The Pharma Innovation

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Estimation of genetic parameters for yield and yield contributing characters in blackgram [*Vigna mungo* (L.) Hepper] genotypes

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Abstract
Blackgram is the third most important legume crop in India and due to very less genetic variability, improvement in yield now requires more emphasis in research for the development of improved varieties. An experiment was conducted with the objective to determine the estimates of genetic parameters for yield and its contributing traits on 40 blackgram genotypes during Rabi/Summer- 2020/21. All the genotypes were sown in three replications by employing randomized complete block design. The observation on different quantitative traits were recorded and the parameters of genetic variability *viz.* GCV, PCV, heritability and genetic advance were determined. As per ANOVA, all the genotypes differed significantly for all the characters. The highest GCV and PCV was recorded for number of clusters per plant, number of pods per plant, seed yield per plant, number of primary branches per plant, biological yield per plant and plant height. The estimate of heritability was found to be high for characters; number of pods per plant, 100 seed weight, plant height, biological yield per plant height, days to maturity, number of primary branches per plant, number of clusters per plant, number of secondary branches per plant, number of seeds per pod and harvest index. The characters plant height and number of pods per plant exhibited medium genetic advance. High heritability coupled high genetic advance as percent of mean was recorded for number of pods per plant, number of clusters per plant, seed yield per plant, biological yield per plant, number of primary branches per plant and plant height.

Keywords: Blackgram, variability, heritability genetic advance

Introduction
In the family Leguminosae and sub-family Papilionaceae, the blackgram [*Vigna mungo* (L.) Hepper] with chromosome number (2n=22) is a significant self-pollinated, short-duration legume crop. Blackgram is a crop that is grown as a single crop or as a follow-up crop using the leftover moisture of a previous crop. It is native to India (Mehra *et al*., 2016) [1]. Blackgram which is also known as urdbean, urd or mash is a significant grain legume because of its nutritive value and crop adaptability. Blackgram is primarily used to make dals, curries, soup, desserts, and snacks. The abundant and easily digestible protein in urdbean is what gives it its nutritional worth. On a dry weight basis, its seeds have 25–28% protein, 1.0–1.5% oil, 3.5–4.5% fibre, 4.5–5.5% ash, and 62–65% carbs. Similar to other pulses, it increases soil fertility, strengthens soil structure, and is utilised as green cattle feed (Kumaresan *et al*., 2016) [3]. The reason being numerous desirable features must be combined to develop the right plant type for a certain growing zone and cropping strategy, the breeding process has been inconsistent. The total area occupied by urdbean in India is 4703.35 ha with a production of 2682.18 tonnes and Madhya Pradesh being the lead producer of the country shares the area, production and productivity of 1647.20 ha, 875.09 tonnes and 531.25 kg/ha respectively (Singh *et al*., 2021) [2]. In order to adopt a successful breeding programme, knowledge of the type and degree of genetic variability existing in the available population is a prerequisite for the development of high yielding crop varieties. Therefore the present investigation was carried out with an objective to assess genetic variability by computing its parameters to find out the contribution of yield related traits on the seed yield.

Materials and Methods
The experimental material comprised 40 blackgram genotypes received from the Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi

Vishwavidyalaya, Jabalpur, Madhya Pradesh, India. The field trial was conducted during Rabi/Summer (2020-21) by employing randomized complete block design in 3 replications. The genotypes were grown in four rows of 2 meters each maintaining a row to row distance of 40 cm and plant to plant distance of 10 cm. Thirteen quantitative traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, pod length (cm), number of seeds per pod, number of pods per plant, number of clusters per plant, 100 seed weight (g), biological yield (g), harvest index (%) and seed yield per plant (g) were recorded for five randomly selected plants in each of the genotypes per replication. Analysis of variance was computed as per (Burton, 1952). Estimates of heritability and genetic advance were calculated as per Heritability (Hanson *et al*., 1956) and (Johnson *et al*., 1955) respectively.

Results and Discussion

The mean sum of squares due to genotypes were significant for all the 13 characters suggesting that the genotypes were genetically variable and considerable amount of variability existed among them (Table 1). Per se performance exhibited wide range of variations for the characters studied i.e. Days to 50% flowering (45.66-51.66), days to maturity (68.00-76.33) Plant height (19.4146.41), number of primary branches per plant (12.34-7.47), number of secondary branches per plant (5.74-13.18), number of pods per plant (6.94-27.62), number of clusters per plant (2.03-8.84), pod length (3.37-4.47), number of seeds per pod (3.39-6.71), biological yield per plant (8.79-19.33), seed yield per plant (2.50-6.62), harvest index (24.36-37.87) and 100 seed weight (3.04-5.07) (Table 2).

Estimates of the phenotypic coefficient of variation were higher than the corresponding genotypic coefficient of variation for all the traits, suggesting that the environment factors impacted the characters under study. These results were in accordance with the findings of Sowmini and Jayamani (2013) [4] and Ramya *et al*., (2014) [5]. The high values of GCV and PCV was recorded for number of clusters per plant (29.14, 31.31), number of pods per plant (28.39, 28.75), seed yield per plant (23.73, 25.02), number of primary branches (21.92, 23.61), biological yield (20.40, 20.92) and

plant height (19.42, 19.86) (Table 2). These results are supported by (Kumar *et al*., 2015) [6].

