

ASSESSMENT OF GENETIC VARIABILITY PARAMETERS IN BLACK GRAM [*VIGNA MUNGO* (L) HEPPER] GENOTYPES

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Abstract: The present investigation was conducted during *kharif*-2021 at Agricultural Research Station, Ummadganj, Kota (Agriculture University, Kota), to examine 40 black gram diverse genotypes in Randomize Block Design with three replications. The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed high for number of primary branches per plant, number of clusters per plant, number of pods per plant, biological yield per plant, harvest index and seed yield per plant. High heritability coupled with high genetic advance as per cent of mean was obtained for number of primary branches per plant, number of clusters per plant, number of pods per plant, biological yield per plant, harvest index and seed yield per plant. Based on the mean performance of the genotypes, KPU 1097, KPU410-31, KPU1102, KPU1116 and KPU12-155 were superior not only for seed yield per plant but also for other yield contributing traits.

Keywords: Black gram, Genetic variability, Heritability, Genetic advance

INTRODUCTION

Black gram [*Vigna mungo* (L.) Hepper] is an important annual, autogamous, short duration, pulse crop widely cultivated in India which give us an excellent source of easily digestible good quality protein and ability to restore the fertility of soil through symbiotic nitrogen fixation. It widely cultivated on marginal lands with low inputs during *Kharif*, *Rabi* and *Summer* seasons in different part of the country. The whole plant of this crop is utilized as fodder for animals. It is also an excellent green manure and soil conservation crop.

It is grown as a mixed crop, catch crop, sequential crop besides as sole crop under residual moisture conditions after the harvest of rice and also before and after the harvest of other crops under semi irrigated and dry land conditions (Yashoda *et al.*, 2016). To achieving higher yield in this crop are lack of genetic variability, poor harvest index, suitable varieties and genotypes with adaptation to local condition are the main constraints. To achieve a genotype with high yield potential is considered as ultimate aim of plant breeder which is possible only by incorporating various desirable traits in a genotype. This is very difficult often to improve yield directly as it is controlled by poly genes and interlinked with other yield components traits.

Black gram is the fourth main pulse crop in India. According to recently data, the area of black gram is about 4.14 million hectares with the estimated production 2.23 million tones and productivity of about 538 kg/ hectare in India. Whereas, in Rajasthan

black gram is grown in 4,24,857 hectares with the production 1,55,626 tones and productivity of 366 kg/hectares (Anonymous, 2021). India, in spite of being largest producer of black gram, its production is not sufficient to meet out the consumption demand. Hence, to raise the production of black gram, there is a need of developing high yielding varieties or improve existing genotypes for better performance and production of greater quality of seeds, which requires the adoption of systematic breeding approaches. Assessment of variability is an initial step in any breeding programme. Higher the diversity of the material, better are the chances of improvement, provided that heritability and genetic advance is more. The ultimate goal of any breeding programme is to get higher yield. Since, yield is a complex character, thus the selection is more effective when it is practice simultaneously for the characters which have desired association with the traits of ultimate interest.

The major constraints in black gram genetic improvement are lack of exploitable genetic variability, absence of suitable ideotype for different cropping systems, poor harvest index and susceptibility to biotic and abiotic stresses and non-availability of quality seeds of improved varieties. It is mainly due to the repeated usage of few parents with high degree of relatedness in crossing programmes. One of the factors responsible for the poor productivity of black gram is lack of stable cultivars (Gowsalya *et al.*, 2016). Further, it has been the least studied crop among the pulses and no international system under the CGIAR has this as a

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mandate crop. Genetic improvement and development of high yielding varieties are dependent upon genetic variability as it provides the base for selection. Yield, being a complex quantitative trait, is not amenable to improvement through individual plant selection based on per se performance. Success of yield improvement largely depends upon the magnitude and nature of genetic variability present in yield contributing traits (Johnson *et al.*, 1955). Thus, it becomes necessary to select for those traits that contribute to yield with high heritability, and the selection based on such component traits of yield would be more effective and beneficial in genetic enhancement of yield of the crop. To raise the production of black gram, there is a need of developing high yielding varieties which requires the adoption of systematic breeding approaches.

