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## Evaluation of genetic parameters in black gram [*Vigna mungo* (L.) Hepper] for seed yield and its related traits

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### Abstract

The genetic parameters for seed yield and its related traits were assessed by the evaluation of thirty five genotypes of Black gram along with two checks (*i.e.*, Pratap Urd-1 and Pant Urd-31). The experiment was carried out during *khariif* 2018 in Randomized Block Design. The results of ANOVA revealed that all the genotypes differ significantly. The high GCV and PCV estimates were observed for number of branches per plant, seed yield per plant, biological yield per plant and harvest index. High heritability coupled with high genetic advance as percent of mean was recorded for Plant height, number of branches per plant, number of clusters per plant, seed yield per plant, harvest index and 100-seed weight hence, these traits should be considered during selection of parents as these are controlled by the additive gene action.

**Keywords:** Black gram, GCV, genetic advance, heritability, PCV

### 1. Introduction

Black gram is an excellent source of protein and also rich in carbohydrate, minerals and vitamins. It is mostly grown on poor soils and its play a key role in sustainable agriculture in Indian conditions. Regardless of its importance, its cultivation is ignored as little consideration is given towards its improvement. The productivity of Black gram is very low due to various constraints *i.e.*, agronomic, genetic and physiological constraints, therefore efforts should make to improve the productivity of this crop by following suitable breeding procedures. This requires huge information about the variability parameters because presence of variability in a population is prerequisite for success of any breeding program. Prior to start any breeding program it is essential to determine nature and degree of genetic variability in the population to enhance the seed yield and its attributing traits (Chauhan *et al.* 2018) [6]. Therefore, the present investigation was planned to estimate the genetic variability with help of various genetic parameters *viz.*, genotypic and phenotypic coefficients of variation, heritability and genetic advance as a percent of mean.

### 2. Materials and Methods

#### 2.1. Experimental site

The experiment was conducted at Instructional Research Farm, Department of Genetics and Plant breeding, Rajasthan College of Agriculture, MPUAT, Udaipur during *khariif* 2018. The site is situated at an elevation of 579.5 meters above mean sea level, latitude of 24° 35' North and longitude of 74°42' East.

#### 2.2. Experimental material and design

In this experiment the material used consisted of thirty three diverse genotypes of Black gram and two varieties *viz.*, Pratap Urd-1 and Pant Urd-31 were used as check. These genotypes were collected from the Pulse Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyaapeeth, Akola (Maharashtra) and Agriculture Research Station, Kota (Rajasthan). The experimental materials were analyzed in Randomized Block Design with three replications keeping inter and intra row spacing of 30 cm and 10 cm respectively. The agronomical practices were adopted according to the package of practices of zone IV A throughout the period of crop growth.

#### 2.3. Recording of observations

Except days to 50 percent flowering and days to 75 percent maturity, for all the traits *viz.*, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, pod length (cm), number of seeds per pod, seed yield per

plant (gm), biological yield per plant (gm), harvest index (%), 100-seed weight (gm) and seed protein content (%), observations were recorded on five randomly selected plants from each plot in each replication. Observations for days to 50 percent flowering and days to 75 percent maturity were recorded on whole plot basis.

#### 2.4. Statistical analysis

Statistical analysis was done by using mean values. Analysis of variance, genotypic coefficient of variation (GCV) & phenotypic coefficient of variation (PCV), heritability and genetic advance were estimated by the procedures suggested by Panse and Sukhatme (1985) [15], Burton (1952) [4], Burton and Devane (1953) [3] and Johnson *et al.* (1955) [9] respectively. Seed protein content was estimated using

Kjeldahl's method (Kjeldahl, 1883) [11].

### 3. Results and Discussion

Genetic analysis of quantitative traits is a prerequisite for a plant breeding program whereby a method of systematic design and proper planning for a breeding strategy can be prepared. Success of any crop improvement program depends on the genetic variability which is present in the experimental material. Therefore, information of genetic variability is essential for effective selection.

The analysis of variance (Table 1) revealed that the genotypes differed significantly at one percent level of significance for all the traits studied indicates that the ample amount of genetic variability was present among various genotypes that fulfills the requirements of present investigation.

**Table 1:** Analysis of variance for seed yield per plant and its contributing traits in black gram

Characters	Mean sum of square		Error	CV (%)
	Replication	Genotype		
	[2]	[34]		
Days to 50% flowering	1.32	13.55**	2.19	3.55
Days to 75% maturity	1.80	18.70**	2.45	2.13
Plant height (cm)	3.08	54.09**	4.55	8.00
Number of branches/plant	0.16	9.24**	0.34	6.64
Number of clusters/plant	0.41	5.19**	0.41	7.97
Number of pods/plant	2.29	19.00**	4.22	10.28
Number of pods/cluster	0.04	0.36**	0.04	7.62
Pod length (cm)	0.08	0.83**	0.08	6.27
Number of seeds/pod	0.05	1.52**	0.26	9.08
Seed yield/plant (gm)	0.30	3.44**	0.29	10.19
Biological yield per plant (gm)	0.01	20.95**	4.48	12.48
Harvest index (%)	10.46	110.95**	14.84	12.12
100-seed weight (gm)	0.07	1.50**	0.09	6.48
Seed protein content (%)	1.12	4.35**	0.76	3.77

Degrees of freedom; \*, \*\* Significant at 5% and 1% respectively.

