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Assessment of variability parameters for seed yield and related component traits in blackgram [*Vigna mungo* (L). Hepper] generations

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Abstract

The research was carried out to assess the nature and magnitude of genetic variability, along with proportions of heritability and genetic advance among 14 crosses and ten parents by considering 11 yield and its related traits in blackgram. The investigation was undertaken in the Experimental Farm of Department of Genetics and Plant Breeding, College of Agriculture, CSKHPKV, Palampur (H.P.) during *Kharif* 2018 and 2019 in Randomized Complete Block Design over three replications. Analysis of Variance revealed significant differences among the genotypes for all the traits in both the generations. High PCV and GCV was recorded for biological yield per plant (g), seed yield per plant (g) and harvest index (%). High heritability along with high genetic advance was recorded for pods per plant, biological yield per plant, seed yield per plant and harvest index in both the generations indicating the preponderance of additive gene action to develop desirable and stable genotypes during breeding programme.

Key words: Blackgram, variability, heritability, genetic advance.

Blackgram [*Vigna mungo* (L).Hepper], 2n=22, also known as uradbean, minapa, pappu, mungo bean is an important self-pollinated true diploid, short duration *Kharif* legume crop belonging to family Fabaceae and progenitor as *V. mungo* var. *silverstris*. It is believed to be originated in India with its secondary centre of origin in Central Asia. India is the largest producer as well as consumer of urdbean with production of approx. 2.93 million tons annually from about 4.49 million hectare of area with an average productivity of 500 kg per hectare (Anonymous 2019). In Himachal Pradesh, it is one of the important *Kharif* pulse grown in an area of 12 thousand ha with annual production and productivity of 9.4 thousand tons annually (Anonymous 2018). The yield and productivity is less and stagnant over years due to narrow genetic base and lack of genetic variability, poor ideotype, lack of high yielding varieties, cultivation in harsh and marginal lands and susceptibility of the crop to various biotic and abiotic stresses which results in drastic reduction in yield. It has been evident that transgressive segregation facilitates the successful establishment of hybrid lineages is indirect and comes principally from research on plants (Gupta *et al.* 1993; Sood *et al.* 2000). Selection of parental material for hybridization with wider adaptability, genetic variability and high yielding potential will greatly be helpful in resolving the problems and thus influences the success of any breeding programme. So, focusing on achieving the goals of increased production, the breeder must have firm knowledge about related genetic parameters like variability *viz*; phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance, for determining the inheritance of qualitative and quantitative traits which serves as a pre-requisite for a plant breeder in devising efficient breeding strategy. Also the nature and magnitude of genetic variability in the population provides a clear cut idea about a particular trait to be selected for improving the yield potential of the genotypes. Keeping the above points in context, the present research was conducted to estimate the nature and magnitude of genetic variability, heritability and genetic advance in F_2 and F_3 generations of urdbean.

Materials and Methods

The genetic materials in the present study comprised of nine genotypes including seven lines & two testers of urdbean (*Vigna mungo* L. Hepper) forming 14 different crosses *viz*., IC-281980 x HPBU-111, IC-281982 x HPBU-111, IC-281993 x HPBU-111, IC-436852 x HPBU-111, IC-398973 x HPBU-111, IC-413306 x HPBU-111, IC-413304 x HPBU-111, IC-281980 x Him Mash-1, IC-281982 x Him Mash-1, IC-281993x Him Mash-1, IC-436852 x Him Mash-1, IC-398973 x Him Mash-1, IC-413306 x Him Mash-1 and , IC-413304 x Him Mash-1 to derive $F_2$and F_3 generations. The investigation was carried out at Experimental Farm, Department of Genetics and Plant Breeding, College of Agriculture, CSK HPKV, Palampur during *Kharif* 2018 and 2019. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each genotype as well as cross combinations was grown in three rows of 2m length in $F_2$and 10 progeny rows in F_3 generation with inter and intra- row spacing of 30 x 10cm respectively. The recommended package of practices was followed to raise the crop. 20 random plants were selected in F_2generation whereas ten were selected in F_3 generation from each parent as well as cross for plant height, branches per plant, pods per plant, pod length, seeds per pod, biological yield per plant, seed yield, harvest index, 100-seed weight (individual plant basis), days to 50% flowering and days to 75% maturity (plot basis). Data for Analysis of variance (ANOVA) was analyzed statistically as per method suggested by Panse and Sukhatme (1985). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated as per method of Burton and De Vane (1953), whereas estimates of heritability (h^2_{bs}) and genetic advance were done as suggested by Burton and De Vane (1953) and Johnson *et al.* (1955).