MATERIALS AND METHODS

The experimental material for the present investigation consisted of 40 genotypes obtained from the Agriculture Research station, Kota, Rajasthan. Recommended cultural practices were followed to raise healthy crop. The observations were recorded on five randomly selected plants per plot for twelve characters *viz.*, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, 100-seed weight

(g), biological yield per plant (g), harvest index (%), and seed yield per plant (g). Whereas, the observations for days to 50 % flowering and days to maturity were recorded on plot basis.

Analysis of variance was carried out as per standard procedure (Fisher, 1938). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) (Burton, 1952), heritability (Burton and Devane, 1953), genetic advance (Johnson *et al.*, 1955), were estimated.

RESULTS AND DISCUSSION

Analysis of variance

Genetic variability in any crop is pre-requisite for selection of superior genotype over the existing cultivars. Variance analysis for all the characters revealed significant variation among the genotypes studied (Table 1). The analysis of variance showed significant differences among 40 black gram genotypes for all the characters under study, indicates that there is ample scope for selection of promising genotypes from present germplasm for yield improvement. High amount of genetic variability for most of these traits has also been reported earlier by Punia *et al.* (2014), Kumar *et al.* (2015), Panda *et al.* (2017), Bandi *et al.* (2018), Senthiamiahselvi *et al.* (2019) and Chowdhary *et al.* (2020).

Table 1. Analysis of variance for yield and its contributing traits in black gram genotypes

Source of variation	D.F.	Mean sum of square											
		Days to 50% Flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of clusters per plant	Number of pods per cluster	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Replication	2	1.90	1.30	6.03	1.17	0.46	0.00	0.30	0.06	0.06	13.30	6.61	0.05
Genotypes	39	29.22**	24.97**	17.98**	3.27**	5.74**	0.12**	31.22**	0.27**	0.23**	114.35**	56.80**	3.79**
Error	78	0.89	1.92	4.14	0.61	1.11	0.01	5.36	0.09	0.08	7.00	10.72	0.88

** Significant at 1% significance level

Variability parameters and per se performance

Mean values of 40 genotypes for twelve characters were recorded carefully and presented in Table 2. The mean performance of different genotypes for the characters gave the first hand information for the variability present in the materials under study and gives an opportunity to the plant breeders to select the diverse parents as per objective of the breeding in black gram crop. Among 40 genotypes of black gram KPU1097 (10.72 g) genotype was observed highest mean performance for seed yield per plant followed by KPU410-31 (10.02 g) and KPU1102 (9.85g) indicating that these genotypes can be used in hybridization programmes in order to achieve target environment in yield. KPU13-21 and KPU1105 (38.67) was earliest in flowering and KPU1073 in maturity (66 days). These genotypes can be used as a donor in hybridization programmes for evolving

early maturity or short duration black gram varieties. Genotype KPU1729-133 (19.11 cm) was the shortest and KPU111-183 (28.78 cm) was the tallest among all 40 genotypes of black gram.

The highest mean performance for number of primary branches per plant was observed in genotype KPU1147 and KPU63-189 (10.27) followed by KPU1102 (10.23), KPU410-31 (10.17), KPU23-96 (9.73) and lowest in KPU1079 (6.07).

The highest mean performance for number of clusters per plant was observed in genotype KPU1097 (12.93) followed by KPU111-183 (12.23), KPU 514-75 (11.57), PratapUrad-31 (11.37), KPU63-189 (11.23) and lowest in KPU1727-133 (6.53). The highest mean performance for number of pods per cluster was observed in genotype KPU1139 (3.13) followed by KPU410-31 (3.11), KPU1711-149 (3.08), KPU 23-96 (3.02), PratapUrad-1 (2.99); for pods per plant

KPU1097 (32.58 pods) followed by KPU 1147 (32.27 pods), PratapUrad-31 (31.30 pods), KPU1102 (31.07 pods), KPU12-1731A (30.64 pods); for number of seeds per pod KPU111-333 and

KPU12-155 (6.27) followed by KPU1121 (6.23), KPU410-31 (6.20), KPU11-40 (6.17); for 100-seed weight

Table 2. Mean values of different genotypes with respect of twelve characters in black gram

