

Original Research Article

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Genetic Parameters of Variation for Seed Yield and its Component Traits in Black Gram (*Vigna mungo* L. Hepper)

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ABSTRACT

Black Gram (*Vigna mungo* L. Hepper) is most prevalent types out of pluses crops 80 genotypes of Black gram collected from Bastar Region (Dantewad, Sukma, Bijapur, Kondagoan, Narayanpur, Kanker districts). The experiment was conducted in Randomized Complete Block Design (RCBD) with two replications comprising two check varieties viz. Indira Urd Pratham and T.U. 94-2. Crop growing spacing 30×10cm during *Kharif* 2019 in Research cum Instructional Farm of SGCARS Kumhrawand, Jagdalpur, Bastar (C.G.). Analysis of variances indicated presences of significant genetic variability for thirteen biometrical traits in Black Gram genotypes. Highest GCV and PCV estimated for seed yield per plant, plant height (cm), number of primary branches per plant and test weight of thousand seeds. High heritability and genetic advances indicated least influenced of environment on the expression of character and characters governed by additive genes respectively. High heritability accompanied with high Genetic Advance as percent of mean observed for the traits plant height (cm), Test weight of thousand seeds, seed yield per plant (g), harvest index (%) and petiole length (cm) due to additive gene effect abundant sources provided for improving the traits though section.

Keywords

Seed yield,
Component traits,
Black gram,
Analysis of
variances

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Introduction

Black gram [*Vigna mungo* (L)] belongs to kingdom plantae, division magnoliophyta class magnoliopsida sub class rosidae, order fabales, family Fabaceae, (alt. Leguminosae) Sub family Papilionaceae, genus *vigna* species *mungo* with chromosome number $2n = 22$ (Cronquist, 1988). Black gram is classified in two groups *Vigna mungo* var. *niger* and *Vigna mungo* var. *viridis*, in *niger* includes varieties which mature early and

have black coloured seeds and in *viridis* includes varieties which mature late and their seeds are smaller and green in colour. Synonym of Black gram is locally known as Urd, Biri and Mash. It is originated in India from wild progenitor *Phaseolus sublobatus* was found domesticated in south Asian countries. It is an annual erect growing herb with height of 0.3-1.0 m and stem are ribbed and covered by brown hairs. Leaves are trifoliate and dark green covered with profuse purplish small hairs. Leaflets are broad, ovate

and entire in margins. Flower is clusters of 5-6, born on long hair peduncle. They have 5 sepal, 5 petals, 9+1 stamen, and hairs are twisted in style (Ram, 2011). Pods are dehiscent, long and cylindrical (4-6 cm), having 4-10 dark brown/black /dull olive green seed black gram is self pollinated crops. It is mainly grown in India as well as in Myanmar, Pakistan, Bangladesh and Srilanka. Occupying both tropical and sub tropical regions. It has grown over 3.4 million hectare in the world, out of which 2.97 million hectare is grown in India. Black gram contributing 10% of the total pulse production from 13% in total area in India (Joshi, 2015). High values of lysine make urd bean an excellent complement to rice in terms of balanced human nutrition (Sakila and Pandiyan, 2018). Nutritive value of urd bean hold protein 26-27%, calcium -154 mg/100g, fat-1.4%, phosphorus-385mg/100g, Minerals -3.2%, Iron - 9.1mg/100g, Fiber-0.9%, calorific value-347Kcal/100g, carbohydrate-60%, moisture 10.9% and vitamins (mg/100gm) B₁, B₂ and Niacine 0.42, 0.37 and 2.0 respectively (Panigrahi *et al.*, 2014). Black gram can be grown on different types of soils from light sandy to heavy clay soils having well drained condition. It should be temperature range between 25°C to 35°C, relative humidity 50 to 85% and annual rainfall of 600- 1000 mm for better growth and development. But it grows better on rich black vertisols or loamy soils with a pH 6-7. It can withstand acidic soil (down to pH 4.5). It is drought tolerant and thus suitable for semi arid areas. Urd is sensitive to saline and alkaline soils (Sharma *et al.*, 2011). In rainfed agriculture, it has special status, as it is an effective soil binder over all soil conservation and also act as green manuring crop. Black gram is an important food legume with excellent source of good quality protein and having ability to restore fertility of soil through symbiotic nitrogen fixation (Gupta *et al.*, 2008).

