

Evaluation of Genetic Variability Parameters in 185 F₃ Progenies of Black Gram [*Vigna mungo* (L.) Hepper] for Seed Yield and Related Components

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ABSTRACT: Black gram is an important autogamous pulse crop with cleistogamous condition, hence showing minimal variation. So, the experiment was done to assess the black gram F₃ progenies of cross NUK-15-02 × GU-1 along with four checks GU-1, GU-2, GU-3 and T-9 for genetic variability parameters of eleven quantitative traits related to seed yield in Augmented Block Design. Analysis of variance showed that F₃ progenies exhibit substantial variability for all the attributes considered in this study. The highest seed yield per plant was depicted by progenies A-74 (31.38 g), A-193 (30.60 g) and A-11 (29.08 g). High GCV and PCV values were observed for seed yield per plant, pods per plant, clusters per plant, branches per plant and harvest index, demonstrating the potential for improvement through selection. Plant height, branches per plant, clusters per plant, pods per plant, harvest index and seed yield per plant showed strong heritability in conjunction with high genetic advance. So, selection for such traits is recommended to improve black gram due to additive gene action.

Keywords: Variability, Heritability, Genetic advance, Augmented Block Design, Black gram, Urdbean.

INTRODUCTION

Black gram has an approximate genome size of 0.59 pg/1C(574 Mbp) and is autogamous diploid ($2n = 2x = 22$) (Arumuganathan and Earle 1991). From long ago, green gram and urdbean have been chief pulses in Asia. (Paroda and Thomas 1987). Urdbean, mash, or urid are among of its more common names. It is a crucial grain legume from sub-family *Papilionaceae* of *Fabaceae* family. It is an annual herb with dense hair and of erect, sub erect or trailing habit with narrow and cylindrical pods. Branching roots with rounded, smooth nodules are produced from the tap root of urdbean. *V. mungo* var. *silvestris* is the wild ancestral type, from which, urdbean originated in India. (Lukoki *et al.*, 1980).

Black gram is rich in protein, vitamin, mineral and devoid of cholesterol. Black gram seeds typically contain 3.2 percent mineral, 1.4 percent fat, 24 percent protein, and 57.3 percent carbohydrates (Aykroyd and

Doughty 1964). It is rich in amino acid like lysine and tryptophan, which are present in traces in cereals. It serves as a repository for minerals like manganese, iron, copper, calcium, and magnesium. Additionally, it has vitamins and nutritional fibers. Black gram contains a lot of potassium, which lowers hypertension or high blood pressure by balancing sodium and potassium levels and also is an aphrodisiac. A significant portion of the protein needed in a vegetarian diet is provided by black gram, which is a necessary addition to a cereal-based diet. Due to the complimentary nature of the essential amino acids like phenylalanine, lysine, valine, isoleucine, leucine and arginine, the biological value of combining wheat or rice with a pulse like black gram is enhanced (Goyal *et al.*, 2010). Both split and whole, dehusked and husked, varieties are eaten as food in the form of "Dal". It is a key component of "Papad." Additionally, it is a component of the preparations for "Dosa," "Idli," "Halwa," and "Imarti Sweets". Additionally, it enhances soil fertility by symbiotically

fixing air nitrogen in root nodules. The entire urdbean plant is utilized as nutritious food for animals and it is sown in a variety of cropping patterns, including catch, mixed, situational and solo crops (Amruta *et al.*, 2016). Black gram is produced and consumed primarily in India (Raju, 2019). It is the third-most significant pulse in India. It was grown over 5.44 Mha (*Rabi + Kharif*) and produced 3.56 Mt with 655 kg/ha productivity (Singh *et al.*, 2021). Although India is the world's biggest consumer and producer of urdbean, crop production there has exceptionally poor yields, which makes it more dependent on imports from other producing nations to meet consumer demand (Rawal and Navarro 2019; Somta *et al.*, 2019 and 2020). Genotypic variation, which is assessed as genotypic variance, is crucial for any crop development effort because it is the variation that is passed down to the following generation. A good indicator of how attributes are passed down from parents to their progenies is heritability, which measures the proportion of genetic variation to the total amount of phenotypic variation in the attributes (Falconer, 1960). It supports the selection of desirable genotypes from a variety of populations by plant breeders. The improvement of progeny of selected plants over parental populations is known as genetic advance and genetic advance estimates along with heritability are generally exceptional in speculating the gain under selection instead of using heritability solitary.

