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## Studies on genetic variability in Black gram (*Vigna mungo* L. Hepper) germplasm

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#### Abstract

The present investigation was conducted during *kharif-2014* in the Field Experimentation Centre of the Department of Genetics and Plant Breeding to examine 36 black gram genotypes along with one check (SHEKHAR-2) to study Genetic variability, correlation and path analysis for yield in black gram. The experiment was laid out in an in Randomize Block Design with three replications. Analysis of variance showed highly significant differences among 36 genotypes of black gram for 13 characters studied. Moderate genotypic coefficient of variation and phenotypic coefficient of variation was recorded for number of clusters per plant, primary branches per plant and seed yield per plant. All characters showed High broad-sense heritability and high genetic advance as percent of mean was recorded for seed yield per plant and plant height.

**Keywords:** Black gram, genetic variability, correlation and path coefficient analysis

#### 1. Introduction

Among pulses, black gram (*Vigna mungo* L.) is an important short duration 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. The major constraints in achieving higher yield of this crop are lack of genetic variability, poor harvest index, suitable varieties and genotypes with adaptation to local condition. Yield is considered as an end product of a set of plant processes which are related to each other. It is very complex trait which controlled by poly genes and interlinked with other yield components, hence it is very difficult often to improve yield directly. It can be achieved by improving closely related traits. The systematic collection of black gram has displayed inadequate variability for biotic and abiotic genes. It is possible that genes for high productivity could have been lost due to overriding role of natural selection (Roopalakshmi *et al.*, 2003) [10] and the genetic base of the present day collection remains poor (Delannay *et al.*, 1983) due to lac of variability owing to its autogamous nature. The creation of variability is difficult through hybridization due to its high self-pollination and flower droop (Deepalakshmi and Anandakumar, 2004) [4]. Besides the major constrains in achieving higher yield of blackgram is absence of suitable ideotypes for different cropping system, poor harvest index and susceptibility to disease (Souframanien and Gopalakrishnan, 2004) [13]. In order to improve yield and other polygenetic characters, mutation breeding can be effectively utilized (Deepalakshmi and Anandakumat, 2004) [4]. Therefore genetic variability is the basic requirement for making progress in crop breeding (Appalaswamy and Reddy, 2004) [1]. In India black gram is grown both in winter and summer as monocrop and inter crop, respectively. That is why no single plant type is appropriate for all production system. So the variability among the existing germplasm or the accessions is the primary need to develop appropriate plant type for specific production system. Black gram originated in India where it has been in cultivation from ancient times and is one of the most highly prized pulses of India. A successful breeding programme in black gram would need information on the nature and degree of genetic divergence in the available stock for choosing the right parents for further improvement (Falconer, 1981) [5]. Grain yield is complex character, which depends on its main components viz; number of pod per plant, pod length, number of seed per pod and 100 seed weight. These components are further dependent for their expression on several morphological and developmental traits, which are interrelated with each other and therefore, the parent selected for the breeding programmes aimed at increased seed yield should possess wide range of genetic variation for the above said morphological and developmental characters. Besides, it could be of 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. In other words, for the improvement in any crop species, the knowledge of genetic variability for characters of economic importance and their heritability and genetic advance is of utmost importance in planning future breeding programme (Singh *et al.*, 2007) [12].

### Materials and Methods

The experimental material for the present investigation consisted of 36 genotypes obtained from the Agriculture Research station, Kota, Rajasthan. The present experiment was conducted in randomized block design at Field Experimentation Centre, Department of Genetics and Plant Breeding, Allahabad during *khari*, 2014. Recommended cultural practices were followed to raise healthy crop. Five competitive plants from each genotype were randomly selected for recording observations on thirteen characters, *viz.*, days to 50 per cent flowering, Days to 50 per cent pod setting, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, Pod

length (cm), days to maturity, number of seeds per pod, Biological yield per plant (g), Harvest index (%), Seed index (g) and Seed yield per plant (g). Analysis of variance was carried out as per standard procedure (Fisher, 1938) [6]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) (Burton, 1952) [2], heritability (Burton and Devane, 1953) [3], genetic advance (Johnson *et al.*, 1955) [7], were estimated.

### Results and Discussion

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 36 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

**Table 1:** Analysis of variance for 13 different quantitative characters in 36 genotypes of Black gram

S. No	Characters	Mean Sum of Squares		
		Replication (d. f.=02)	Treatments (d. f=35)	Error (d. f=70)
1	Days to 50% Flowering	18.78	20.13**	11.57
2	Days to 50% Pod Setting	23.68	22.88**	12.31
3	Plant Height	30.32	220.76**	28.45
4	Primary Branches/ Plant	0.00	0.58**	0.15
5	Clusters/ Plant	1.25	24.39**	5.76
6	Pods/ Plant	0.67	8.21**	1.20
7	Pod Length	0.04	0.06**	0.02
8	Seeds/ Pods	0.01	0.23**	0.11
9	Days to maturity	3.23	4.39**	1.82
10	Seed Index	0.00	0.21**	0.01
11	Harvest Index	0.03	21.73**	0.96
12	Biological Yield/ Plant	0.11	23.72**	0.85
13	Seed Yield/ Plant	0.02	4.58**	0.01

\*\* Significant at 1% level of significance

### Per se mean performance of genotypes

The *per se* mean performance of various genotypes exhibited wide range of variation for most of the traits studied (Table 2). Despite that some traits showed more variation like as Days to 50% Flowering (34.67-45.33cm), Days to 50% Pod Setting (45.33-56.00), plant height (41.75-85.81cm), Primary Branches/ Plant (2.97-5.06), clusters/plant (8.8-22.06), pods/plant (59.2-67.00), pod length (4.59-5.50), seed per pod (5.2-6.93), days to maturity (66.67-71.33 days), seed index (3.84-4.93), harvest index (32.14-44.84%), biological yield/plant (27.9-39.83), seed yield/plant (11.42-15.90g), etc. indicates sufficient variation among the genotypes for the traits studied. The mean value for grain yield was found 14.18g. This reflected that there is greater opportunity to improve the yield and its related traits in black gram.