Heritability serves as a good index for transmission of characters from parents to their offspring and helps a breeder as a tool for selecting elite genotypes from diverse genetic population. It gives an exact idea of heritable portion of variability. In the present study, highest heritability was recorded for number of pods per plant (97.5), followed by 100 seed weight (96.9), plant height (95.6), biological yield (95.1), days to maturity, (93.2), seed yield per plant (89.9), number of seeds per pod (86.3), number of clusters per plant (86.2), number of secondary branches per plant (85.2) and harvest index (80.5). Medium and high heritability was exhibited by pod length and days to 50% flowering respectively. Panigrahi *et al*., (2014) [7] also reported very high heritability for seed yield per plant, number of clusters per plant and number of pods per plant. The moderate heritability was recorded for 100 seed weight (43.7) and number of seeds per pod (43.6) indicating that selection of these characters are in a condition to accumulates more additive gene leading to further improvement of their performance (Table 2).

Genetic advance determines the genetic gain under selection. Genetic advance as percentage of mean is more reliable index for understanding the effectiveness of selection in improving the traits because its estimated value is derived by involvement of heritability, phenotypic standard deviation and intensity of selection. In this investigation, medium genetic advance was exhibited by plant height (10.70) and number of pods per plant (10.18) while remaining characters like harvest index (6.00), biological yield per plant (5.57), days to maturity (4.36), number of clusters per plant (3.16), number of secondary branches (3.06), days to 50% flowering (2.48), seed yield per plant (1.99), number of primary branches per plant (1.86), 100 seed weight (1.25), number of seeds per pod (1.21) and pod length (0.26) exhibited low genetic advance. High heritability coupled high genetic advance as percentage of mean was noted for number of pods per plant (86.2, 57.75) and number of clusters per plant (97.5, 57.75), seed yield per plant (89.9, 46.35) biological yield per plant (95.1, 40.98), number of primary branches per plant (86.3, 41.95) and plant height (95.6, 39.12) (Sushmitharaj *et al*., 2018) [8] also reported high heritability coupled with high genetic advance as percentage of mean for number of clusters per plant.

Table 1: Analysis of variance for different quantitative characters in 40 genotypes of blackgram.

S. No	Characters	Mean sum of squares		
		Replication (d.f=2)	Treatment (d.f=39)	Error (d.f=78)
1	Day to 50% flowering	0.10	7.50**	1.78
2	Days to maturity	0.00	15.48**	1.05
3	Plant height (cm)	6.57	88.63**	3.88
4	No. of primary branches/plant	2.14	3.31**	0.45
5	No. of Secondary branches/plant	3.93	9.15**	1.35
6	No. of pods/plant	8.19	77.12**	1.92
7	No. of clusters/plant	1.28	9.40**	1.25
8	Pod length (cm)	0.13	0.20**	0.10
9	No. of seeds/pod	1.22	1.39**	0.19
10	Biological yield (g)	0.42	24.26**	1.19
11	Seed yield/plant (g)	0.23	3.49**	0.35
12	Harvest index (%)	5.18	39.30**	7.65
13	100 seed weight (g)	0.02	1.19**	0.03

**&* Significant at 1 and 5% level

Table 2: Mean, range, variability, heritability (broad sense), genetic advance and genetic advance as per cent of mean for 13 characters in blackgram

S. No.	Characters	GCV	PCV	h² (%)	Genetic Advance (%)	Genetic Advance as (%) of mean	Per se performance Rang		Mean
							Min	Max	
1	Day to 50% flowering	2.85	3.27	76.2	2.48	5.14	45.66	51.66	48.31
2	Days to maturity	3.09	3.19	93.2	4.36	6.14	68.00	76.33	71.01
3	Plant height (cm)	19.42	19.86	95.6	10.70	39.12	19.41	46.41	27.35
4	No. of primary branches/plant	21.92	23.61	86.3	1.86	41.95	2.34	7.47	4.44
5	No. of Secondary branches/plant	16.54	17.92	85.2	3.06	31.47	5.47	13.18	9.74
6	No. of pods/plant	28.39	28.75	97.5	10.18	57.75	6.94	27.62	17.63
7	No. of clusters/plant	29.14	31.31	86.2	3.16	55.89	2.03	8.84	5.65
8	Pod length (cm)	4.77	6.85	48.5	0.26	6.84	3.37	4.47	3.80
9	No. of seeds/pod	12.00	12.92	86.3	1.21	22.97	3.39	6.71	5.27
10	Biological yield (g)	20.40	20.92	95.1	5.57	40.98	8.79	19.33	13.58
11	Seed yield/plant (g)	23.73	25.02	89.9	1.99	46.35	2.50	6.62	4.31
12	Harvest index (%)	10.27	11.45	80.5	6.00	18.99	24.36	37.87	31.60
13	100 seed weight (g)	16.17	16.43	96.9	1.25	32.80	3.04	5.07	3.83

Conclusion

The traits found to possess high heritability coupled with high genetic advance as percent of mean could be considered for the identification of high yielding breeding traits to enhance the genetic yield potential of the crop. A systematic hybridization programme can also be developed considering the traits with high heritability with high genetic advance as percent of mean for the selection of transgressive segregants in the segregating generations. The segregants may have some improved breeding value and will be of great importance to enhance the production and productivity of the urdbean crop in future.

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