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Genetic variability and correlation studies of seed yield and its components in black gram (*Vigna mungo* (L.) Hepper)

Bhanu Partap, Mukesh Kumar, Vipin Kumar and Arvind Kumar

Abstract

An experiment was carried out to estimate the genetic parameters like variability, heritability and correlation studies for eleven quantitative characters viz., days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of pods plant⁻¹, pod length, number of seeds pod⁻¹, biological yield plant⁻¹, test weight, harvest index, and grain yield plant⁻¹ in 40 genotypes of Black gram (*Vigna mungo* (L.) Hepper). High phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were observed for all the characters studied. The phenotypic coefficient of variance was higher in magnitude than the respective genotypic coefficient of variance for all the characters indicating the important role of environment in the expression of characters. High heritability coupled with high genetic advance was observed for plant height only indicating the heritability is due to additive gene action and simple selection for this trait. Hence, yield studies revealed that, grain yield plant⁻¹ shows significant positive correlation with biological yield per plant, number of pods per plant, number of seeds per pod, test weight, plant height, number of primary branches per plant and pod length both at phenotypic and genotypic level. Path analysis studies revealed that biological yield per plant, number of pods per plant, number of seeds per pod, test weight, plant height, number of primary branches per plant and pod length both at phenotypic and genotypic level.

Keywords: Genetic variability, heritability, genetic advance, path analysis, black gram

Introduction

Black gram (*Vigna mungo* L. Hepper) popularly known as urdbean or mash, is a grain legume domesticated from *V.mungo* var. *silvestris*. It belongs to family leguminosae with chromosome number $2n=2x=22$. Blackgram is reported to be originated in India. It is grown mainly in rainy and/or summer seasons. In India the area production and productivity of blackgram was 4.49mha with 2.93 m tonne and 651 kg ha⁻¹ (Agricultural Statistics, 2016) [2]. During 2016-17 its share towards total pulse production was 11%. In Uttar Pradesh Blackgram occupied an area of 0.99 lakh ha, production 0.32 lakh tonne and productivity 323 kg ha⁻¹ (DPD 2016-17). The reason for low yield is i) adaption of crop to marginal lands of rain-fed nature, ii) unavailability of suitable cultivars with high potential, iii) stress to diseases insects and environmental fluctuations, etc. Hence, large parts of the genetic variability for yield contributing characters were lost during the course of evolution. Thus, the crop requires due attention to increase its production and productivity. Blackgram is very nutritious as it contains high levels of protein (25g/100g), potassium (983 mg/100g), calcium (138 mg/100g), iron (7.57 mg/100g), niacin (1.447 mg/100g), Thiamine (0.273 mg/100g), and riboflavin (0.254 mg/100g).

Yield is a complex quantitative trait which controlled by polygene and interlinked with other yield components, and cannot be improved by selecting individuals on *per se* performance basis. Thus, it can be improved by practicing selection for other traits which are highly heritable and are interrelated with the yield as well. Progresses in any breeding programme depend upon the extent and nature of variability existing in the base population. Thus, the success of any breeding programme depends on choice of breeding stocks that have sufficient variability. Low productivity in this crop is also attributable to its narrow genetic base due to common ancestry of various superior genotypes, poor plant type and their cultivation in marginal and harsh environments. The improvement of crop yield largely depends upon the magnitude of genetic variability and the extent to which the determining characters are heritable from generation to generation. Correlation coefficients reveal the magnitude and direction of association of yield components. Character association helps in formulating an effective breeding strategy to develop productive genotypes. Thus knowledge of genetic variability, genetic advance and correlation are very essential for breeder to choose good

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parents and to decide the correct breeding method for crop improvement.

The creation of variability is difficult through hybridization due to its high self-pollination and flower droop (Deepalakshmi and Anandakumar, 2004) ^[12]. Therefore, mutation breeding can also be effectively utilized to improve yield and other polygenetic characters, (Deepalakshmi and Anandakumar, 2004) ^[12]. Hence, genetic variability is the basic requirement for making progress in crop breeding (Appalaswamy and Reddy, 2004) ^[4]. Keeping the above points in the view, the present study was undertaken with the following objectives of (a) interest to know the magnitude of variation due to heritable component, which in turn would be a guide for selection for the improvement of a population, (b) the inheritance of various developmental and productive traits through the estimation of different genetic parameters, (c) to study the genetic variability parameters for yield and yield attributing traits i.e. components of variances, genotypic and phenotypic coefficients of variability, heritability and genetic advance, (d) to assess the correlation among yield and component traits.