India is larger producer (25% of global production), consumer (27% of world consumption) and importer (14%) of pulses in the world. Pulses can be produced with a minimum use of resources and hence, it becomes less costly even than animal protein. Important states growing black gram in India total area (lakh ha) and production (lakh tonnes) of black gram is 44.78, 28.32 respectively in which Madhya Pradesh (12.03) (8.17), Uttar Pradesh (6.44)(3.57), Andhra Pradesh (5.00) (3.29), Rajasthan (4.77) (3.05), Tamilnadu (4.30) (2.74), Maharashtra (3.38) (1.83), Gujarat, (1.97) (1.19), Jharkhand (1.57) (1.39), Orissa (1.09) (0.49) and Other states (3.29) (2.06) respectively (Anon, 2016).

In the year 2018–19 during *rabi* and 2019-20 during *kharif* in India area (lakh ha) and production (lakh tonnes) is 7.629, 26.5, 37.52 and 25.6, respectively (Anon. 2019). In Chhattisgarh black gram area (000 ha) and production (kg/ha) according to the year wise in 2015-16(154.51) (305), 2016-17(144.94) (320), 2017-18(164.44) (332) occupies respectively (Anon. 2019).

All the varieties developed to date are mainly by single plant selection from locals. There is greater need to increase the yield and quality of this crop by breeding while understanding the genetic makeup of this crop. Hence, it is essential to generate new variability through hybridization. By germplasm exploration superior germplasm's can be identified from these local varieties which can be ultimately used for developing superior lines in breeding programme. Hence looking to the above facts investigation entitled "Diversity analysis in black gram [*Vigna mungo* (L.) Hepper] genotypes collected from Bastar region" is being carried out with the objective "to study the genetic variability in black gram for seed yield and its yield related components traits"

Materials and Methods

The present experiment entitled “Diversity analysis in black gram [*Vigna mungo* (L.) Hepper] was conducted at “Research cum Instructional Farm, Shaheed Gundadhoor College of Agriculture and Research Station, Kumhrawand, (Jagdarpur), Indira Gandhi Krishi Vishwa vidyalaya, Raipur (Chhattisgarh)” located at N 19°5’39’’ longitude E 81°59’33’’ latitude and at an altitude 553.400 meters above mean sea level (MSL) with an annual rainfall 14.39 mm. The experimental material comprised of eighty two black gram genotypes along with two check varieties Indira Urd Pratham and T.U. 94-2. The experimental material was planted in a Randomized Complete Block Design with two replications during *kharif* 2019. Each genotype was planted in two rows of 3 m length × 1 m width having 30 ×10 cm spacing between rows and plants. The observations were recorded on five randomly selected plants per replication for each accession. The analysis of variance for different characters was carried out using the mean data through method given by Ponce and Sukhatme (1964).

The phenotypic and genotypic variances and genetic advance were calculated as suggested by Johnson *et al.*, (1955) and Sivasubramaniam and Madhavamenon (1973). Genotypic and phenotypic coefficients of variations were estimated by using the formula suggested by Burton and De Vane (1953). Heritability in broad sense for each character was analysed by using the method suggested by Hanson *et al.*, (1956). The coefficient of variation (CV) being a unit less measurement, is a good basis for comparing the extent of variation between different characters with different scales. The genotypic and phenotypic variance was calculated as per the formulae proposed by Burton (1952). Broad sense heritability was

computed as “the ratio of genetic variance to the total or phenotypic variance as suggested by Hanson *et al.*, (1956) and expressed as percentage”. The expected genetic gain for each character was analyzed by using the following method suggested by Johnson *et al.*, (1955).