Results and Discussion

The results of statistical analysis of variance highlighted that mean sum of squares due to genotypes for11 traits namely days to 50 per cent flowering, days to 75 per cent maturity, plant height, number of branches per plant, pods per plant, pod length, seeds per pod, biological yield per plant, seed yield per plant, harvest index and 100-seed weight were significant among all the 24 genotypes (including 14 crosses and 10 parents) in both the segregating generations which means that there is presence of sufficient genetic variation for different agro-morphometric traits enhancing the scope for selecting better genotypes with desirable aspects (Table 1). These results are in accordance with the earlier reports of Blessy *et al.* (2018), Priya et al. (2018), Reddy et al. (2018), Tank *et al*. (2018), Chaithanya *et al.* (2019), Senthamizhselvi *et al.* (2019), Chowdhury *et al.* (2020) and Singh *et al.* (2020) who reported significant amount of genetic variation for all the traits similar to our study.

The PCV values were higher than corresponding GCV for all the characters studied in both generations thereby meaning that the variation present is not only due to the genotypes but also due to the environmental effect (Table 2) & (Fig. 1 and Fig.2). Similar results in relation to PCV and GCV were reported by Priya *et al*. (2018), Chaithanya et al. (2019), Senthamizhselvi *et al*. (2019), Sathees *et al*. (2019), Chowdhury *et al*. (2020) and Singh *et al*. (2020). For F_2 generation, PCV and GCV values were recorded high (>30%) for biological yield per plant (49.25%, 48.85%) followed by seed yield (46.36%, 45.08%), harvest index (37.01%, 36.52%), also number of pods per plant (30.28%) had high PCV. In F_3 population, high values of PCV (>30%) and GCV (>30%) were recorded for seed yield (44.62%, 44.33%), biological yield per plant (43.80%, 43.69%), harvest index (33.29%, 32.59%) and number of pods per plant (32.13%, 31.83%). Similar results were reported by Panda *et al*. (2017) for seed yield per plant and pods per plant, Kurer (2010) for pods per plant and seed yield per plant in F_2 generation and for seed yield per plant in F_3 generation in cowpea, Hemalatha *et al*. (2017) & Singh *et al*. (2020) for harvest index, pods per plant and seed yield per plant and Panwar *et al*. (2019) for seed yield per plant, biological yield per plant, pods per plant and harvest index in urdbean.

PCV and GCV in F_2 generation were moderate (15-30%) for plant height (27.12%, 26.58%) and branches per plant (22.12%, 19.01%), also pods per plant showed response to moderate GCV (29.19%). For F_3 population, moderate GCV and PCV (15-30%) were recorded for branches per plant (25.15%, 22.84%) and plant height (23.55%, 23.10%). Similar findings were reported by Senthamizhselvi *et al*. (2019) & Chowdhury *et al*. (2020) for plant height, Rolaniya *et al*. (2017) & Aftab *et al*. (2018) for branches per plant, Sushmitharaj *et al*. (2018) observed for plant height and number of pods per plant while Tank *et al*. (2018) observed moderate GCV for branches per plant and plant height, whereas PCV for only plant height in blackgram.

Table 1. Analysis of variance for 11 traits among blackgram genotypes in F_2 and F_3 generations

Traits		Mean sum of squares					
		F_2 generation			F_3 generation		
	Source	Replication	Genotypes	Error	Replication	Genotypes	Error
	Df	2	23	46	2	23	46
Days to 50% flowering		0.04	11.46*	0.04	0.29	6.85*	0.16
Days to 75 % maturity		0.07	65.92*	0.06	0.26	50.04*	0.09
Plant height (cm)		3.69	67.14*	0.91	2.83	324.61*	4.22
Branches per plant		1.43	0.75*	0.08	0.98	1.46*	0.10
Pods per plant		0.17	20.18*	0.50	0.27	135.92*	0.84
Pod length (cm)		0.03	0.08*	0.01	0.10	0.60*	0.01
Seeds per pod		0.28	0.17*	0.06	0.28	0.83*	0.04
Biological yield per plant (g)		0.26	90.73*	0.50	11.56	1139.18*	1.90
Seed yield per plant (g)		0.04	2.15*	0.04	0.64	23.23*	0.10
Harvest index (%)		4.87	127.77*	1.16	0.48	90.14*	1.29
100-seed weight (g)		0.01	0.18*	0.03	0.31	0.95*	0.06

