44.7	4.4	4.7	4.5	12.9	23.4	44.9	10.5
TU-94-2 × LBG-20	42.0	74.7	31.6	8.3	41.3	4.3	4.7	4.8	12.1	24.0	40.1	9.6
TU-94-2 × IPU-02-43	40.3	71.7	34.3	9.0	42.7	4.1	5.3	3.8	11.5	25.3	36.5	9.2
TU-94-2 × TU 40	42.3	73.0	34.1	8.3	37.3	4.1	4.3	3.6	10.9	23.3	36.8	8.6
TBG-104 × LBG-17	41.0	71.7	30.8	8.3	38.0	4.4	5.3	3.9	9.6	22.5	37.4	8.4
TBG-104 × LBG-20	42.3	72.0	31.2	9.3	41.7	4.1	4.0	4.5	10.7	22.9	38.0	8.7
TBG-104 × IPU-02-43	40.7	71.7	30.0	8.7	42.0	4.3	4.0	4.2	11.1	24.0	35.6	8.5
TBG-104 × TU-40	42.0	73.0	31.6	9.7	44.3	4.6	4.7	4.2	12.9	25.4	41.1	10.4
PU-31 × LBG-17	42.7	74.0	32.9	8.7	43.3	3.9	3.7	4.3	11.2	24.8	37.1	9.2
PU-31 × LBG-20	41.3	72.3	31.0	9.3	42.7	4.1	3.7	4.5	10.7	26.4	34.8	9.2
PU-31 × IPU-02-43	41.7	72.3	29.9	8.3	41.3	4.0	4.7	3.5	11.0	25.5	35.1	9.0
PU-31 × TU-40	43.0	73.7	33.4	9.7	43.3	4.1	4.3	4.1	11.4	27.2	34.1	9.3
GBG-1 × LBG-17	42.0	73.3	30.7	10.3	41.3	3.8	3.3	4.5	10.5	23.3	36.2	8.4
GBG-1 × LBG-20	40.0	71.0	33.5	9.7	45.7	4.3	4.3	4.6	11.8	28.9	33.9	9.9
GBG-1 × IPU-02-43	43.7	74.0	33.7	10.0	39.3	4.4	4.7	3.4	11.3	25.4	35.7	9.1
GBG-1×TU-40	43.0	75.0	33.9	10.3	46.0	3.8	3.3	4.7	11.7	25.9	36.8	9.5
MBG-1080 × LBG-17	41.7	72.7	41.3	13.7	49.0	4.2	4.7	4.0	13.5	28.5	37.9	10.8
MBG-1080 × LBG-20	41.3	72.0	28.0	10.3	39.3	4.3	4.7	3.5	10.7	23.3	37.0	8.6
MBG-1080×IPU-02-43	43.3	74.0	33.3	8.3	42.0	4.4	4.0	3.9	10.4	22.8	36.7	8.4
MBG-1080 × TU-40	45.0	75.3	36.9	9.3	48.0	4.0	4.7	4.3	10.8	24.8	34.7	8.6
MBG-207 × LBG-17	41.7	72.7	37.2	10.7	39.0	3.6	5.0	2.7	11.3	26.2	33.5	8.8
MBG-207 × LBG-20	42.0	73.3	34.2	10.7	39.3	3.8	3.7	4.4	10.7	24.4	34.6	8.4
MBG-207 × IPU-02-43	43.7	75.0	31.4	9.7	40.0	4.3	4.3	3.8	10.4	22.6	36.3	8.3
MBG-207 × TU-40	42.7	74.3	32.9	9.3	37.0	4.2	3.7	3.9	10.6	23.0	37.0	8.2
TU-94-2	41.7	73.0	35.5	13.0	41.7	4.7	5.3	4.3	11.6	24.6	38.3	9.4
TBG-104	43.0	75.3	30.5	9.0	36.3	4.4	4.3	4.3	11.6	21.5	41.0	8.8
PU-31	42.3	73.3	26.5	9.7	40.3	4.4	5.7	3.3	12.0	22.5	40.4	9.1
GBG-1	46.0	77.0	32.3	7.7	42.3	4.5	4.0	4.1	11.2	22.9	38.6	8.8
MBG-1080	41.3	74.7	31.1	11.1	41.3	4.2	4.3	3.7	11.3	22.1	40.4	9.0
MBG-207	43.7	75.7	30.1	9.3	40.3	4.7	3.3	3.5	10.5	21.3	38.6	8.2
LBG-17	42.3	74.0	35.3	10.7	42.0	4.2	4.7	4.6	11.7	22.1	42.2	9.3
LBG-20	42.0	74.3	31.5	9.0	38.7	4.7	5.3	3.6	10.6	22.7	36.7	8.6
IPU-02-43	44.3	76.3	32.3	11.0	36.0	4.3	4.7	3.5	10.5	21.7	38.8	8.4
TU-40	46.3	77.3	29.9	8.3	33.0	4.3	4.3	4.1	9.6	22.3	34.0	7.6
TBG-104	43.7	75.0	30.4	9.7	40.3	4.3	4.0	4.4	11.6	22.4	39.8	8.9
Mean	**42.5**	**73.8**	**32.5**	**9.7**	**41.2**	**4.2**	**4.4**	**4.0**	**11.2**	**24.0**	**37.5**	**9.0**
S.E.	0.7	0.7	0.9	0.6	1.1	0.1	0.4	0.1	0.2	0.4	0.7	0.2
C.D. 5%	2.1	2.0	2.6	1.7	3.1	0.3	1.0	0.3	0.7	1.0	2.0	0.5
C.V.	3.0	1.6	4.9	11.0	4.6	4.1	13.8	4.0	3.7	2.6	3.2	3.1
Range Lowest	40.0	71.0	26.5	7.7	33.0	3.6	3.3	2.7	9.6	21.3	33.5	7.6
Range Highest	46.3	77.3	41.3	13.7	49.0	4.7	5.7	4.8	13.5	28.9	44.9	10.8

"DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height, NCP = No. of clusters per plant, NPP= No. of pods per plant, PL= Pod length, NSP= No. of seeds per pod, YPP= Yield per plant, PYPP= Pod yield per plant, BYPP= Biological yield per plant, TW=100 seed weight and HI= Harvest index."

Knowing the genetic variation inherent in a specific crop species for a particular trait under development is critical for the success of any breeding programme. The coefficient of variation is used to calculate how much variation there is in a crop species. Estimates of heritability provide information on the amount of transmissible genetic variation among total variation, which defines its responsiveness to selection and the scope of genetic advance in the new population over the original population. If a character is governed by non-additive gene action, it may have a high heritability but a low genetic advance, whereas if it is governed by additive gene action, it will have a high heritability (above 60%) and a high genetic advance, with a lot of potential for improvement. As a result, increasing these characteristics through selection is the most important technique for making genetic gains over generations. The genotypic and phenotypic coefficients of variation, heritability, genetic advance, and genetic advance as a percent of the mean for the genotypes were calculated and given in Table 4.

For all of the traits investigated, the phenotypic coefficient of variation (PCV) was larger than the genotypic coefficient of variation (GCV), indicating that they were governed by non-additive gene action. Similar results have been recorded by Muthuswamy *et al.* (2019); Sushmitharaj *et al.* (2018); Govardhan *et al.* (2018); Moderate estimates of GCV and PCV were observed for number of clusters per plant (GCV:11.44%, PCV:15.99%), number of seeds per pod (GCV:11.30%, PCV:17.86%) and 100 seed weight (GCV:11.57%, PCV:12.25%). Similar findings for moderate GCV and PCV for number of clusters per plant Tambe *et al.* (2018); Tank *et al.* (2018); Rehman *et al.* (2021). For 100 seed weight similar results for moderate GCV and PCV were obtained earlier by Tank *et al.* (2018); Panwar *et al.* (2019); Sathees *et al.* (2019); Veni *et al.* (2019); Priya *et al.* (2021). For number of seeds per pod similar results for moderate GCV and PCV were found earlier by Panigrahi *et al.* (2015); Sathees *et al.* (2019). Number of pods per plant (GCV:9.61%, PCV:10.91%) shows moderate PCV with low GCV. Similar line of findings were given by Tambe *et al.* (2018); Chaitanya *et al.* (2019).

Table 4: Genotypic (σ^2g) and phenotypic variance (σ^2p) and other genetic parameters for all the traits in blackgram.