Results and Discussion

Analysis of variance was performed for thirteen quantitative traits including yield and yield attributes of 82 genotypes. From the analysis of variance it was observed that mean sum of squares due to genotypes was significant for all characters at 5% level of significance under study, thus exhibiting the presence of significant considerable genetic variability for all the traits in the experimental material. The results found were presented in Table 1. These findings are authorization with the finding of Singh *et al.*, (2020), Shalini and Lal (2019), Aftab *et al.*, (2018), Chauhan *et al.*, (2018), Vidya *et al.*, (2018), Bishnoi *et al.*, (2017), Rolaniya *et al.*, (2017), Tank *et al.*, (2017), Jyothsna *et al.*, (2016), Priyanka, *et al.*, (2016), Sohail *et al.*, (2016), Usharani and Kumar (2016), Veeramani *et al.*, (2005) in black gram.

Genetic variability

The results pertaining to genetic parameters viz., range, mean, genotypic variance, phenotypic variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean were calculated to estimate the amount of genetic variability for different characters. The results related to genetic parameters are presented in the Table 2. The data of mean and range reveals the extent of phenotypic and genotypic variability of characters under study.

Table.1 Analysis of variances for seed yield and its attributing traits in black gram

Source of variation	Degrees of freedom	DFP	NPBPP	NPPP	PL (cm)	PH (cm)	NSPP	DFMP	DM	PeL (cm)	NPPC	HI	TW (g)	SYPP (g)
Replication	1	3.51	0.13	22.08	0.20	204.87	0.09	383.91	384.15	3.53	0.01	0.01	11.14	65.05
Treatments	81	9.15**	0.42**	38.88**	0.42**	450.39**	0.42**	20.42**	14.91**	5.32**	0.41**	157.34**	65.07**	130.96**
Error	81	4.18	0.03	5.69	0.10	8.96	0.12	7.11	9.77	0.67	0.10	7.34	2.17	5.75
SE(d)	-	2.04	0.16	2.39	0.31	2.99	0.35	2.67	3.13	0.82	0.32	2.71	1.47	2.40
C.D. at 5%	-	4.08	0.33	4.76	0.63	5.97	0.69	5.32	6.23	1.63	0.64	5.40	2.94	4.78
C.V. (%)	-	5.07	8.08	5.11	6.51	6.30	5.27	4.18	4.08	7.91	9.01	5.25	5.34	10.76

*Significant at 5% level of significance DFP= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height (cm), NPBPP= Number of primary branches per plant, NPPP= Number of pods per plant, DFMP= Days to first mature pod, NPPC= Number of pods per cluster, PeL= Petiole length (cm), PL= Pod length(cm), NSPP= Number of seeds per pod, SYPP= Seed yield per plant (g), HI= Harvest index(%), TW (g) = Test weight of 1000 Seed.

Table.2 Genetic parameters of variation for seed yield and its component traits in black gram

Characters	Mean	Range		CV		h ² bs (%)	GA as % mean
		Min	Max	GCV (%)	PCV (%)		
DFF	40.34	34.50	45.00	3.91	6.40	37.28	4.91
NPBPP	2.02	1.00	3.20	22.00	23.44	88.10	42.53
NPPP	46.67	41.40	56.40	8.73	10.12	74.47	15.52
PL (cm)	4.83	3.53	6.03	8.27	10.52	61.74	13.38
PH (cm)	47.52	24.60	101.51	31.26	31.89	96.10	63.13
NSPP	6.54	5.62	7.81	5.96	7.95	56.08	9.19
DFMP	63.75	57.50	73.00	4.05	5.82	48.34	5.80
DM	76.65	70.50	83.00	2.09	4.58	20.83	1.97
PeL (cm)	10.35	7.04	13.77	14.74	16.73	77.63	26.74
NPPC	3.57	2.50	4.60	10.93	14.16	59.56	17.38
HI (%)	51.58	26.32	69.32	16.79	17.59	91.09	33.01
TW of 1000 Seeds (g)	27.62	20.70	47.22	20.31	21.00	93.54	40.46
SYPP (g)	22.28	11.06	41.53	35.51	37.10	91.59	70.00

GCV= Genotypic coefficient variance, PCV= Phenotypic coefficient variance, h² bs = Heritability in broad sense, DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height (cm), NPBPP= Number of primary branches per plant, NPPP= Number of pods per plant, PeL= Petiole length (cm), PL= Pod length (cm), NSPP= Number of seeds per pod, NPPC=Number of pods per cluster, DFMP=Days to first mature pod, HI= Harvest index (%), SYPP= Seed yield per plant (g), TW= test weight of 1000 seeds.