S. N.	Genotype	Days to 50% Flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
1	KPU1102	49.67	69.33	26.53	10.23	10.67	2.94	31.07	5.63	6.02	43.11	22.97	9.85
2	KPU1116	45.67	69.00	28.70	9.00	10.27	2.50	29.80	5.50	5.90	44.40	22.15	9.84
3	KPU113-120	47.67	71.00	23.03	8.47	9.33	2.94	27.05	6.10	5.67	30.61	27.92	8.54
4	KPU520-69A	48.00	72.00	26.83	9.70	8.70	2.76	27.97	5.96	6.13	32.23	27.68	8.86
5	KPU11097	48.33	69.33	23.28	7.60	9.27	2.71	26.39	5.69	5.86	26.71	30.93	8.25
6	KPU111-183	49.00	71.00	28.78	8.73	12.23	2.73	30.03	5.93	5.69	46.86	19.25	9.02
7	KPU1101	48.00	69.67	24.90	6.87	8.27	2.83	24.99	5.64	5.79	30.94	24.40	7.46
8	KPU1079	45.33	66.67	22.49	6.20	7.73	2.99	23.60	5.65	5.57	23.62	28.76	6.79
9	KPU1097	48.67	71.00	26.39	9.53	12.93	2.65	32.58	6.05	5.50	40.35	26.59	10.72
10	KPU13-21	38.67	64.00	20.03	7.07	7.07	2.47	24.15	5.13	5.43	26.78	29.56	7.94
11	KPU128-105	48.33	70.00	23.95	7.20	8.73	2.74	26.81	5.87	5.77	30.48	27.46	8.31
12	KPU1139	48.33	73.33	25.87	8.27	9.17	3.13	28.63	6.00	5.88	28.32	32.91	9.27
13	KPU12-219	48.67	73.00	26.39	9.00	10.67	2.64	30.64	5.80	5.76	30.85	30.41	9.37
14	KPU1147	49.33	75.33	26.75	10.27	10.60	2.75	32.27	6.01	5.69	46.20	20.88	9.63
15	KPU119-225	49.00	73.67	25.69	9.47	9.17	2.86	28.09	6.00	5.86	31.92	27.76	8.87
16	KPU63-189	48.67	74.33	26.25	10.27	11.23	2.84	30.21	5.77	5.93	31.23	30.32	9.46
17	KPU23-96	49.33	76.67	25.47	9.73	9.60	3.02	28.27	6.13	6.02	44.73	20.67	9.23
18	PU-31	49.00	70.00	28.07	9.27	11.37	2.84	31.30	5.83	5.75	42.42	21.27	9.02
19	KPU12-144A	47.33	71.67	26.17	8.27	8.80	2.33	21.48	5.83	5.58	30.96	21.41	6.64
20	KPU1711-149	49.00	72.67	23.73	8.33	10.07	3.08	30.33	5.77	5.97	41.06	23.34	9.55
21	KPU12-1731A	39.00	72.33	23.17	8.37	10.60	2.43	30.64	4.90	5.55	32.38	30.16	9.72
22	KPU1073	48.67	66.00	21.53	8.60	10.50	2.90	27.79	5.60	5.07	40.78	18.00	7.24
23	KPU514-75	48.33	72.00	19.80	9.47	11.57	2.71	29.24	5.60	5.76	35.02	24.41	8.57
24	KPU111-333	49.00	73.33	27.40	8.67	10.50	2.95	26.75	6.27	6.01	40.20	21.15	8.46
25	KPU410-31	48.67	72.00	27.60	10.17	9.87	3.11	29.30	6.20	6.01	36.24	27.56	10.02
26	KPU1531	49.00	76.00	27.90	8.87	9.47	2.90	27.60	5.43	5.91	34.62	22.60	7.68
27	KPU1529	49.00	73.00	23.90	7.20	9.47	2.81	26.03	6.04	6.23	38.81	20.88	8.06
28	KPU1115	48.67	72.00	24.87	8.40	8.80	2.71	24.51	5.67	5.60	25.73	27.58	7.14
29	KPU527-62	47.33	74.00	23.60	8.13	10.37	2.74	29.24	5.79	5.80	28.13	31.81	8.97
30	Pratap Urd-1	49.00	70.33	27.40	9.07	9.73	2.99	25.30	5.63	6.40	39.79	19.43	7.73
31	KPU1105	38.67	67.33	27.20	8.40	8.90	2.43	25.60	5.50	5.37	32.69	21.47	7.02
32	KPU11-40	47.33	70.00	24.97	9.40	8.77	2.56	25.42	6.17	6.05	31.58	27.53	8.67
33	KPU1121	47.67	69.00	23.50	8.60	8.97	2.72	24.75	6.23	5.99	29.14	29.81	8.53
34	KPU1729-133	47.67	69.67	19.11	6.07	6.63	2.82	20.69	5.87	6.16	33.62	20.39	6.83
35	KPU12-155	47.00	71.00	22.05	8.00	8.93	2.83	30.52	6.27	5.89	32.23	30.32	9.76
36	KPU1727-133	40.33	68.00	28.17	8.80	6.53	2.38	25.06	5.63	6.04	29.52	29.35	8.48
37	KPU13-241	47.00	70.00	24.73	9.40	8.53	2.69	17.65	5.96	5.70	30.64	17.65	5.38
38	KPU520-69	47.33	69.33	24.80	9.07	10.63	2.49	29.97	5.67	6.09	31.23	30.29	9.44
39	KPU524-65	40.00	63.67	23.13	9.33	8.60	2.55	25.36	6.10	5.67	26.23	29.32	7.67
40	KPU1724-136	48.33	69.67	26.57	8.00	8.47	2.73	26.88	5.43	6.49	31.66	26.85	8.48
	Minimum	38.67	63.67	19.11	6.07	6.53	2.33	17.65	4.90	5.07	23.62	17.65	5.38
	Maximum	49.67	76.67	28.78	10.27	12.93	3.13	32.58	6.27	6.49	46.86	32.91	10.72
	Mean	47.10	70.81	25.02	8.64	9.54	2.75	27.35	5.81	5.84	34.10	25.58	8.51
	CD @ 5%	1.53	2.25	3.31	1.27	1.72	0.18	3.76	0.50	0.44	4.30	5.32	1.53
	CV %	2.00	1.96	8.13	9.07	11.09	3.97	8.46	5.26	4.67	7.76	12.80	11.05

