



Evaluation of genetic variability, heritability and genetic advance in blackgram [*Vigna mungo* (L.) Hepper]

Shilpa Chauhan, Raj Kumar Mittal, Vinod Kumar Sood, Ranjana Patial

10.18805/LR-4002

ABSTRACT

An attempt was made to study blackgram germplasm with an objective to develop genetically diverse genotypes accompanied with high heritable components of yield contributing traits. The experimental material comprised of 21 blackgram genotypes, was examined during *kharif* 2015 and 2016. Experimental study conducted during *kharif* 2015, was mainly relied on selection of transgressive segregants, which were further analyzed in Compact Family Block Design during *kharif* 2016. The results depicted that families and progenies within families were significantly different for majority of the traits and found to be highly variable for biological yield, harvest index and seed yield. High heritability coupled with high genetic advance were recorded for plant height (74.15%, 33.12%), branches per plant (84.34%, 40.55%), biological yield (83.51%, 69.11%) and seed yield (84.50%, 66.11%). Thus, the present findings could be beneficial to develop superior genotypes through selection in blackgram breeding program.

Key words: Agro-morphometric, Black gram, Genetic advance, Genetic variability, Heritability, Transgressive segregants.

INTRODUCTION

Blackgram, also known as urdbean and mash is an important short duration and self pollinated *kharif* legume crop and is an important part of Indian diet. It is a rich source of protein (25-28%), carbohydrates (62-65%), fibre (3.5-4.5%), ash (4.5-5.5%), oil (0.5-1.5%), amino acids like lysine, vitamins like thiamine, niacin, riboflavin and much needed iron and phosphorus Sohel *et al.* (2016). Being a leguminous crop, it restores the soil fertility by fixing atmospheric nitrogen and thus prevents soil erosion. India is the largest producer as well as consumer of the blackgram. The major producing states are Andhra Pradesh, Maharashtra, Madhya Pradesh, Tamil Nadu and Uttar Pradesh. India accounts for about 1.5 million tonnes annually from 3.25 million hectare of area with an average productivity of 400 kg per ha Anonymous (2016). Despite its great importance, blackgram cultivation is neglected as little attention is given towards its improvement. There are various reasons for the low production of crop like lack of genetic variability, absence of suitable ideotype, susceptibility to biotic and abiotic stresses and planting in marginal areas of farming. Hence, it is vital to improve the productivity of blackgram. This can be achieved by studying the genetic architecture of the crop.

The knowledge of the inheritance of various quantitative and qualitative traits through estimation of genetic parameters like phenotypic and genotypic coefficients of variability, heritability and genetic advance is a prerequisite in conducting an effective breeding programme. Before starting any breeding program, it is necessary to assess the nature and magnitude of genetic variability in the population to improve the yield and its component traits Singh *et al.* (2016). Along with genetic variability, knowledge of heritability and genetic advance is essential to formulate selection criteria for improvement of seed yield. Heritability

Department of Crop Improvement, College of Agriculture, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062, Himachal Pradesh, India.

Corresponding Author: Shilpa Chauhan, Department of Crop Improvement, College of Agriculture, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062, Himachal Pradesh, India. Email: thakurshilpa627@gmail.com

How to cite this article: Chauhan, S., Mittal, R.K., Sood, V.K. and Patial, R. (2020). Evaluation of genetic variability, heritability and genetic advance in blackgram [*Vigna mungo* (L.) Hepper]. Legume Research. 43(4): 488-494.

Submitted: 07-02-2018 **Accepted:** 25-09-2018 **Published:** 03-01-2019

is the heritable portion of phenotypic variance which is a good index of transmission of traits from parents to their offspring. Heritability in broad sense provides an idea about the additive and non-additive gene action in the expression of traits. The estimates of heritability along with genetic advance are more important than genetic advance alone to know the resulting effect of the best individuals Johnson *et al.* (1955). Keeping in view these points, the present investigation is conducted to assess the variability, heritability in broad sense and genetic advance in F_3 generation of blackgram.