Results obtained from these components of genetic parameter indicate presence of abundant amount of genetic variability in the material under present investigation. These findings are in authorisation with the findings on the reports of Chowdhury *et al.*, (2020), Singh *et al.*, (2020), Sathees *et al.*, (2019), Chauhan *et al.*, (2018), Priya *et al.*, (2018), Verma *et al.*, (2018), Sinha *et al.*, (2018), Panigrahi *et al.*, (2014), Singh *et al.*, (2014), Sowmini and Jayamani (2013).

Data obtained from the experiment showed high PCV and GCV have in seed yield per plant (37.10%, 35.51%), plant height (31.89%, 31.26%), number of primary branches (23.44%, 22.00%) and 1000 seed weight (21.00%, 20.31%) respectively. Moderate PCV and GCV have in harvest index (17.59%, 16.79%), petiole length (16.73%, 14.74%) and number of pods per cluster (14.16, 10.93) respectively. Moderate PCV and low GCV values recorded both traits pod length (10.52%, 8.27%) and number of pods per plant (10.12%, 8.73%). Low PCV and GCV for days to maturity (4.58%, 2.09%), days to first mature pod (5.82%, 4.05%), days to 50% flowering (6.40%, 3.91%) and number of seeds per pod (7.97%, 5.96%). if the genetic coefficient of variance (GCV) is higher than phenotypic coefficient of variance (PCV) it indicate that there is little influence of environment on the expression of character. Selection for improvement of such characters will be regarding. when less than PCV as compared to GCV the Apparent variation is not only due to genotype but also due to the influence of environment. These approximations of the current study were authorized with the outcomes of Chowdhury *et al.*, (2020a), Singh *et al.*, (2020), Chaithany *et al.*, (2019), Shalini and Lal (2019), Singh *et al.*, (2019), Sathees *et al.*, (2019), Veni *et al.*, (2019), Aftab *et al.*, (2018), Chauhan *et al.*, (2018), Priya *et al.*, (2018), Sinha *et al.*, (2018), Tank *et al.*, (2018), Verma *et al.*,

(2018), Bishnoi *et al.*, (2017), Mahesha and Lal (2017), Hemalatha *et al.*, (2017), Deepshika *et al.*, (2014), Panigrahi *et al.*, (2014), Sowmini and Jayamani (2013).

High heritability coupled with high genetic advance indicated presence of additive gene action in these traits *viz.* plant height (96.10%, 63.13%), test weight of 1000 seeds (93.54%, 40.46%), seed yield per plant (91.59, 70%), harvest index (91.09%, 33.01%), number of primary branches per plant (88.10%, 42.53%) and petiole length (77.63%, 26.74%) additive gene action is pronounced in the expression of these characters, early generation selection would be effective in breeding program (Singh and Narayanan, 2015). High heritability coupled with low genetic advance it is indicated non-additive gene action, the high heritability is being exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding. Low heritability accompanied with high genetic advance it reveals that the character is governed by additive gene effects. The low heritability accompanied with low genetic advance for the characters *viz.* days to first mature pod (48.34%, 5.80%), days to 50% flowering (37.28%, 4.91) and days to maturity (20.83%, 1.97%) it indicates that the character is highly influenced by environmental effect and selection would be ineffective.

Moderate heritability was recorded for the characters pod length (61.74%), number of pods per cluster (59.56%) and number of seeds per pod (56.08%). The findings of present study were in agreement with the findings of Sathees *et al.*, (2019), Sushmitharaj *et al.*, (2018), Aftab *et al.*, (2018), Chauhan *et al.*, (2018), Mahesha and Gabriel (2017), Rolaniya *et al.*, (2017), Anand *et al.*, (2016), Sohel *et al.*, (2016) and Panigrahi *et al.*, (2014).

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