Materials and Methods

The material under investigation consisted of forty genotypes of black gram Gram (*Vigna mungo* L. The field experiment was conducted at Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut (U.P.) research farm (29° 04' N latitude and 77° 42' E longitude at a height of 237m above mean sea level) U.P., during spring, 2017. The design adopted was Randomised Block Design with three replications. Each plot consisted of four rows of 5.0 meters length with a spacing of 30 × 10 cm and seeds were sown by hand dibbling. The area receives an average annual rainfall of 695 mm (constituting 44% of pan evaporation) of which about 80% is received during the monsoon period. The soil analysis revealed that the soil was sandy-loam with 55, 18, and 27% sand, silt, and clay, respectively, *Typic Ustochrept*; non-saline (EC 0.42 dS m⁻¹) but mild alkaline in reaction (pH 7.98). The soil (0-15 cm depth) initially had 4.1 g kg⁻¹ of SOC and 16.4, 96, and 14.5 kg ha⁻¹ of available P, K, and S, respectively. Observations on plot basis were recorded for days to 50% flowering and days to maturity. For recording single plant observations, from each replication five random plants were tagged for observing yield and other quantitative characters. The mean value of the five plants was computed and taken for analysis in respect of plant height, number of primary branches plant⁻¹, number of pods plant⁻¹, number of seeds plant⁻¹, number of seeds pod⁻¹, 1000-seed weight, biological yield plant⁻¹, harvest index and seed yield plant⁻¹ as suggested Fisher (1936) ^[14]. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were given by Burton (1952) ^[10]. Heritability in broad sense was given by Lush (1949) ^[21] and Burton and Devane (1953) ^[11]. Genetic advance was given by Lush (1949) ^[21].

Results and Discussion

A broad-spectrum of genetic variability is fundamental requisite for success of a plant breeding programme since it provides opportunity to breeders to make selection for desirable superior individuals from genetically diverse base population. Since, many characters of economic importance are highly influenced by environmental conditions; the improvement of a crop mainly depends upon the amount, nature and magnitude of genotypic variability present in the population. Wide range of variability existing among the

genotypes to be tested for all the characters is also necessary to isolate significantly superior genotypes.

The mean performance of forty genotypes of black gram lines are presented in Table 1 revealed that highly significant differences among the genotypes for all the traits viz., days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of pods plant⁻¹, pod length, number of seeds pod⁻¹, biological yield plant⁻¹, harvest index, test weight and grain yield plant⁻¹ indicating the presence of considerable genetic variability in the experimental material. These results were in agreement with the findings of Balachandran *et al.* (2010) ^[7], Kumar *et al.* (2015) ^[19, 20], Priyanka *et al.* (2016) ^[32], Rolaniya *et al.* (2017) ^[38] and Nagmi and Lal (2017) ^[26].

The success of any breeding programme depends upon the extent of genetic variability in base population and it is essential to subject a population for selection to achieve improvement in a particular trait. The estimates of genotypic co-efficient of variance (GCV), and phenotypic co-efficient of variance (PCV) for different characters are presented in Table 2. The highest estimate variation GCV and PCV was registered for single plant yield (>20%) for plant height, number of pods plant⁻¹ and number of primary branches plant⁻¹. Moderate (10-20%) PCV and GCV values were observed in the present study for the traits viz., biological yield plant⁻¹, pod length, days to 50% flowering, number of seeds pod⁻¹, grain yield plant⁻¹, harvest index and days to maturity. However, low PCV and GCV value was (<10%) for test weight. Moreover, the present findings exhibited that the estimate of PCV were magnitudinally higher than their corresponding GCV for all the traits. It's suggested that phenotypic expression of the genotypes was least influenced by environmental factors and desirable improvement can be achieved through simple selection procedures. These results were in consonance with the findings of Sharma *et al.* (2006) ^[41], Konda *et al.* (2009) ^[18], Senapati and Mishra (2010) ^[40], Kodanda Rami reddy *et al.* (2011) ^[17], Meshram *et al.* (2013) ^[24], Deepshikha *et al.* (2014) ^[13], Patel *et al.* (2014) ^[30], Ramya *et al.* (2014) ^[36], Kumar, *et al.* (2015) ^[19, 20], Patel *et al.* (2015) ^[29], Gowsalya *et al.* (2016) ^[15] and Patidar *et al.* (2018) ^[31].