MATERIALS AND METHODS

Experimental site

Experiment was laid out in the farm situated at an elevation of about 1290 m above mean sea level with 36°6' N latitude and 76°3' E longitude representing the mid-hill zone (Zone-II) of Himachal Pradesh, India and characterized by humid sub-temperate climate with high rainfall (2500 mm per annum).

Experimental design

21 blackgram genotypes viz. COBG-653 x Palampur-93, DU-1 x Him Mash-1, KU-553 x HPBU-111, COBG-653 x HPBU-111, KU-553 x Palampur-93, 1 x DU- Palampur-93, KU-216 x Him Mash-1, IPU-02-33 x Palampur-93, IPU-05-13 x Palampur-93, KU-553 x Him Mash-1, KU-223 x HPBU-111, HPBU-126 x HPBU-111, HPBU-124 x HPBU-111, KUG-540 x Palampur-93, TU-17-4 x Palampur-93, HPBU-126 x Palampur-93, TU-94-2 x HPBU-111, KUG-540 x HPBU-111, TU-17-4 x Him Mash-1, TU-94-2 x Him Mash-1, TU-94-2 x Palampur-93 which were developed by crossing 12 lines viz., COBG-653, DU-1, HPBU-124, HPBU-126, IPU-02-33, IPU-05-13, KU-223, KU-553, KUG-216, KUG-540, TU-17-4, TU-94-2 with three testers i.e. Palampur-93, Him Mash-1, HPBU-111, selected on the basis of desirable gca and sca effects in randomised block design with three replications during *kharif* 2014. The resultant F_1 s were advanced to F_2 during *kharif* 2015. Individual plant selection was attempted from F_2 population of 21 cross combinations. The selection of segregants was done phenotypically on the basis of desirable traits like optimum plant height, more number of primary branches per plant, pods per plant, seeds per pod, large pod length, high biological yield per plant and high seed yield per plant. The final experiment was laid out with F_3 population of 21 crosses in compact family block design with three replications during *kharif* 2016-17. The families were randomized in main plots and progenies in sub-plots. Six progenies of each family were planted in each replication. Each progeny was grown in two rows with 1.5 m length. The plants were grown with a spacing of 30 x 10 cm.

Recording of data

Observations were recorded on plot basis as well as single plant basis. Plot basis data were recorded for days to flower initiation, days to 50 per cent flowering and days to 75 per cent maturity while single plant basis data recording was done for plant height, branches per plant, pods per plant, pod length, seeds per pod, biological yield per plant, harvest index, 100-seed weight and seed yield per plant. Ten randomly competitive plants were taken for single plant recording of data.

Statistical analysis

The analysis of variance was conducted as per Chandel (1970) and Bartlett's test was applied according to the

Table 1: Parentage/ source of genotypes/ varieties used in cross combination.

Genotypes/ Varieties	Source/ parentage
Him Mash-1	Pure line selection from local material of Himachal Pradesh by CSKHPKV, Palampur
HPBU-111	Pure line selection from local material of Himachal Pradesh by CSKHPKV, Palampur
Palampur-93	Pure line selection from local material of Himachal Pradesh by CSKHPKV, Palampur

Table 2: Analysis of variance among all families.