* Significant at $P \leq 0.05$

Table 2. Estimates of variability parameters for 11 characters in F_2 and F_3 generations of blackgram

	F_2 generation						F_3 generation					
Characters	**General Mean±SE (m)**	**Range**	**PCV (%)**	**GCV (%)**	**h^2bs (%)**	**GA (% of Mean)**	**General Mean±SE (m)**	**Range**	**PCV (%)**	**GCV (%)**	**h^2bs (%)**	**GA (% of Mean)**
Days to 50%flowering	40.41±0.11	35.32-43.60	4.85	4.83	99.10	9.91	39.93±0.24	36.67-42.47	3.87	3.74	93.21	7.43
Days to 75 % maturity	96.23±0.15	78.17-99.58	4.88	4.87	99.73	10.02	96.55±0.18	78.60-99.63	4.24	4.23	99.45	8.68
Plant height (cm)	17.68±0.55	12.67-37.37	27.12	26.58	96.06	53.67	44.74±1.19	28.33-65.57	23.55	23.10	96.20	46.67
Branches per plant	2.49±0.16	1.47-3.15	22.12	19.01	73.89	33.67	2.95±0.18	1.80-4.37	25.15	22.84	82.47	42.73
Pods per plant	8.77±0.41	5.64-15.73	30.28	29.19	92.94	57.98	21.08±0.53	12.00-35.43	32.13	31.83	98.17	64.97
Pod length (cm)	4.06±0.05	3.82-4.67	4.42	3.87	76.59	6.98	4.65±0.06	3.82-5.25	9.81	9.55	94.84	19.16
Seeds per pod	5.47±0.14	4.75-5.86	5.63	3.45	37.41	4.34	6.44±0.12	5.45-7.20	8.57	7.97	86.46	15.27
Biological yield per plant (g)	11.23±0.41	6.10-23.03	49.25	48.85	98.36	99.80	44.56±0.80	13.93-71.77	43.80	43.69	99.50	89.78
Seed Yield per plant (g)	1.86±0.12	0.74-3.68	46.36	45.08	94.55	90.30	6.26±0.19	2.85-12.15	44.62	44.33	98.69	90.71
Harvest index (%)	17.79±0.62	10.65-33.57	37.01	36.52	97.34	74.22	16.70±0.66	4.96-25.94	33.29	32.59	95.82	65.71
100-seed weight (g)	4.93±0.10	4.19-5.29	5.67	4.52	63.70	7.44	5.28±0.14	3.19-6.04	11.29	10.34	83.90	19.52