In general genetic parameters estimates were observed to be that plant height, number of pods plant⁻¹ and number of primary branches plant⁻¹ exhibited high phenotypic and genotypic coefficient of variation suggesting that the existence of sufficient genetic variability for these traits in the population. Thus, it provided the basis for selection of desirable genotypes from the diverse population for enhancement of black gram production. The present study indicated that the highest heritability was recorded for the trait of plant height, number of pods plant⁻¹ and number of primary branches plant⁻¹ and thereby suggested that parental selection on the performance of these characters may be utilized in the hybridization programme for achieving desirable transgressive segregants. However, also found that the genetic gain will be high when there is additive gene action and genetic advanced would be low. In the present investigation, high heritability coupled with high genetic advance (GAM) was recorded for the traits viz., plant height only indicated that the heritability is involved in the additive gene control of these traits and simple selection for such traits could be practiced for improved them. Similar results were obtained by Sharma *et al.* (2006) ^[41], Konda *et al.* (2009) ^[18], Balachandran *et al.* (2010) ^[7].

The genotypic correlation coefficients between different characters studied are presented in Table 3. From the

correlation studies, data predicted that for most of the character pairs, genotypic and phenotypic associations were in the same direction and the genotypic estimates were higher than the phenotypic ones. Hence, these traits would be an inherited association between the characters studied as also observed by Ali *et al.* (2008)^[1], Begum *et al.* (2012)^[8], Bharti *et al.* (2013)^[9], Reni *et al.* (2013)^[37], Sarkar (2014)^[39], Kumar *et al.* (2015)^[19, 20], Gowsalya *et al.* (2016)^[15] and Arya *et al.* (2017)^[5].

From the inter correlation studies, grain yield plant⁻¹, showed positive and significant association with biological yield plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹, test weight, plant height, number of primary branches plant⁻¹ and pod length both at phenotypic and genotypic level. Similar findings were reported by Sharma *et al.* (2006)^[41], Ali *et al.* (2008)^[1], Shivade *et al.* (2011)^[42, 43], Punia *et al.* (2014)^[33], Kumar *et al.* (2015)^[19, 20], Mehra *et al.* (2016)^[23], Gowsalya *et al.* (2016)^[15] and Mohammad *et al.* (2016)^[25].

The results suggested that the characters biological yield plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹, test weight, plant height, and number of primary branches plant⁻¹ and pod length were positively and significantly correlated

with grain yield plant⁻¹ which might be due to linkage of genes determining these traits. These results indicated that simultaneous improvement in seed yield through these traits could be achieved within a short period by simple selection procedures.

Table 4 and 5 reported that biological yield per plant and day to maturity established high direct effect on grain yield plant⁻¹ along with highly significant correlation in the desirable direction towards grain yield per plant. Hence, obtained true and perfect relationship between grain yields. However, these characters indicated direct selection based in selecting the high yielding genotypes of black gram. These results were in agreement with the earlier findings of Babu *et al.* (2010)^[6], Punia *et al.* (2014)^[33], Sohel *et al.* (2016)^[45], Mohammad *et al.* (2016)^[25], Arya *et al.* (2017)^[5]. The contribution of residual effects that influenced seed yield was low at both genotypic and phenotypic levels, reflected that the traits in study were sufficient enough to account the variability in the dependent character. Similar results were also supported earlier by Rameshwari Netam (2010)^[35], Shivade *et al.* (2011)^[42, 43], Pushpa *et al.* (2013)^[34], Punia *et al.* (2014)^[33], Mohammad *et al.* (2016)^[25] and Arya *et al.* (2017)^[5].

Table 1: Analysis of variance (ANOVA) for eleven characters of forty genotypes in Blackgram (*Vigna mungo* (L.) Hepper)

Source of variations	d. f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Pod length (cm)	Number of Seeds per pod	Biological yield per plant	Harvest index (%)	Test weight (100 seed)	Grain yield per plant
Replication	2	1.34	1.76	9.52	0.09	6.78	0.29	0.13	0.03	0.089	0.11	0.07
Treatments	39	275.50**	193.01**	524.02**	1.19**	259.14**	1.11**	1.05**	98.89**	13.99**	0.63**	1.57**
Error	78	1.20	1.48	5.11	0.01	1.47	0.07	0.03	1.53	1.06	0.04	0.07

** Significant at 1% level

Table 2: Estimates of general mean, range, GCV, PCV, heritability h^2 % (BS), genetic advance and genetic advance as percentage of mean for eleven characters in Blackgram (*Vigna mungo* (L.) Hepper).