Source of variation	Df	Mean sum of squares											
		Days to flower initiation	Days to 50% flowering	Days to 75% maturity	Plant height (cm)	Branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	Biological yield (g)	100-seed weight (g)	Harvest index (%)	Seed yield (g)
Replications	2	1.82	0.29	3.57	58.52	0.03	0.49	0.01	0.01	0.27	0.12	9.71	0.01
Families	20	17.94*	31.12	41.21*	1436.36*	4.02*	102.25*	0.62*	2.28*	527.75*	1.32*	417.91*	13.79*
Error	40	2.31	21.46	4.87	88.92	0.09	2.23	0.02	0.13	23.11	0.17	24.45	1.01
Bartlett's test	20	45.41*	23.91	30.84	355.80*	194.51*	75.12*	50.99*	122.77*	134.24*	102.69*	207.92*	143.32*

*Significant at $P \leq 0.05$.

procedure given by Snedecor and Cochran (1989). The phenotypic coefficient of variation and genotypic coefficient of variation was calculated by the formula given by Burton (1952). Heritability in broad sense was estimated according to Burton and De Vane (1953). The estimates of genetic advance were obtained by the formula given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of variance

Genetic variability in any crop improvement program is a basic requirement for deciding the efficiency of selection. Its existence is essential for resistance to biotic and abiotic factors as well as for wide adaptability. The assessment of genetic variability was main objective of present investigation. The analysis of variance presented in Table 2, indicated that mean sum of squares of families were significantly different at 5% level of significance for days to flower initiation, days to 75 per cent maturity, plant height, branches per plant, pods per plant, pod length, seeds per pod, biological yield, 100-seed weight, harvest index and seed yield. Bartlett's test for homogeneity of variances given in Table 2, showed significant heterogeneity between error variances of families for all the traits except for days to 50 per cent flowering and days to 75 per cent maturity. Table 3 depicted pooled analysis of variance for the traits where error variances between families were homogeneous indicated significant differences among progenies within families for these two traits. For the characters, where error variances were heterogeneous, analysis of variance calculated separately for each family (Table 4), revealed significant differences between progenies within family for majority of the traits in most of the families except for days to flower initiation. The results indicated a wide range of variability among families, between progenies within family and between progenies of different families. Similar observations were recorded by Jain (2004), Kant and Srivastava (2012) in blackgram.

Parameters of variability

The phenotypic coefficient of variation and genotypic coefficient of variation ranged from 3.56-40.18% and 1.99-

36.72%, respectively. The phenotypic coefficient of variation was greater than genotypic coefficient of variation for all agro-morphometric traits studied indicating the influence of environment on the expression of these traits (Table 5). Similar results were recorded by Reddy *et al.* (2011) and Priyanka *et al.* (2016) in blackgram and Jain *et al.* (2017) in soybean. High phenotypic coefficient of variation and genotypic coefficient of variation were found for biological yield (40.18%, 36.72%) followed by harvest index (37.92%, 25.98%) and seed yield (37.98%, 34.91%) (Table 5). This provides an evidence for the existence of sufficient variability for these traits in the population with more contribution of genetic factors and also provides the basis for selection of desirable genotypes from the population. These results are in agreement with Babu *et al.* (2016). Low estimates of variability were observed for days to 75 per cent maturity (3.56%, 1.99%), days to 50 per cent flowering (5.67%, 3.01%), days to flower initiation (6.12%, 2.92%), pod length (8.25 %, 8.07%), seeds per pod (9.19%, 8.40%), 100-seed weight (11.84%, 6.03%) and pods per plant (16.78%, 15.56%). This suggested the prevalence of low genetic variability for these traits in the population and selection will not be effective for these traits. Similar findings were reported by Konda *et al.* (2009) and Deepsikhai *et al.* (2014) for days to 50 per cent flowering, days to 75 per cent maturity, pod length and seeds per pod.

Heritability

Heritability provides the assessment of transmissible traits from one generation to other. Heritability in broad sense is of remarkable significance to the breeders as its extent indicates the reliability with which a genotype can be documented by its phenotypic expression. It was recorded from 22.68 % to 95.71 %. Highest heritability was found for pod length (95.71 %) followed by pods per plant (86 %), seed yield (84.50 %), branches per plant (84.34 %), seeds per pod (83.63 %), biological yield (83.52 %) and plant height (74.15 %) (Table 5). This revealed the lesser influence of environment but selection for improvement of these traits may not be useful due to the involvement of additive and non-additive variances. Such high heritable estimates has been reported by Narasimhan *et al.* (2013) and Bishnoi *et al.* (2017) for plant height, branches per plant, pods per plant, pod length, seeds per pod and seed yield in blackgram and Ramachandra and Lavanya (2017) for pod length, seeds per pod and branches per plant.