Results of variability parameters (Table 2) revealed that the extent of PCV was higher than GCV for all the traits studied indicated that the expression of the trait is considerably influenced by the environment. Panwar *et al.* (2019) [16], Priyanka *et al.* (2016) [17], Ramya *et al.* (2014) [18], Vinoth and Jayamani (2014) [22] and Panigrahi *et al.* (2014) [14] were also

observed similar results. The influence of environment on any character is measured by the magnitude of the difference among GCV and PCV; large difference reflect more effect of environment while small difference reveal low environmental influence and high genetic effect (Tuhina-Khatun *et al.* 2015) [21].

**Table 2:** Variability parameters for seed yield per plant and its contributing traits in black gram

Characters	Mean	GCV	PCV	ECV	h <sup>2</sup>	GA	GG
Days to 50% flowering	41.65	4.67	5.87	3.55	63.40	3.19	7.66
Days to 75% maturity	73.43	3.17	3.82	2.13	68.88	3.98	5.42
Plant height (cm)	26.66	15.25	17.22	8.00	78.41	7.41	27.81
Number of branches/plant	8.84	19.48	20.58	6.64	89.59	3.36	37.97
Number of clusters/plant	8.01	15.76	17.66	7.97	79.62	2.32	28.97
Number of pods/plant	19.99	11.10	15.13	10.28	53.86	3.36	16.78
Number of pods/cluster	2.53	12.91	14.99	7.62	74.14	0.58	22.90
Pod length (cm)	4.47	11.20	12.83	6.27	76.16	0.90	20.13
Number of seeds/pod	5.58	11.63	14.76	9.08	62.12	1.05	18.88
Seed yield/plant (gm)	5.31	19.30	21.82	10.19	78.20	1.87	35.16
Biological yield per plant (gm)	16.96	13.81	18.61	12.48	55.07	3.58	21.12
Harvest index (%)	31.79	17.80	21.54	12.12	68.34	9.64	30.32
100-seed weight (gm)	4.75	14.41	15.80	6.48	83.17	1.29	27.07
Seed protein content (%)	23.09	4.74	6.05	3.77	61.30	1.76	7.64

The degree of various variability parameters was categorized on the basis of mean plus/minus half standard deviation. Values more than (mean + 1/2SD) categorized as high, equal to (mean + 1/2SD)/ (mean - 1/2SD) as medium and it is less than (mean - 1/2SD) as low (Diwakar *et al.* 2016) [7].

High magnitude of GCV and PCV were recorded for number of branches per plant, seed yield per plant, biological yield per plant and harvest index indicating ample variability for these traits thus, selection based on these traits would make possible successful isolation of desirable genotypes. Results also found

in accordance with the findings of Panwar *et al.* (2019) [16], Chaithanya *et al.* (2019) [5], Reddy *et al.* (2018) [19], Aftab *et al.* (2018) [1], Gowsalya *et al.* (2016) [8] and Babu *et al.* (2016) [2]. Whereas, moderate GCV and PCV estimates were observed for plant height, number of clusters per plant, number of pods per plant, number of pods per cluster, pod length, number of seeds per pod and 100-seed weight recommended that enhancement in these traits might be gained up to considerable level. Panigrahi *et al.* (2014) [14] also reported similar results for plant height, number of pods per plant, pod length and 100-seed weight.

Heritability alone is not much reliable for predicting the effect of selection since it includes the effect of both additive and non-additive gene actions therefore, heritability in combination with genetic advance as percent of mean would be more useful because genetic advance depends on the magnitude of genetic variability, environmental influence and intensity of selection (Lyngdoh *et al.* 2018) [13]. High heritability combined with high genetic advance as percent of mean was observed for plant height, number of branches per plant, number of clusters per plant, seed yield per plant, harvest index and 100-seed weight. The findings are in agreement with the results of Chaithanya *et al.* (2019) [5], Reddy *et al.* (2018) [19], Aftab *et al.* (2018) [1], Kuralarasan *et al.* (2017) [12], Gowsalya *et al.* (2016) [8], Singh *et al.* (2014) [20] and Kant and Srivastava (2011) [10]. This indicates preponderance of additive gene action which responds to simple selection therefore, selection based on these traits will be more effective for crop improvement.

#### 4. Conclusion

It can be concluded from the present investigation, traits like plant height, number of branches per plant, number of clusters per plant, seed yield per plant, harvest index and 100-seed weight may respond more to the selection since these traits showed high heritability along with high genetic advance as percent of mean. Thus, these traits could be considered during selection for yield improvement of this crop at desired level.

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