MATERIALS AND METHODS

In late *kharif* 2021–2022, the trial was organized at Farm of College, N. M. College of Agriculture, Navsari Agricultural University, Navsari (Gujarat). The trial material comprised of 185 F₃ progenies derived from the cross NUK-15-02 × GU-1 and four checks (GU-1, GU-2, GU-3 and T-9) of black gram. All one hundred and eighty five F₃ progenies, along with checks GU-1, GU-2, GU-3 and T-9 were evaluated in Augmented Block Design, where each and every check was replicated in five blocks. Each row comprised of 13 plants of single progeny with 45 × 20 cm² spacing. In each block, F₃ progenies were distributed at random. The crop was successfully raised by implementing the entire recommended agronomic package of procedures and plant protection measures. Eleven quantitative parameters, including days to fifty flowering, plant height (cm), branches per plant, clusters per plant, pods per plant, pod length (cm), seeds per pod, 100 seed weight (g), days to maturity, harvest index (%) and seed yield per plant (g) were examined. The observations were made on five randomly chosen plants from each F₃ progenies, eliminating border plants, with the exception of days to maturity and days to fifty flowering. Selected plants were marked before the first flower emergence. On a population basis, data were collected for days to maturity and days to fifty flowering. The five plants that were chosen at random

served as the source of the data for the other attributes and means of them were employed in the statistical analysis.

Analysis of variance of the attributes was carried out as per standard statistical procedure for Augmented Randomized Complete Block Design (Augmented Design II) as given by Federer (1956). The approach proposed by Allard (1999) was used to calculate heritability in a broad sense (h_{bs}^2) and genetic advance.

RESULTS AND DISCUSSION

Table 1 displays the analysis of variance for all attributes. For all the attributes in F₃ progenies, the analysis of variance depicted significant mean sum of square values, designating that there was enough variation in the progenies for every attributes taken into study. Similar kind of result was also found by Konda *et al.* (2009), Gowsalya *et al.* (2016); Bishnoi *et al.* (2017); Kondagari *et al.* (2017); Bandi *et al.* (2018); Samuel *et al.* (2019); Patel and Madhu Bala (2020); Barik *et al.* (2021); Chaturvedi *et al.* (2021); Deekshith *et al.* (2022).

Table 2 and Fig. 1 show the findings from the variability parameters. Mean values displayed a wide range for days to fifty percent flowering (46-56), plant height (30.88-63.04 cm), branches per plant (1.20-9.60), clusters per plant (3.20-29.20), pods per plant (10.20-112.80), pod length (3.28-5.10 cm), seeds per pod (3.80-8.00), 100 seed weight (3.10-6.50 g), days to maturity (87-99), harvest index (12.46-63.96 %) and seed yield per plant (1.18-31.38 g). According to mean values, the progenies A-74 (31.38 g), A-193 (30.60 g) and A-11 (29.08 g) were classified as excellent F₃ progenies because they produced significantly more seeds per plant than the control varieties GU-1, GU-2, GU-3, and T-9.

Progenies indicated higher GCV and PCV values for branches per plant (36.60% and 36.94%), clusters per plant (42.76% and 43.99%), pods per plant (47.84% and 48.11%), harvest index (22.64% and 26.67%), and seed yield per plant (56.50% and 59.38%, respectively), indicating less environmental influence on these traits and the potential to improve these traits using selection (Table 2). Plant height (15.61% and 19.28%, respectively) and 100 seed weight (12.52% and 13.79%) both had moderate values of GCV and PCV, designating a lesser level of response of these variables for selection. Meanwhile lower values of GCV and PCV were unveiled for days to fifty percent flowering (6.03% and 6.17%, respectively), pod length (7.68% and 8.39%, respectively), and days to maturity (3.82% and 3.93%, respectively), with the exception of seeds per pod (8.61% and 10.40%, respectively), which disclosed a moderate value of PCV, specifying restricted variability for these traits and limiting the scope of selection for these traits. Same kind of outcomes were also achieved for seed yield per plant, harvest index and seeds per pod by Patel and Madhu

Bala (2020); for branches per plant by Barik *et al.* (2021); for clusters per plant by Barik *et al.* (2021); Teja and Lal (2021); for pods per plant by Sathees *et al.* (2019); Barik *et al.* (2021); for plant height by Priya *et al.* (2018); Barik *et al.* (2021); for 100 seed weight by Meshram *et al.* (2012); Barik *et al.* (2021); Deekshith *et al.* (2022);

for days to fifty percent flowering by Kondagari *et al.* (2017); Barik *et al.* (2021); Deekshith *et al.* (2022); for pod length by Gill *et al.* (2017); Deekshith *et al.* (2022) and for day to maturity by Rolaniya *et al.* (2017); Barik *et al.* (2021); Deekshith *et al.* (2022).