Moderate heritability was observed for days to 75 per cent maturity (31.29%), 100-seed weight (30.98%) and harvest index (46.95%), indicated non-additive gene effect and influence of environment and requires high intensity of selection for improvement of these traits. Similar observations were reported by Veeramani *et al.* (2005) for 100-seed weight.

Genetic advance

Genetic advance is helpful in the improvement of mean genotypic value of selected plants over the parental

Table 3: Pooled analysis of variance for progenies among all the families.

Source of variation	df	Mean sum of squares	
		Days to 50% flowering	Days to 75% maturity
Blocks	2	0.29	3.57
Families	20	31.12	41.21*
Error (a)	40	21.46	4.87
Main plots	62	23.89*	16.55*
Progenies within families	105	8.01*	7.02*
Error (b)	210	5.38	5.28

* Significant at $P \leq 0.05$.

Table 4: Analysis of variance for progenies within family.

Families	Source of variation	df	Days to flower initiation	Plant height (cm)	Branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	Biological yield (g)	100-seed weight (g)	Harvest index (%)	Seed yield (g)
COBG-653 x Palampur-93	Replications	2	0.38	1.43	0.24	6.07	0.08	0.09	4.27	0.12	12.70	2.20
	Progeny	5	5.25	165.30	0.14*	23.36*	0.34*	0.04	20.42*	0.02	15.79	0.68*
	Error	10	4.05	62.83	0.02	1.32	0.01	0.04	1.50	0.01	36.37	0.18
DU-1 x Him Mash-1	Replications	2	1.55	9.45	0.08	5.02	0.02	0.48	5.11	0.02	61.36	1.21
	Progeny	5	1.02	22.86	0.10*	1.31	0.19*	0.21	21.16	0.14	25.03	1.05
	Error	10	1.02	17.79	0.02	1.42	0.01	0.08	7.98	0.26	10.85	0.32
KU-553 x HPBU-111	Replications	2	2.38	1018.79	0.25	6.92	0.02	0.29	17.46	0.10	151.54	2.99
	Progeny	5	15.38	56.923	0.61*	14.05*	0.16*	0.04	14.53	0.02	77.86	0.70
	Error	10	7.98	266.28	0.04	1.33	0.01	0.03	4.66	0.01	28.35	1.43
COBG-653 x HPBU-111	Replications	2	6.88	263.73	0.08	7.86	0.01	0.25	22.94	0.29	15.56	12.71