Parameters/Characters	General Mean	Range		GCV (%)	PCV (%)	Heritability h^2 % (BS)	Genetic Advance (GA)	GA as % of mean
		Lowest	highest					
Days to 50% flowering	62.12	40.00	81.00	15.39	15.49	98.71	19.57	31.50
Days to maturity	79.18	66.00	97.00	10.09	10.21	97.73	16.27	20.55
Plant height (cm)	30.55	17.62	61.27	43.05	43.68	97.13	26.70	87.41
Number of primary branches per plant	3.04	2.00	4.67	20.64	20.93	97.20	1.28	41.91
Number of pods per plant	35.99	24.00	67.00	25.75	25.97	98.32	18.93	52.60
Pod length (cm)	3.92	2.97	7.03	15.03	16.47	83.28	1.11	28.25
Number of Seeds per pod	4.25	3.27	6.11	13.74	14.24	93.10	1.16	27.32
Biological yield per plant	30.04	20.60	45.33	18.97	19.41	95.51	11.47	38.18
Harvest index (%)	18.64	15.46	23.83	11.14	12.43	80.30	3.83	20.56
Test weight (100 seed)	4.89	3.87	6.39	9.01	9.97	81.77	0.82	16.79
Grain yield per plant	5.51	4.05	7.45	12.83	13.68	87.95	1.37	24.78

Table 3: Estimates of genotypic (G) correlation coefficients among eleven characters in Blackgram (*Vigna mungo* (L.) Hepper)

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Pod length (cm)	Number of Seeds per pod	Biological yield per plant	Harvest index (%)	Test weight (100 seed)	Grain yield per plant
Days to 50% flowering	G	1.000	0.953**	-0.486**	-0.282**	-0.386**	-0.118	-0.535**	-0.452**	0.312**	-0.014	-0.350**
	P		0.946**	-0.476**	-0.273**	-0.380**	-0.100	-0.510**	-0.444**	0.280**	-0.015	-0.332**
Days to maturity	G			-0.366**	-0.217*	-0.273**	-0.172	-0.388**	-0.293**	0.241**	-0.001	-0.197*
	P			-0.360**	-0.215*	-0.262**	-0.154	-0.356**	-0.288**	0.208*	-0.009	-0.195*
Plant height (cm)	G				0.430**	0.400**	0.367**	0.471**	0.446**	-0.256**	-0.250**	0.414**
	P				0.417**	0.389**	0.332**	0.441**	0.432**	-0.234*	-0.211*	0.379**
Number of primary branches per plant	G					0.344**	0.237**	0.054	0.375**	-0.313**	0.118	0.284**
	P					0.335**	0.221*	0.031	0.363**	-0.286**	0.105	0.260**
Number of pods per plant	G						0.261**	0.373**	0.667**	-0.304**	0.358**	0.665**
	P						0.235**	0.361**	0.645**	-0.270**	0.322**	0.617**
Pod length (cm)	G							-0.113	0.169	0.001	-0.037	0.256**
	P							-0.104	0.150	0.011	-0.018	0.222*
Number of Seeds per pod	G								0.520**	-0.174	0.121	0.572**
	P								0.477**	-0.136	0.079	0.511**
Biological yield	G									-0.710**	0.330**	0.815**

per plant	P											-0.668**	0.311**	0.770**
Harvest index (%)	G												0.020	-0.180*
	P												0.057	-0.052
Test weight (100 seed)	G													0.505**
	P													0.487**
Grain yield per plant	G													1.000
	P													1.000

Table 4: Estimates of path coefficient showing direct and indirect effects of component characters on grain yield at genotypic level in Blackgram (*Vigna mungo* (L.))