Table 1: Result of Analysis of variance for characters under study.

Source	df	DTF	PH	BPP	CPP	PPP	PL	SPP	SW	DTM	HI	SY
Treatment (ignoring blocks)	188	10.12**	84.89*	5.50**	43.95**	929.9**	0.15**	0.40*	0.41**	13.68**	156.10**	78.62**
Treatment: Check	3	11.53**	264.90**	0.21 ^{NS}	149.90**	12.46 ^{NS}	0.38**	0.70*	0.31*	16.85**	622.60**	66.71**
Treatment: Test vs. Check	1	31.53**	8.40 ^{NS}	188**	42.44**	25079.80**	4.55**	0.93*	0.14 ^{NS}	48.02**	22.79 ^{NS}	430.50**
Treatment: Test	184	9.98**	82.38*	4.60**	42.23**	813.60**	0.12**	0.40*	0.42**	13.45**	149.30**	76.90**
Block (eliminating treatments)	4	0.75 ^{NS}	24.97 ^{NS}	0.96**	39.53**	12.35 ^{NS}	0.02 ^{NS}	0.39 ^{NS}	0.04 ^{NS}	0.93 ^{NS}	64.01 ^{NS}	2.32 ^{NS}
Residuals	12	0.45	28.36	0.08	2.34	9.28	0.02	0.12	0.07	0.73	38.34	7.27

** - Significant at a probability of 1.0%, * - Significant at a probability of 5.0%

df = Degree of freedom

DTF = Days to 50% flowering

PH = Plant height (cm)

BPP = Branches per plant

CPP = Clusters per plant

PPP = Pods per plant

PL = Pod length (cm)

SPP = Seeds per pod

SW = 100 seed weight (g)

DTM = Days to maturity

HI = Harvest index

SY = Seed yield per plant (g)

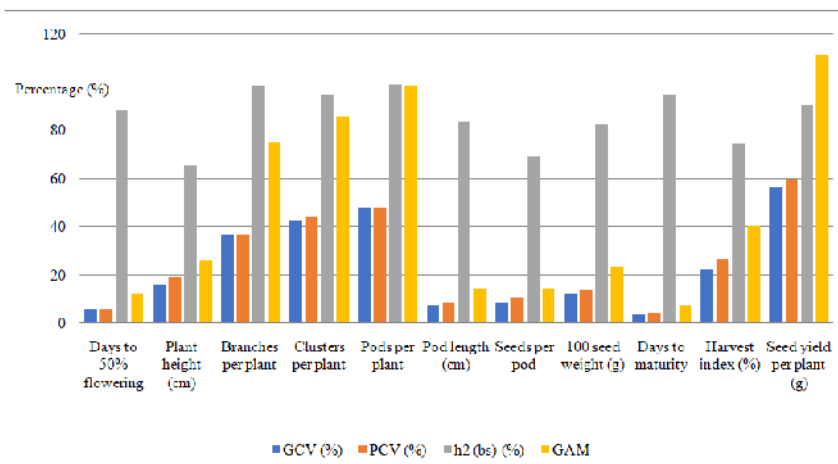
Table 2: Result of measures of variability parameters of all the characters studied.

Character	Range		Grand mean	GCV (%)	PCV (%)	h ² _{bs} (%)	GA	GAM
	Min.	Max.						
Days to 50% flowering	46.00	56.00	51.21	6.03	6.17	95.49	6.22	12.16
Plant height (cm)	30.88	63.04	47.07	15.61	19.28	65.58	12.28	26.09
Branches per plant	1.20	9.60	5.80	36.60	36.94	98.17	4.34	74.82
Clusters per plant	3.20	29.20	14.77	42.76	43.99	94.45	12.66	85.72
Pods per plant	10.20	112.80	59.29	47.84	48.11	98.86	58.18	98.12
Pod length (cm)	3.28	5.10	4.13	7.68	8.39	83.69	0.60	14.49
Seeds per pod	3.80	8.00	6.05	8.61	10.40	68.92	0.89	14.72
100 seed weight (g)	3.10	6.50	4.69	12.52	13.79	82.43	1.10	23.45
Days to maturity	87.00	99.00	93.35	3.82	3.93	94.61	7.16	7.67
Harvest index (%)	12.46	63.96	46.52	22.64	26.67	74.32	18.74	40.27
Seed yield per plant (g)	1.18	31.38	14.77	56.50	59.38	90.54	16.38	110.91

GCV = Genotypic coefficient of variation
PCV = Phenotypic coefficient of variation

h²_{bs} (%) = Heritability (Broad sense)
GA = Genetic advance

GAM = Genetic advance as per cent of mean (%)



GCV (%) = Genotypic coefficient of variation
PCV (%) = Phenotypic coefficient of variation

h²_{bs} (%) = Heritability (Broad sense)
GAM = GA as per cent of mean (%)

Fig. 1. GCV, PCV, h²_{bs} and GAM for eleven quantitative characters in F₃ progenies in black gram.