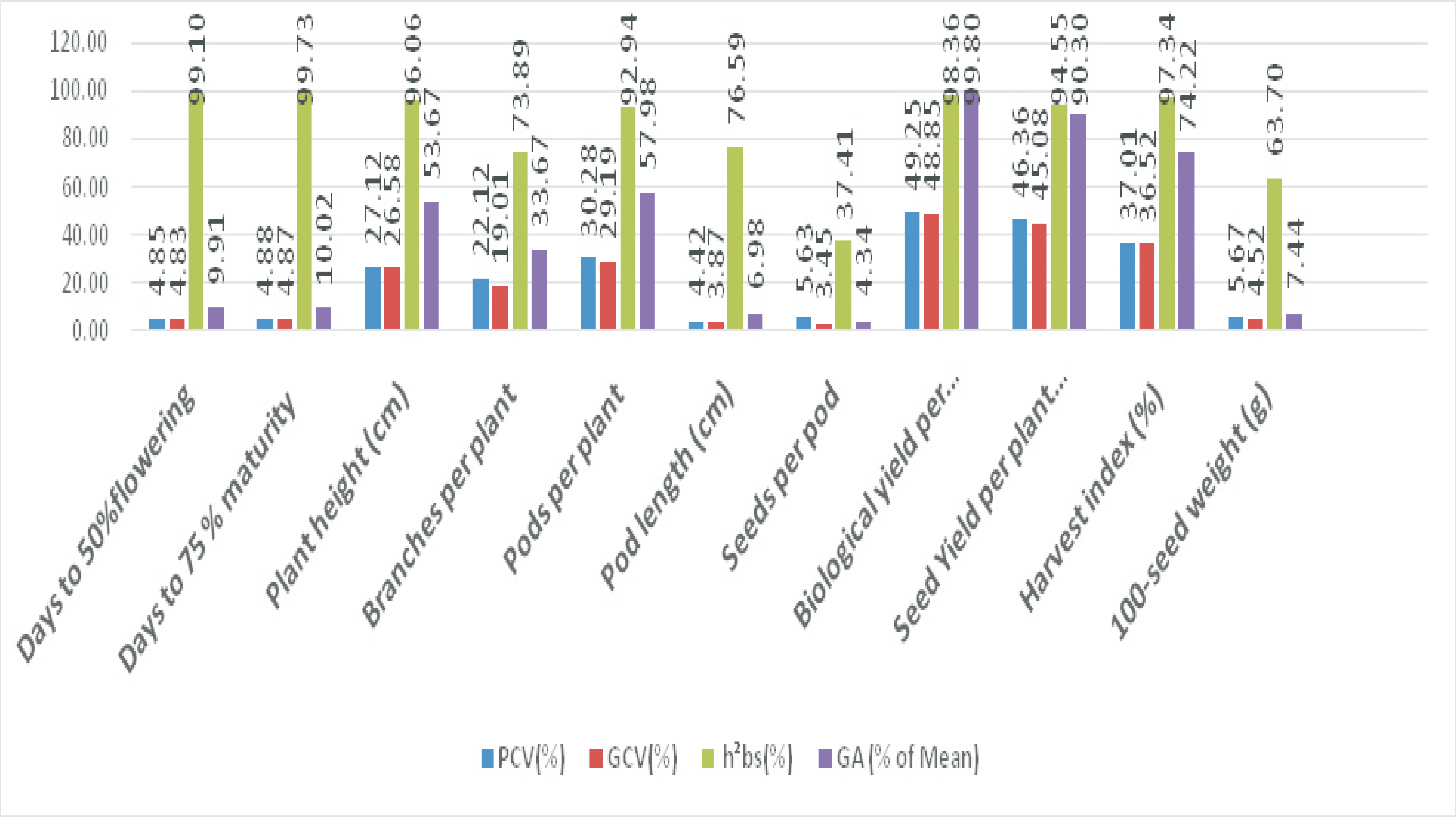

Fig.1 Estimates of variability parameters for 11 characters in blackgram (F_2 generation)