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

KPU1742-136 (6.49 g) followed by PratapUrad-1 (6.40 g), KPU1529 (6.23 g), KPU1729-133 (6.16), KPU520-69A (6.13 g); for biological yield per plant KPU111-183 (46.86 g) followed by KPU1147 (46.20 g), KPU23-96 (44.73 g), KPU1116 (44.40 g), KPU1102 (43.11 g) and for harvest index KPU1139 (32.91 %) followed by KPU527-62 (31.81 %), KPU11097 (30.93 %), KPU12-219 (30.41 %), KPU12-155 (30.32).

Higher seed yield is the ultimate goal of any breeding programme, which is the product of different combinations of desirable and non-desirable traits. A wide range of seed yield per plant (5.38 g-10.72 g)

has been observed in the present investigation. KPU1097, (10.72 g), KPU410-31 (10.02 g), KPU1102 (9.85 g), KPU 1116 (9.84 g) and KPU12-155 (9.76 g) were found to be the top five yielders

among the 40 genotypes with significant mean value over average value.

It is understandable from the above discussion that the genotypes included in the study illustrated extensive range of variability in respect of all the twelve characters. Among the 40 genotypes KPU13-21 and KPU1105 was found to be earliest in respect to days to 50% flowering and KPU524-65 was found to be days to maturity. The genotype KPU1729-133 was shortest in plant height and genotype KPU1147 also showed highest number of primary branches per plant. The mean performance of KPU1097 was highest for number of clusters per plant and number of pods per plant whereas, KPU1139 for number of pods per cluster and harvest index, KPU111-333 and KPU12-155 for number of seeds per pod, KPU1742-136 for 1000-seed weight and KPU111-183 for biological yield per plant were the best performing genotypes for the respective characters. Among the 40 genotype KPU1097 recorded highest seed yield per plant which also exhibited higher number of clusters per plant, and higher number of pods per plant. High amount of genetic variability for most of these characters including seed yield per plant have been reported earlier by Punia *et al.* (2014), Kumar *et al.* (2015), Priyanka *et al.* (2016), Rolaniya *et al.* (2017), Bandiet *et al.* (2018), Singh *et al.* (2019), Chowdhary *et al.* (2020) and Sood *et al.* (2021).