Analysis revealed that all of the traits exhibited high heritability (broad sense) in F₃ progenies (Table 2). The traits viz., days to 50% flowering (95.49 %), plant height (65.58 %), branches per plant (98.17 %), clusters per plant (94.45 %), pods per plant (98.86 %), pod length (83.69 %), seeds per pod (68.92 %), 100 seed weight (82.43 %), days to maturity (94.61 %), harvest index (74.32 %) and seed yield per plant (90.54 %) showed high heritability, which suggests that the environmental effect had the least impact on these attributes. Because total variance, which includes both non-fixable (dominance and epistasis) and fixable (additive) variance, is the basis for broad sense heritability, choosing to improve such specified attributes may not be beneficial. Similar to this, Patel and Madhu Bala (2020) and Barik *et al.* (2021) found high heritability for the seed yield per plant, pods per plant, clusters per plant, branches per plant, days to 50% flowering and days to maturity; Barik *et al.* (2021); Deekshith *et al.* (2022) found high heritability for plant height and 100 seed weight, Kondagari *et al.* (2017) found high heritability for seeds per pod and Deekshith *et al.* (2022) found high heritability for pod length.

Plant height (26.09%), branches per plant (74.82%), clusters per plant (85.72%), pods per plant (98.12%), 100 seed weight (23.45%), harvest index (40.27%) and seed yield per plant (110.91%) demonstrated higher genetic advance as per cent of mean. Selection is successful to improve these attributes with higher genetic advance as percent of mean, which highlights the critical function of additive gene action. Days to fifty percent flowering (12.16%), pod length (14.49%) and seeds per pod (14.72%) depicted moderate genetic advance as percent of mean, meanwhile days to maturity (7.67%) showed low genetic advance as a percent of mean. Direct selection for improvement is inefficient because low to moderate genetic advance as percent of mean suggests that the traits were governed by non-additive gene actions. Similar outcomes were noted for days to maturity and harvest index by Patel *et al.* (2014); for clusters per plant, pods per plant and pod length by Priya *et al.* (2018); Chaturvedi *et al.* (2021); for seed yield per plant by Kiran and Lal (2021). Estimates of heritability that take genetic advance into account are more beneficial than heritability alone in forecasting the impact on choosing the best progenies. High heritability along with high genetic advance were observed in the current study for plant height (65.58 and 26.09%, respectively), branches per plant (98.17% and 74.82%, respectively), clusters per plant (94.45% and 85.72%, respectively), pods per plant (98.86% and 98.12%, respectively), 100 seed weight (82.43 and 23.45%, respectively), harvest index (74.32% and 40.27%, respectively) and seed yield per plant (90.54% and 110.91%, respectively), suggesting that these attributes were controlled by additive gene action, therefore pure line selection has a fair chance of improving these features. Days to 50% flowering

showed high heritability and moderate genetic advance (95.49% and 12.16%, respectively), as did pod length (83.69% and 14.49%, respectively), seeds per pod (68.92% and 14.72%, respectively), whereas days to maturity showed high heritability and low genetic advance (94.61% and 7.67%, respectively). Selection under such conditions should be avoided since the high heritability in combination with the moderate to low genetic advance demonstrates the major role of environment for high heritability expression.

CONCLUSION

The entire research trial manifested that there is a lot of variation in the progenies for every attributes incorporated in this study. For all the traits, PCV was higher than the GCV but values are very close to each other, depicting that environment has little influence. Due to high heritability coupling with high genetic advance as per cent of mean (additive gene action), it will be simple to select for plant height, branches per plant, clusters per plant, pods per plant and harvest index, which will be helpful in future seed yield enhancement programmes of black gram breeding.

FUTURE SCOPE

Black gram has a very low yield since it is frequently grown on marginal fields with insufficient irrigation, fertilizer and insect pest management. Furthermore, it is difficult to find seeds from better kinds. Farmers are thus obliged to employ locally available, variable-productivity and disease-prone materials for sowing. Taking into account the aforementioned aspects, there is a significant opportunity to increase the productivity of this crop by generating and utilizing variability and selecting for attributes that are connected to seed yield.

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Conflict of Interest. None.

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