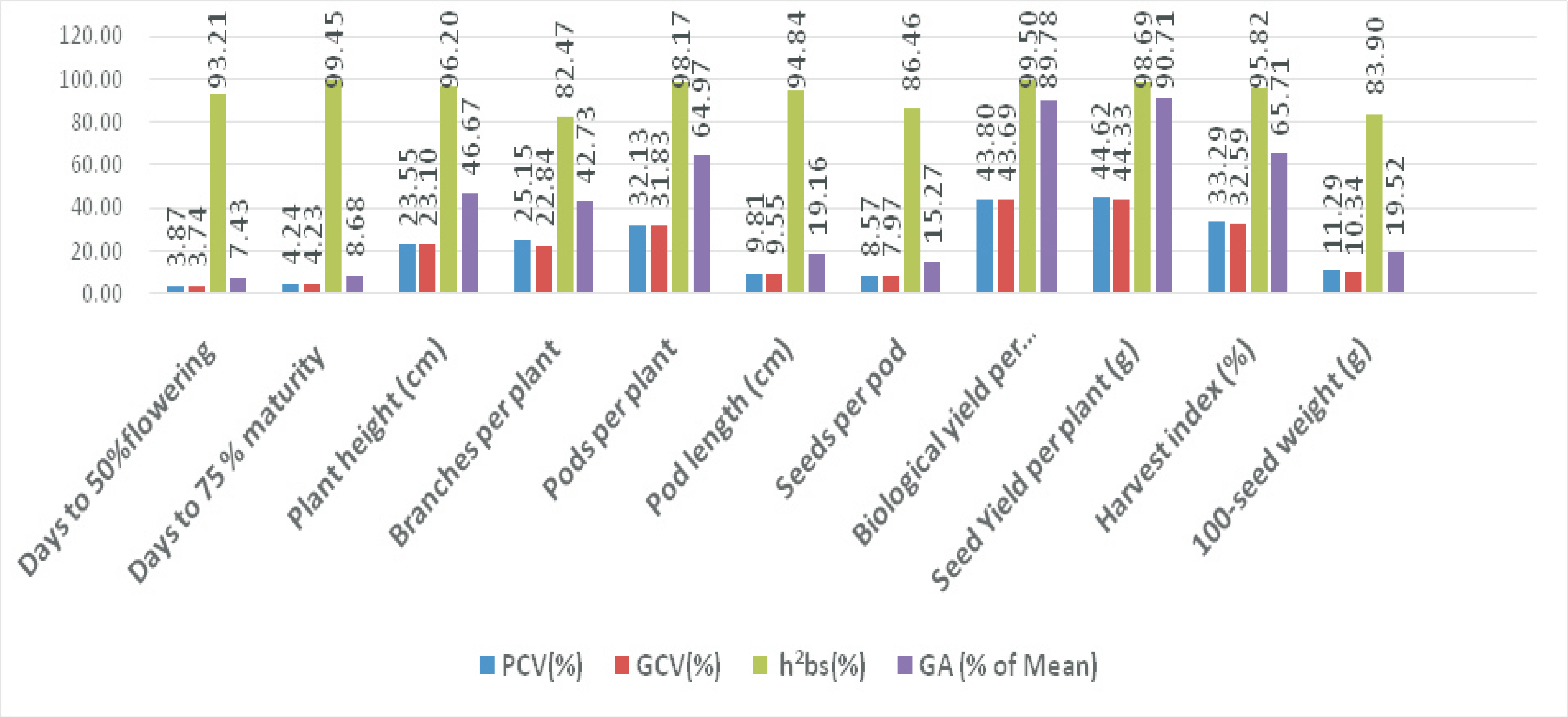

Fig.2 Estimates of variability parameters for 11 characters in blackgram (F_3 generation)

100-seed weight (5.67%, 4.52%) seeds per pod (5.63%, 3.45%), days to 75% maturity (4.88%, 4.87%), days to 50% flowering (4.85%, 4.83%), and pod length (4.42%, 3.87%) showed low estimates (<15%) of PCV and GCV in F_2 generation. However, in F_3 generation they were observed low (<15%) for 100-seed weight (11.29%, 10.34%), pod length (9.81%, 9.55%), seeds per pod (8.57%, 7.97%), days to 75% maturity (4.24%, 4.23%) and days to 50 per cent flowering (3.87%, 3.74%) respectively. Similar results were reported by Ozukum and Sharma (2017), Aftab *et al.* (2018) and Gandi *et al.* (2018) in urdbean.

Heritability in F_2 generation was high (>80%) for days to 75% maturity (99.73%), days to 50% flowering (99.10%), biological yield per plant (98.36%), harvest index (97.34%), plant height (96.06%), seed yield per plant (94.55%) and pods per plant (92.94%). Similar results were revealed by Rajasekhar *et al*. (2017) for harvest index and seed yield per plant, Priya *et al.* (2018) noted for plant height, pods per plant and plant yield and Chaithanya *et al*. (2019) for pods per plant, harvest index, biological yield and seed yield per plant in blackgram. The traits which exhibited high heritability implied that the influence of environment was very low and genetic variation played a greater part in the research. Moderate heritability (50-80%) was observed for pod length (76.59%), branches per plant (73.89%) and 100-seed weight (63.70%). Sohel *et al*. (2016) noted lowest heritability in seeds per pod. The estimates of moderate and low heritability indicated that the characters are highly affected by the environmental factors and influence of non-additive gene action, so genetic improvement through selection would be difficult or virtually impractical for such traits due to masking effects of the environment at the genotypic level.