	Progeny	5	5.92	167.67*	0.60*	5.44*	0.45*	0.25	26.48*	0.23	66.01	0.85*
	Error	10	7.22	42.97	0.08	1.59	0.01	0.11	5.93	0.28	74.33	0.15
KU-553 x Palampur-93	Replications	2	2.05	472.09	0.16	0.33	0.02	0.13	7.40	0.19	0.86	0.06
	Progeny	5	3.12	283.89	0.61*	4.61	0.41*	0.18*	13.46*	0.15	21.74	0.26
	Error	10	10.92	246.89	0.09	1.79	0.01	0.02	2.85	0.24	12.36	0.13
DU-1 x Palampur-93	Replications	2	0.66	7.38	0.03	4.33	0.03	0.09	13.72	0.06	10.34	0.01
	Progeny	5	6.36	130.53*	0.54*	24.42*	0.28*	0.14*	6.42	0.14	8.36	0.33*
	Error	10	4.53	2.93	0.01	3.70	0.01	0.01	3.65	0.30	5.69	0.08
KU-216 x Him Mash-1	Replications	2	2.00	1.67	0.18	1.68	0.01	0.01	16.82	0.58	10.38	0.01
	Progeny	5	3.16	26.44*	0.72*	16.67*	0.45*	0.49*	17.46	0.04	17.06	0.25*
	Error	10	2.26	2.46	0.14	2.42	0.01	0.03	10.02	0.18	7.13	0.07
IPU-02-33 x Palampur-93	Replications	2	4.16	0.79	0.80	2.43	0.01	0.35	7.48	0.17	1.33	0.11
	Progeny	5	6.23	63.56*	0.52	7.17	0.26*	0.07	23.13*	0.11	6.84	0.31*
	Error	10	8.10	1.25	0.24	3.75	0.01	0.07	4.56	0.11	3.62	0.05
IPU-05-13 x Palampur-93	Replications	2	0.50	0.15	0.03	0.05	0.01	0.03	49.68	0.40	6.47	0.06
	Progeny	5	12.36	60.59*	0.29*	2.86*	0.19*	0.25*	17.01	0.22	4.89	0.14
	Error	10	6.16	1.54	0.01	0.76	0.01	0.02	8.84	0.14	11.98	0.04
KU-553 x Him Mash-1	Replications	2	2.38	0.54	0.01	0.70	0.04	0.15	14.53	0.02	8.38	0.21
	Progeny	5	3.02	59.55*	0.23*	4.43*	0.09*	0.05	24.09	0.08*	18.30*	0.41*
	Error	10	1.12	1.34	0.02	0.43	0.01	0.04	8.37	0.01	4.39	0.08
KU-223 x HPBU-111	Replications	2	1.05	0.34	0.02	0.52	0.01	0.01	41.98	0.11	46.87	0.06
	Progeny	5	0.62	42.87*	0.06	4.24*	0.24*	0.21*	14.02	0.07	9.21	0.06
	Error	10	1.32	1.92	0.44	0.04	0.01	0.01	18.92	0.04	34.44	0.02
HPBU-126 x HPBU-111	Replications	2	0.05	1.05	0.01	0.63	0.05	0.22	3.86	0.31	3.87	0.06
	Progeny	5	1.82	123.28*	0.65*	11.16*	0.30*	0.06	19.67	0.19	39.63	0.60*
	Error	10	1.58	2.83	0.02	1.03	0.01	0.04	22.40	0.35	72.65	0.02