### Genotypic and phenotypic coefficient of variation

Phenotypic variance was higher than the genotypic variances for all the characters thus indicating the influence of the environmental factors on these traits. The genotypic and phenotypic variations were obtained for different characters, and they are presented in Table 2. The maximum (64.11 and 92.55) genotypic variation ( $V_g$ ) and phenotypic variation ( $V_p$ ) were obtained from the plant height followed by biological yield per plant (7.62 and 8.47), respectively.

Similar findings were reported by Konda *et al* 2009 [8]. Lowest values were recorded in pod length (0.01 and 0.04), followed by seed per pod (0.04 and 0.15), seed index (0.07 and 0.08) respectively. The lowest values showed there was considerably low influence of environment for the expression of the traits. A comparison by the estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) suggested that estimates PCV were higher than the estimates of GCV for all the characters (Table 2.). This may be due to the involvement of environment and genotype environment interaction effects in characters expression. The estimates of GCV and PCV maximum for number of cluster per plant (14.25,19.79) followed by plant height (11.51,13.83), primary branches per plant (9.88,14.26), seed yield per plant (8.70,8.74), biological yield per plant (7.81,8.23) and lowest Days to maturity (1.34,2.38), followed by pod per plant (2.44,3.00) respectively. Konda *et al* (2009) [8] also reported high value of PCV for pods per plant, number of branches per plant and plant height. Moreover, Uma devi and Ganesan (2006) [15], Samad *et al* (2013) [11] also reported high GCV values for the number of clusters per plant, number of pods per plant, pod length and number of seeds per pod in black gram and suggested for a greater scope of selection for these traits.

**Table 2:** Genetic parameters for 13 biometrical characters of 36 black gram genotypes

S. No.	Characters	Range	Mean	Vg	Vp	GCV	PCV	h <sup>2</sup> (bs) (%)	GA	GA as % of mean
1	Days to 50 % Flowering	34.67-45.33	41.67	2.86	14.42	4.06	9.12	20	1.55	3.72
2	Days to 50 % Pod Setting	45.33-56.00	50.29	3.52	15.84	3.73	7.91	22	1.82	3.63
3	Plant Height	41.75-85.81	69.55	64.11	92.55	11.51	13.83	69	13.73	19.74
4	Primary Branches/ Plant	2.97-5.06	3.81	0.14	0.30	9.88	14.26	48	0.54	14.11
5	Clusters/ Plant	8.8-22.06	17.48	6.21	11.97	14.25	19.79	52	3.70	21.14
6	Pods/ Plant	59.2-67.00	62.8	2.34	3.54	2.44	3.00	66	2.56	4.08
7	Pod Length	4.56-5.50	4.82	0.01	0.04	2.47	3.91	40	0.16	3.23
8	Seeds per Pod	5.2-6.93	5.91	0.04	0.15	3.37	6.62	26	0.21	3.53
9	Days to Maturity	66.67-71.33	68.8	0.86	2.68	1.34	2.38	32	1.08	1.56
10	Seed Index	3.84-4.93	4.45	0.07	0.07	5.91	6.16	92	0.52	11.68
11	Harvest Index	32.14-44.84	40.19	6.92	7.88	6.55	6.98	88	5.08	12.64
12	Biological Yield/ Plant	27.9-39.83	35.35	7.62	8.47	7.81	8.23	90	5.40	15.26
13	Seed Yield/ Plant	11.42-15.9	14.18	1.52	1.54	8.70	8.74	99	2.53	17.85

**Heritability and Genetic Advance:** 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. In the present study high estimates of heritability in percentage and were observed for seed yield per plant (99), followed by seed index (92), biological yield per plant (90), harvest index (88) and plant height (69) (Table2). High heritability estimates for these traits indicating that these traits are more likely to be controlled by additive genetic component. Sowmini and Jayamani (2013) [13], Wani *et al.* (2007) [16] reported high heritability for the traits such as number of pods per plant, number of pods per cluster, plant height and seed yield per plant and suggested the additive genetic control in the inheritance of these characters. High heritability, genetic advance and per cent of mean were observed for traits seed yield per plant, biological yield per plant, harvest index and seed index. Wani *et al.*, (2007) [16] also reported high heritability for plant height. Konda *et al* 2009 [8] also reported high genetic advance for cluster per plant. Jonson *et al.* (1995) and Panse & Sukhatme (1985) [9] suggested high estimates of heritability and genetic advance as per cent of mean should be taken into consideration for selection for base improvement. Heritability along provides no indication of the amount of genetic improvement that would result from selection of the individual genotypes.

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