Genotypic and phenotypic coefficient of variation

Variation is one of the basic requirements for selection and genetic improvement in a crop. Selection is ineffective and useless without variation. The study of nature and extent of variability present in genotype is required for effective selection. Genotypic and phenotypic coefficients of variation were estimated to study the comparative magnitude of variability present in different traits (Table 3). In general, the values of phenotypic coefficient of variation (PCV) were higher than that of corresponding genotypic coefficient of variation (GCV), indicating influence of environmental factors in the expression of the traits as also reported by Pratap *et al.* (2019). However, narrow differences were observed between the PCV and GCV in certain cases indicated that these characters were less influenced by the environment. The estimates of genotypic and phenotypic coefficient of variation are necessary to understand the role of environmental

influence on different traits. The differences between the GCV and PCV indicate the level of environmental variations that contributes a major part in the expression of traits.

Moderate magnitude of GCV and PCV (10-20 %) was recorded for biological yield per plant, harvest index, number of clusters per plant, seed yield per plant, number of primary branches per plant and number of pods per plant indicating a good deal of genetic variability for the characters under study to allow further improvement by selection of the individual traits. Similar results were also reported by Kumar *et al.* (2015), Gowsalya *et al.* (2016), Sushmitharajet *et al.* (2018), Satheeset *et al.* (2019), Suvarchala *et al.* (2020) and Sood *et al.* (2021).

The relative magnitude of difference between phenotypic and genotypic coefficient of variation was low for days to maturity, 100-seed weight, number of seeds per pod, days to 50 % flowering, number of pods per cluster and plant height indicating that these characters were less influenced by the environment. Similar results were also supported by Kumar *et al.* (2015), Priyanka *et al.* (2016), Mahesha and Lal (2017) and Pratap *et al.* (2019).

Heritability and Genetic Advance as per cent of mean

Knowledge in heritability of character is important as it indicates the possibility and extent to which improvement is possible through selection. It is a measure of genetic relationship between parents to progeny and has been widely used to assess the degree to which a character may be transmitted from parents to off springs. The coefficient of variation alone is not sufficient to determine the amount of heritable variability from one generation to the next generation. Heritability is the ratio of genotypic variance to the total variance or the phenotypic variance. In the present investigation, high heritability (more than 60 %) was recorded for number of pods per plant (61.67 %), number of pods per cluster (75.81 %) and days to maturity (79.98 %). Days to 50 per cent flowering (91.37 %) and biological yield per plant (83.63 %) exhibited highest heritability. Similar findings were reported earlier by Miah *et al.* (2016), Babu *et al.* (2016), Ozukum and Sharma (2017) and Rolaniya *et al.* (2017).

Table 3. Genetic variability parameters for yield and its contributing characters in black gram genotypes.

S. No.	Characters	Range		Mean	GCV	PCV	Heritability (bs) %	Genetic Advance as % of mean
		Lowest	Highest					
1.	Days to 50% flowering	38.67	49.67	47.10	6.52	6.82	91.37	12.85
2.	Days to maturity	63.67	76.67	70.81	3.91	4.38	79.98	7.21
3.	Plant height (cm)	19.11	28.78	25.02	8.59	11.82	52.72	12.84
4.	No. of pri. branches per plant	6.07	10.27	8.64	10.89	14.17	59.05	17.24
5.	Number of clusters per plant	6.53	12.93	9.54	13.01	17.09	57.92	20.39
6.	Number of pods per cluster	2.33	3.13	2.76	7.02	8.07	75.81	12.60

7.	Number of pods per plant	17.65	32.58	27.35	10.74	13.67	61.67	17.37
8.	Number of seeds per pod	4.90	6.27	5.81	4.18	6.71	38.73	5.36
9.	100-seed weight (g)	5.07	6.49	5.84	3.85	6.06	40.48	5.05
10.	Biological yield per plant (g)	23.62	46.86	34.10	17.54	19.18	83.63	33.05
11.	Harvest index (%)	17.65	32.91	25.58	15.32	19.96	58.89	24.22
12.	Seed yield per plant (g)	5.38	10.72	8.51	11.56	15.99	52.26	17.21

Satheeset al. (2019), Senthamiazhselviet al. (2019), Singh et al. (2019), Suvarchalaet al. (2020) and Soodet al. (2021).