Table 4: Continue...

Table 4: Continue...

HPBU-124 x HPBU-111	Replications	2	6.50	7.89	0.01	2.35	0.03	0.01	247.41	0.04	150.26	0.30
	Progeny	5	7.56	118.13*	0.51*	21.61*	0.26*	0.16*	39.39	0.05	178.85	1.19*
	Error	10	3.16	5.93	0.01	2.14	0.01	0.01	12.96	0.01	173.17	0.11
KUG-540 x Palampur-93	Replications	2	1.38	5.43	0.02	0.72	0.04	0.03	6.04	0.28	5.50	0.01
	Progeny	5	0.85	189.81*	0.30*	15.63*	0.65*	0.09*	35.69*	0.36	17.22	0.02
	Error	10	1.92	2.63	0.01	0.60	0.02	0.01	10.12	0.34	10.30	0.06
TU-17-4 x Palampur-93	Replications	2	0.22	4.51	0.01	0.36	0.03	0.01	0.37	0.16	0.18	0.02
	Progeny	5	8.18	290.78*	0.50*	8.73*	0.74*	0.27*	13.63*	0.17	8.01*	0.19*
	Error	10	2.62	5.65	0.02	0.77	0.01	0.01	0.38	0.15	1.41	0.04
HPBU-126 x Palampur-93	Replications	2	3.16	5.07	0.02	1.60	0.03	0.01	0.67	0.26	0.10	0.05
	Progeny	5	8.23	31.39*	0.43*	7.38*	0.26*	0.24*	18.78*	0.07	1.39*	0.74*
	Error	10	4.10	0.80	0.02	0.52	0.01	0.01	1.90	0.19	0.26	0.02
TU-94-2 x HPBU-111	Replications	2	4.66	5.23	0.02	0.09	0.03	0.24	0.39	0.04	0.76	0.02
	Progeny	5	1.96	67.64*	0.50*	6.26*	0.38*	0.02	4.59*	0.06	2.25	0.08
	Error	10	2.53	2.07	0.02	0.84	0.01	0.05	0.82	0.03	1.21	0.05
KUG-540 x HPBU-111	Replications	2	1.72	14.25	0.02	2.57	0.01	0.01	0.02	0.46	0.19	0.01
	Progeny	5	7.55	7.54	0.66*	9.35*	0.25*	0.33*	11.44*	0.17	7.33	0.16
	Error	10	2.65	5.12	0.01	0.29	0.01	0.01	0.56	0.22	3.67	0.06
TU-17-4 x Him Mash-1	Replications	2	3.38	2.12	0.01	0.14	0.01	0.32	0.91	0.01	1.85	0.03
	Progeny	5	3.12	26.75*	0.23*	6.66*	0.41*	0.34*	3.98*	0.04	13.58	0.17
	Error	10	2.45	2.50	0.01	0.31	0.01	0.08	0.62	0.02	12.30	0.06
TU-94-2 x Him Mash-1	Replications	2	0.05	9.73	0.01	0.10	0.01	0.01	1.13	0.04	8.58	0.01
	Progeny	5	4.85	22.21*	0.41*	2.93*	0.32*	0.07*	3.94*	0.01	4.99	0.06
	Error	10	1.52	4.48	0.02	0.39	0.01	0.01	0.39	0.03	2.96	0.03
TU-94-2 x Palampur-93	Replications	2	2.88	5.28	0.01	0.57	0.00	0.01	0.28	0.01	1.63	0.01
	Progeny	5	5.78	98.99*	0.21*	13.59*	0.26*	0.49*	8.20*	0.01	3.55	0.27*
	Error	10	5.02	2.05	0.01	1.31	0.01	0.01	0.51	0.03	2.57	0.04

*Significant at $P \leq 0.05$.

Table 5: Genetic parameters of variability for different traits in blackgram.

Traits	Mean $\pm$ S.E.(m)	Range	CV(%)	PCV (%)	GCV (%)	h^2 bs (%)	GA (as % of mean)
Days to flower initiation	36.77 $\pm$ 0.36	35.22-38.67	5.37	6.12	2.92	22.68	2.68
Days to 50% flowering	48.29 $\pm$ 1.09	44.50-50.17	5.84	5.67	3.01	28.14	3.29
Days to 75% maturity	77.93 $\pm$ 0.52	75.00-80.17	3.03	3.56	1.99	31.29	2.29
Plant height (cm)	51.70 $\pm$ 2.22	32.28-67.40	14.81	21.69	18.67	74.15	33.12
Branches per plant	2.61 $\pm$ 0.07	1.96-3.65	16.01	23.34	21.44	84.34	40.55
Pods per plant	18.01 $\pm$ 0.35	12.53-22.48	10.69	16.78	15.56	86.00	29.72
Pod length (cm)	4.35 $\pm$ 0.03	4.02-4.68	7.25	8.25	8.07	95.71	16.27
Seeds per pod	4.84 $\pm$ 0.09	3.97-5.42	6.19	9.19	8.40	83.63	15.83
Biological yield (g)	15.14 $\pm$ 1.13	8.98-36.47	22.34	40.18	36.72	83.51	69.11
100-seed weight (g)	3.80 $\pm$ 0.010	3.04-4.20	9.93	11.84	6.03	30.98	6.34
Harvest index (%)	17.85 $\pm$ 1.16	11.20-28.77	28.26	37.92	25.98	46.95	36.67
Seed yield (g)	2.56 $\pm$ 0.24	1.45-4.69	22.26	37.98	34.91	84.50	66.11