Sr. No.	Character	GCV	PCV	h^2_b	GAP	GAM(%)
1.	Days to 50 % flowering	2.93	4.17	49.30	1.80	4.23
2.	Days to maturity	1.88	2.48	57.20	2.16	2.92
3.	Plant height (cm)	8.16	9.54	73.10	4.68	14.37
4.	No. of clusters per plant	11.44	15.89	51.80	1.64	16.96
5.	No. of pods per plant	9.61	10.91	73.00	5.52	13.40
6.	Pod length (cm)	5.54	6.89	64.60	0.39	9.18
7.	No. of seeds per pod	11.30	17.86	40.00	0.65	14.73
8.	100 seed weight (g)	11.57	12.25	89.20	0.91	22.51
9.	Pod yield per plant (g)	7.15	8.05	78.90	1.47	13.08
10.	Biological yield per plant	7.82	8.23	90.30	3.67	15.30
11.	Harvest index (%)	6.72	7.45	81.50	4.68	12.50
12.	Seed yield per plant (g)	7.44	8.06	85.10	1.27	14.13

GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, h_b^2- Heritability in broad sense, GA- Genetic advance GAM - Genetic advance as per cent of mean.

Estimates of high heritability were found for plant height (73.1%), number of pods per plant (73%), pod length (64.6%), harvest index (81.5%), biological yield per plant (90.3%), 100 seed weight (89.2%), pod yield per plant (78.9) and seed yield per plant (85.1%) showing that the environment has the least impact on these traits. 100 seed weight (h^2_b=89.2%, GAM=22.51%) had high heritability along with high genetic advance as a percent of mean, indicating additive gene action and thus phenotypic selection would be more effective for improving these characters. High heritability combined with high genetic advance as per cent of mean for100 seed weight was earlier reported by Tank *et al.* (2018); Sathees *et al.* (2019); Veni *et al.* (2019); Umesh and Bharti (2022). For harvest index (h^2_b = 81.5%, GAM = 12.5%), number of pods per plant (h^2_b = 73%, GAM = 13.4%), seed yield per plant (h^2_b = 85.1%, GAM = 14.13%), biological yield per plant (h^2_b = 90.3%, GAM =15.3%), plant height (h^2_b = 73.1%, GAM =14.37%), pod yield per plant (h^2_b =78.9%, GAM =13.08%) and high heritability coupled with moderate genetic advance percent of mean and suggested that presence of non additive gene action. Similar results were observed by Dharmendra *et al.* (2017) for harvest index. Similar results were observed for plant height by Panda *et al.* (2017), Bandi *et al.* (2018), Reddy *et al.* (2018); Tank *et al.* (2018); Rehman *et al.* (2021); for number of pods per plant by Nagmi and Lal (2017); Chauhan *et al.* (2018); Tambe *et al.* (2018); Chaithanya *et al.* (2019); for seed yield per plant by Nagmi and Lal (2017); Chaithanya *et al.* (2019); for biological yield per plant and harvest index by Rolaniya *et al.* (2017).

High heritability combined with low genetic advance as per cent of mean was recorded for pod length (h^2_b = 64.6%, GAM = 9.18%). Similar line of findings were observed by Nagmi and Lal (2017); Reddy *et al.* (2018); Rehman *et al.* (2021).

CONCLUSION

High heritability estimates were found for the traits *viz.*, plant height, number of pods per plant, pod length, harvest index, biological yield per plant, 100 seed weight, pod yield per plant and seed yield per plant showing that the environment has the least impact on these traits.100 seed weight was the trait with high heritability and high genetic advance as percent of mean. As a result, direct selection for the trait mentioned above would be useful in future breeding programmes to increase yield. For harvest index, number of pods per plant, seed yield per plant, biological yield per plant, plant height, pod yield per plant and high heritability coupled with moderate genetic advance percent of mean and suggested that presence of non additive gene action.

FUTURE SCOPE

Global warming will cause greater environmental variations in the coming days, further worsening the issue with agricultural productivity. Major crop growing areas experience water shortages due to the depletion of the water table and insufficient rainfall, which negatively impacts crop production and creates a drought-like condition. Hence, future challenges in agricultural production to identify resistant cultivars for abiotic stresses.

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Conflict of Interest. None.

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