The heritability estimates alone do not provide authentic information about the gene governing the expression of a particular character and this do not provide the information of the amount of genetic progress that would result from the selection of best individuals. Johansonet al. (1955) had pointed about that the heritability estimates along with genetic advance as percent of mean were more useful than heritability estimates alone in predicting the response to selection. In the present investigation genetic advance as per cent of mean was highest for biological yield per plant (33.05), harvest index (24.22) and number of clusters per plant (20.39). whereas it was moderate for number of pods per plant (17.37), number of primary branches per plant (17.24), seed yield per plant (17.21), days to 50% flowering (12.85), plant height (12.84) and number of pods per cluster (12.60) and It was low for 100-seed weight (5.05), number of seeds per pod (5.36) and days to maturity (7.21). Such a high heritability coupled with high genetic advance has also been reported earlier for biological yield per plant [Rolaniyaet al. (2017), Soodet al. (2021)], for harvest index [Rolaniyaet al. (2017)], Satheeset al. (2019)]. High heritability coupled with moderate genetic advance as per cent of mean for number of pods per plant, number of primary branches per plant, seed yield per plant, number of pods per cluster, plant height [Babu et al. (2016), Ozukum and Sharma (2017), Rolaniyaet al. (2017), Satheeset al. (2019) and Soodet al. (2021)]. High heritability with high genetic advance showed that these traits are controlled by additive gene action and must go for direct selection of these traits for developing improved genotypes. Days to 50 % flowering showed high heritability with moderate genetic advance indicating non-additive gene action. Same results were shown by Reddy et al. (2018) and Senthamiazhselviet al. (2019). Chowdhary et al. (2020) showed high heritability estimates low for days to maturity.

Moderate heritability with moderate genetic advance was showing the presence of additive as well as non-additive gene action, thus providing scope for the improvement through hybridization and selection. Low heritability with low genetic advance was observed for 100-seed weight and number of seeds per pod indicating that selection for these traits

would be ineffective due to the presence of non-additive gene action.

Heritability and genetic advance as per cent of mean are two complementary concepts. Thus, heritability values may be used to estimate the genetic advance through selection for predicting the utility and value of selection.

REFERENCES

Burton, G.W. (1952). Quantitative inheritance in grasses Proc. 6th Int. Grassland cong., **1**:227-283.

[Google Scholar](#)

Burton, G.W. and De Vane, E.M. (1953). Estimating heritability in tall fescues from replicated cloned material. *Journals of Agronomy*, **45**(3): 474-481.

[Google Scholar](#)

Batra, R.L. and Millner, D.P. (1974). Some Asian Fermented Foods and Beverages, and Associated Fungi. *Journal of the Mycological Society of America*, **66**(6): 942-950.

[Google Scholar](#)

Bandi, H.R.K., Rao, K.N., Krishna, K.V. and Srinivasulu, K. (2018). Variability, Heritability and Genetic Advance for Quantitative characters in Rice Fallow Black gram [*Vigna mungo* (L.) Hepper]. *International Journal of Current Microbiology and Applied Sciences*, **7**(2): 171-176.

[Google Scholar](#)

Chowdhary, T., Das, A., Mandal, G.S., Bhattacharya, S. and Chatterjee, S. (2020). Genetic Variability, Character Association and Divergence Study in Urdbean (*Vigna mungo* (L.) Hepper). *International Journal of Current Microbiology and Applied Sciences*, **9**(2): 1726-1734.

[Google Scholar](#)

Fisher, R.A. (1938). Statistical tables for biological, agricultural and mendelian inheritance. *France Royal Society of Edinburgh*, **52**:399- 433.

[Google Scholar](#)

Gowsalya, P., Kumaresan, D., Packiaraj, D. and KannanBapu, R.J. (2016). Genetic variability and character association for biometrical traits in Blackgram (*Vigna mungo* (L.) Hepper). *Electronic Journal of Plant Breeding*, **7**(2): 317-324.

[Google Scholar](#)

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. *Journal of Agronomy*, **47**(7): 314-318.