Whereas, high heritability was observed (>80%) for all the characters in F_3 generation *viz*., biological yield per plant (99.50%) followed by days to 75% maturity (99.45%), seed yield per plant (98.69%), pods per plant (98.17%), plant height (96.20%), harvest index (95.82%), pod length (94.84%). days to 50% flowering (93.21%), seeds per pod (86.46%),100-seed weight (83.90%) and branches per plant (82.47%). Rolaniya *et al.*(2017), Kuralarasan *et al*. (2018) and Priya *et al*. (2018) reported high heritability for all the characters which is in conformity with the present study.

Genetic advance expressed as percentage of mean in F_2 generation was observed to be high (>50%) for biological yield per plant (99.80%) followed by seed yield per plant (90.30%), harvest index (74.22%), pods per plant (57.98%) and plant height (53.67%). Genetic advance expressed as percentage of mean in F_3 generation was recorded highest (>50%) for seed yield per plant (90.71%) followed by biological yield per plant (89.78%), harvest index (65.71%) and pods per plant (64.97%). Priya *et al*. (2018) recorded high genetic advance for plant height, pods per plant and seed yield per plant, Reddy *et al*. (2018) for seed yield per plant and pods per plant whereas Chauhan *et al*. (2018) for plant height, biological yield and seed yield in blackgram genotypes.

It was found moderate (25-50%) for branches per plant (33.67%) in F_2 generation while it was found moderate (25-50%) for plant height (46.67%) and branches per plant (42.73%) in F_3 generation. Chaithanya *et al*. (2019) recorded similar results for branches per plant. Low values in F_2 generation recorded (<25%) for days to 75% maturity (10.02%), days to 50% flowering (9.91%), 100-seed weight (7.44%), pod length (6.98%) and seeds per pod (4.34%) and characters *viz*.,100-seed weight (19.52%), pod length (19.16%),seeds per pod (15.27%), days to 75% maturity (8.68%) and days to 50% flowering (7.43%) had low values (<25%) in F_3 population. Similar results were interpreted by Senthamizhselvi *et al*. (2019) for days to flowering, Chowdhury *et al*. (2020) for days to 50 % flowering, seeds per pod, days to maturity and 100-seed weight.

High heritability with high genetic advance was recorded for pods per plant, plant height, biological yield, seed yield per plant and harvest index. Similarly, in F_3 generation, pods per plant, biological yield, seed yield per plant and harvest index showed high heritability with high genetic advance. This means that these traits are controlled by additive gene action and must go for direct selection of these traits for developing improved genotypes. Results are in accordance with the results of Gandi *et al*. (2018); Reddy *et al*. (2018) and Chowdhury *et al*. (2020)

For F_2 population, high heritability with low genetic advance was found for days to 50% flowering and days to 75% maturity. Same results were shown by Reddy *et al*. (2018) and Senthamizhselvi *et al*. (2019) for days to 50% flowering; whereas in F_3 population, high heritability with moderate and low genetic advance was recorded in branches per plant,

plant height, days to 50% flowering, pod length, seeds per pod, days to 75% flowering and 100-seed weight. The results are in line with the reports of Chaithanya *et al*. (2019) for pod length and branches per plant. Chowdhury *et al*. (2020) showed high heritability estimates with moderate to low GA for days to 50 % flowering, seeds per pod, days to maturity and 100-seed weight.

Moderate heritability with moderate genetic advance was noticed for branches per plant showing the presence of additive as well non-additive gene action, thus providing scope for the improvement of this trait through hybridization and selection. Low heritability with low genetic advance was observed for seeds per pod indicating that the selection for this trait would be ineffective due to the presence of non-additive gene action.

Conclusions

The analysis of variance revealed significant differences among the genotypes for all the traits in both the generations implying the presence of sufficient genetic variability and scope for selecting promising genotypes with desirable attributes under study. The phenotypic coefficient of variation values were higher than corresponding genotypic coefficient of variation for all the characters studied in both generations. Biological yield per plant, harvest index and seed yield per plant should be given top priority for their direct selection as they have recorded high magnitudes of genotypic coefficient of variation as well as high heritability along with high genetic advance for successive breeding programme.

Conflicts of interest: The authors would hereby like to declare that there is no conflict of interests that could possibly arise.

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