populations. It measures the genetic gain under selection. It should be considered in conjugation with genetic advance for effective selection of genotypes. The range of genetic advance as percentage of mean varied from 2.29% to 69.11%. Genetic advance was found to be high (>30%) for biological yield (69.11 %) followed by seed yield (66.11 %), branches per plant (40.55 %), harvest index (36.67%) and plant height (33.12%) (Table 5). High heritability with high genetic advance was recorded for plant height, branches per plant, biological yield and seed yield. This suggesting that mostly these traits were under the control of additive gene action and selection will be more useful for yield improvement. Similar results were observed by Kant and Srivastava (2011) and Singh *et al.* (2014) for plant height, branches per plant and seed yield in blackgram and Meena *et al.* (2017) for biological yield and seed yield in chickpea. High heritability with moderate genetic advance was observed for pods per plant, pod length and seeds per pod, indicating that these traits were less influenced by environment but governed by both additive and non-additive gene action. Hence, simple selection is suggested for improvement of these traits in the later generations. Similar observations were reported by Bharti *et al.* (2016) and Hadimani *et al.* (2015) for pods per plant and seeds per pod. Moderate heritability with high genetic advance was found for harvest index, showing the lesser influence of environment with additive gene action, hence, amenable for selection.

CONCLUSION

The analysis of variance revealed the occurrence of genetic variability among all the families, between progenies belonging to same family and between progenies within families. In general, phenotypic coefficient of variation was greater than the genotypic coefficient of variation for all the agro-morphometric traits. Plant height, branches per plant, biological yield, harvest index and seed yield were important traits and priority should be given for these traits while deciding selection criteria and selection for these traits would be useful in yield improvement. It was concluded that in

case of biological yield and seed yield apart from high genotypic coefficient of variation, estimates of heritability with genetic advance were high, hence direct mass selection may be rewarded for these two traits.

ACKNOWLEDGEMENT

I am thankful to my advisor and Department of Crop Improvement, CSKHPKV, Palampur for rendering necessary help.

REFERENCES

- Anonymous (2016). Indian Institute of Pulses Research, Kanpur (U.P.).
- Babu, J.S., Reni, Y.P. and Ramana, M.V. (2016). Character correlation and path coefficient in black gram [*Vigna mungo* (L.) Hepper]. International Reserach Journal of Natural and Applied Sciences. 3: 178-182.
- Bharti, B. and Kumar, R. (2016). Genetic variability, heritability and genetic advance for seed yield and its components in urdbean germplasm [*Vigna mungo* (L.) Hepper]. Indian Ecological Society, Conference p 255-256.
- Bishnoi A., Gupta P., Meghawal D.R. and Lal G.M. (2017). Evaluation of genetic variability and heritability in blackgram [*Vigna mungo* (L.) Hepper] genotypes. Journal of Pharmacognosy and Phytochemistry. 6: 493-496.
- Burton, G.W. and Devane, E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 45: 478-481
- Burton, G.W. (1952). Quantitative inheritance in grasses. *Proceeding of 6th International Grassland Congress*. 1: 227-283.
- Chandel, R.S. (1970). Handbook of Agricultural Statistics 4th editions. Achal Prakashan Mandir, Parmat, Kanpur-1 pp. 542-546.
- Deepshikha, Lavanya, G.R. and Kumar, S. (2014). Assessment of genetic variability for yield and its contributing traits in blackgram. Trends in Biosciences. 7: 2835-2838.
- Hadimani, A., Konda, C.R., Patil, R., Guru, P.N., Hedge, V.K. and Vijakumar, L. (2015). Assessment of variability, heritability and genetic advance for yield and yield attributing traits in blackgram [*Vigna mungo* (L.) Hepper]. International Journal of Tropical Agriculture. 33: 2473-2475.
- Jain, R.K., Joshi, A., Chaudhary, H.R., Dashora, A. and Khatik, C.L. (2017). Study on genetic variability, heritability and