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Pod length (cm)	Number of Seeds per pod	Biological yield per plant	Harvest index (%)	Test weight (100 seed)	Grain yield per plant
Days to 50% flowering	0.251	-0.185	-0.023	-0.006	0.016	-0.001	-0.016	-0.631	0.247	-0.001	-0.350**
Days to maturity	0.239	-0.194	-0.018	-0.004	0.011	-0.002	-0.011	-0.409	0.190	0.000	-0.197*
Plant height (cm)	-0.122	0.071	0.048	0.009	-0.017	0.003	0.014	0.622	-0.202	-0.013	0.414**
Number of primary branches per plant	-0.071	0.042	0.021	0.020	-0.014	0.002	0.002	0.523	-0.247	0.006	0.284**
Number of pods per plant	-0.097	0.053	0.019	0.007	-0.042	0.002	0.011	0.932	-0.240	0.019	0.665**
Pod length (cm)	-0.030	0.033	0.018	0.005	-0.011	0.009	-0.003	0.237	0.000	-0.002	0.256**
Number of Seeds per pod	-0.134	0.075	0.023	0.001	-0.016	-0.001	0.030	0.726	-0.137	0.006	0.572**
Biological yield per plant	-0.113	0.057	0.022	0.007	-0.028	0.002	0.015	1.396	-0.560	0.017	0.815**
Harvest index (%)	0.078	-0.047	-0.012	-0.006	0.013	0.000	-0.005	-0.991	0.789	0.001	-0.180*
Test weight (100 seed)	-0.004	0.000	-0.012	0.002	-0.015	0.000	0.004	0.461	0.016	0.053	0.505**

Residual Effect = 0.0107

Bold values indicate direct effects

Table 5: Estimates of path coefficient showing direct and indirect effects of component characters on grain yield at phenotypic level in Blackgram (*Vigna mungo* (L.))

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Pod length (cm)	Number of Seeds per pod	Biological yield per plant	Harvest index (%)	Test weight (100 seed)	Grain yield per plant
Days to 50% flowering	0.185	-0.132	-0.013	-0.007	0.012	-0.001	-0.012	-0.595	0.231	-0.001	-0.332**
Days to maturity	0.175	-0.140	-0.010	-0.005	0.008	-0.001	-0.009	-0.386	0.172	0.000	-0.195*
Plant height (cm)	-0.088	0.050	0.028	0.010	-0.012	0.002	0.011	0.579	-0.193	-0.008	0.379**
Number of primary branches per plant	-0.051	0.030	0.012	0.024	-0.010	0.001	0.001	0.486	-0.237	0.004	0.260**
Number of pods per plant	-0.070	0.037	0.011	0.008	-0.030	0.001	0.009	0.864	-0.224	0.012	0.617**
Pod length (cm)	-0.019	0.021	0.009	0.005	-0.007	0.005	-0.003	0.200	0.009	-0.001	0.222*
Number of Seeds per pod	-0.095	0.050	0.012	0.001	-0.011	-0.001	0.024	0.639	-0.112	0.003	0.511**
Biological yield per plant	-0.082	0.040	0.012	0.009	-0.020	0.001	0.012	1.341	-0.553	0.011	0.770**
Harvest index (%)	0.052	-0.029	-0.007	-0.007	0.008	0.000	-0.003	-0.896	0.827	0.002	-0.052
Test weight (100 seed)	-0.003	0.001	-0.006	0.003	-0.010	0.000	0.002	0.417	0.047	0.036	0.487**

Residual Effect = 0.0157,

Bold values indicate direct effects,

*, ** significant at 5% and 1% level

Conclusion

Analysis of variance revealed that sufficient amount of genetic variability existed among the present set of breeding material and study for genetic parameters, with these genotypes, was worth for valuable findings. All the traits viz., days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of pods plant⁻¹, pod length, number of seeds pod⁻¹, biological yield plant⁻¹, harvest index, 100-seed weight and grain yield plant⁻¹ to respond direct selection may be effective. The heritability was high for all the traits under study. This indicated the influence of additive gene action for expression of all characters studied and hence direct selection based on these characters may be useful for effective improvement in black gram crop. High heritability coupled with high genetic advance for plant height only indicating that the heritability is due to additive gene action and simple selection for such traits could be practiced for improving this character. Character association revealed that seed yield plant⁻¹ showed highly significant positive genotypic and phenotypic correlation with biological yield plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹, test weight, plant height, number of primary branches plant⁻¹ and pod length. The path-analysis studies indicated that the seed yield plant⁻¹ received the highest direct effect from biological

yield plant⁻¹, harvest index and days to 50% flowering for both phenotypic and genotypic level. These characters suggesting direct selection, based on these characters would help in selecting the high yielding genotypes in black gram.

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