[Google Scholar](#)

Konda, C.R., Salimath, P.M. and Mishra, M.N. (2009). Genetic variability studies for productivity and its components in black gram [*Vigna mungo*(L.) Hepper]. *Legume Research*, **32**(1): 59- 61.

[Google Scholar](#)

Kumar, V.G., Vanaja, M., Abraham, B., Anitha, Y., Jyothi Laxmi, N. and Maheshwari, M. (2015). Studies on variability, heritability and genetic advance for quantitative traits in blackgram. *International Journal of Current Sciences and Research*, **52**(4): 28-31.

[Google Scholar](#)

Ozukum, C. and Sharma, M.B. (2017). Variability among urdbean (*Vigna mungo* (L.) Hepper) for yield and yield components. *International Journal of Research and Innovation in Applied Science*, **2**(4): 26-28.

[Google Scholar](#)

Panda, D.P., Lenka, D., Dash, A.P., Tripathy, S.K., Behera, C. and Baisakh, B. (2017). Genetic variability and heritability studies in relation to seed yield and its component traits in black gram. *Trends in Biosciences*, **10**(6): 1412-1414.

[Google Scholar](#)

Pratap, B., Kumar, M., Kumar, V. and Kumar, A. (2019). Genetic variability and correlation studies of seed yield and its components in black gram (*Vigna mungo* (L.) Hepper). *Journal of Pharmacognosy and Phytochemistry*, **8**(3): 2035- 2040.

[Google Scholar](#)

Priyanka, S., Rangaiah, S. and Showkath Babu, B.M. (2016). Genetic variability estimates of qualitative and quantitative traits in Blackgram. *International Journal of Agricultural Sciences*, **8**(40): 1821-1840.

[Google Scholar](#)

Punia, S.S., Gautam, N.K., Baldevram, Verma, P., Dheer, M. Jain, N.K., Koli, N.R., Mahavar, R. and Jat, V.S. (2014). Genetic variability and correlation studies in urdbean (*Vigna mungo*(L.) Hepper). *Legume Research*, **37**(6): 580-584.

[Google Scholar](#)

Reddy, A.K., Priya, M.S., Reddy, D.M. and Reddy, B.R. (2018). Genetic variability studies in blakgram. *International Journal of Chemical Studies*, **6**(5): 2569-2572.

[Google Scholar](#)

Rolaniya, D.K., Jinjwadiya, M.K., Meghawal, D.R. and Lal, G.M. (2017). Studies on genetic variability in black gram [*Vigna mungo*(L.) Hepper] germplasm. *Journal of Pharmacognosy and Phytochemistry*, **6**(4): 1506-1508.

[Google Scholar](#)

Sathees, N.D., Shoba, S., Saravanan, Kumari, S.M.P. and Pillai, M.A. (2019). Studies on Genetic Variability, Association and Path Coefficient Analysis in Black Gram (*Vigna mungo* (L.)Hepper). *International Journal of Current Microbiology and Applied Sciences*, **8**(6): 1892-1899.

[Google Scholar](#)

Senthamizhselvi, S., Muthuswamy, A. and Shunmugavalli, N. (2019). Genetic variability, correlation and path coefficient analysis for yield and yield components in black gram (*Vigna mungo* (L.) Hepper). *Electronic Journal of Plant Breeding*, **10**(4): 1600-1605.

[Google Scholar](#)

Sood, R., Mittal, R.K., Sood, V.K. and Sharma, S. (2021). Assessment of variability parameters for seed yield and related component traits in blackgram [*Vigna mungo* (L.) Hepper] generations. *Himachal Journal of Agricultural Research*, **47**(1): 24-32.

[Google Scholar](#)

Sushmitharaj, D.V., Shoba, D. and Pillai, M.A. (2018). Genetic Variability and Correlation Studies in Black Gram (*Vigna mungo* (L.) Hepper) with Reference to YMV Resistance. *International Journal of Current Microbiology and Applied Sciences*, **3**(6): 2849-2856.

[Google Scholar](#)

Yashoda, Gowda, T.H., Ellur, V. and Swetha (2016). Genetic variability and character association for yield and its components in black gram (*Vigna mungo* (L.) Hepper). *The Bioscan*, **11**(2): 1059-1063.

[Google Scholar](#)