- genetic advance in soybean [*Glycine max* (L.) Merrill]. Legume Research. 10: 532-536.
- Jain, S.K. (2004). Induction of variability through mutagenesis in blackgram. Phd. Thesis, Maharana Pratap University of Agriculture and Technology, Udaipur.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. Agronomy Journal. 47: 314-18.
- Joshi, P., Yasin, M. and Sundaram, P. (2018). Genetic variability, heritability and genetic advance study for seed yield and yield component traits in a chickpea Recombinant Inbred Line (RIL) Population. International Journal of Pure and Applied Bioscience. 6: 136-141.
- Kant, R. and Srivastava, R.K. (2012). Heterosis and inbreeding depression studies in urdbean [*Vigna mungo* (L.) Hepper]. Journal of Food Legumes. 25: 102-108.
- Kant, R. and Srivastava, R.K. (2011). Heritability and genetic advance in urdbean [*Vigna mungo* (L.) Hepper]. Legume Research. 34: 226-229.
- Konda, C.R., Salimath, P.M. and Mishra, M.N. (2009). Genotype and environment interactions for yield and its components in blackgram. Legume Research. 32: 195-198.
- Meena, B.L., Das, S.P., Meena, S.K., Kumari, R., Devi, A.G. and Devi, H.L. (2017). Assessment of GCV, PCV, heritability and genetic advance for yield and its components in field pea (*Pisum sativum* L.). International Journal of Current Microbiology and Applied Sciences. 6: 1025-1033.
- Narasimhan, A., Patil, B.R. and Khadi, B.M. (2013). Genetic variability and character association for yield and its components in blackgram [*Vigna mungo* (L.) Hepper]. Journal of Food Legumes. 26: 137-138.
- Priyanka, S., Rangaiah, S. and Showkath, B.B.M. (2016). Genetic variability estimates of quantitative and qualitative traits in black gram. International Journal of Agricultural Sciences. 8: 1821-1824.
- Ramachandra, P. and Lavanya, G.R. (2017). Variability, heritability, genetic advance and correlation coefficients for yield component characters and seed yield in greengram [*Vigna radiata* (L.) Wilczek]. Journal of Pharmacognosy and Phytochemistry. 6: 1202-1205.
- Reddy, D.K.R., Venkateswarlu, O., Jyothi, G.L.S. and Obaiah, M.C. (2011). Genetic parameters and inter-relationship analysis in blackgram. Legume Research. 34: 149-154.
- Singh, A.K., Gautam, R.K., Singh, P.K., Kumar, K., Kumar, N., Swain, S. and Roy, S.D. (2014). Estimation of genetic variability and association analysis in the indigenous landraces of urdbean [*Vigna mungo* (L.) Hepper] of Andaman islands. International Journal of Plant Research. 27: 113-122.
- Singh, M., Swarup, I., Gaikwad, P.D. and Singh, J. (2016). Variability and heritability analysis in black Gram [*Vigna mungo* (L.) Hepper]. Advances in Life Sciences. 5: 2619-2621.
- Snedecor, G.W. and Cockran, W.G. (1989). *Statistical Methods*, eight edition. Iowa State University Press.
- Sohel, M.H., Miah, M.R., Mohiuddin, S.J., Islam, A.K.M.S., Rahman, M.M. and Haque, M.A. (2016). Correlation and path coefficient analysis of blackgram [*Vigna mungo* (L.) Hepper]. Journal of Bioscience and Agriculture Research. 7: 621-629.
- Veeramani, Venkatesan, N.M., Thangavel, P. and Ganesan, J. (2005). Genetic variability, heritability and genetic advance analysis in segregating generation of blackgram. Legume Research. 28: 49-51.