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ASSESSMENT OF VARIABILITY FOR SEED YIELD IN BACK CROSS DERIVED LINES OF BLACKGRAM (*VIGNA MUNGO* L. HEPPER)

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ABSTRACT

The present experiment was conducted with 24 BC_2F_4 progenies of the cross MDU 1 x TU 68 to investigate the variability in seed yield per plant. Results indicated the presence of a wide range of variability in the population. With the recurrent parent MDU 1, eight progenies recorded an on-par yield. All progenies showed high PCV, and 23 progenies showed high GCV. Sixteen progenies recorded high heritability, and 23 progenies had high genetic advance. Eight progenies had on-par seed yield with recurrent parent MDU 1 and high PCV, GCV, and heritability with high genetic advance. These results indicate that additive gene action is present in these progenies. Therefore, selection will be effective in improving the seed yield in these progenies. Additionally, testing these progenies for bruchid resistance could lead to the evolution of a high-yielding bruchid-resistant blackgram variety.

***Keywords* :** Blackgram, Seed yield, Variability

Introduction

Blackgram [*Vigna mungo* (L.) Hepper] (2n = 22) is an important pulse crop of the Leguminosae family. India is the world's largest producer and consumer of blackgram, accounting for 70% of its production (Bag *et al.*, 2014). In India, it is grown in an area of 4.6 million hectares with a production of 2.7 million tonnes (INDIASTAT, 2022). It is one of the major pulse crops grown in the states of Maharashtra, Karnataka, Madhya Pradesh, Gujarat, Uttar Pradesh, Jharkhand, Telangana, Odisha, Andhra Pradesh, and Tamil Nadu.

Blackgram is an important protein source in a vegetarian's diet because it contains easily digestible proteins. It contains protein (20-24%), carbohydrates (61.24%-64.43%), and fat (Nasir & Sidhu, 2012). People refer to this nutritionally rich crop as the king of pulses (Subramaniyan *et al.*, 2022). The nutritional profile of blackgram contains vitamin A and K, thiamine, riboflavin, nicotinic acid, biotin, folic acid, inositol, and pantothenic acid (Pratap *et al.*, 2020). Blackgram seeds contain moderately high amounts of calories and are rich in minerals such as calcium (185 mg/100 g), iron (8.7 mg/100 g), and phosphorous (345 mg/100 g) (Suneja *et al.*, 2011). They also contribute to atmospheric nitrogen fixation by forming a symbiotic relationship with nitrogen-fixing rhizobia (Hanumantharao *et al.*, 2016).

A successful breeding program depends on understanding the range of genetic and phenotypic variation in the population. It makes available diversity for selection, aids in parental selection and direct breeding methodologies, and eventually contributes to the creation of improved agricultural varieties. Against this backdrop, the present study examined the variability in the BC_2F_4 progenies of a cross between MDU 1 and TU 68.

Material and Methods

The recurrent parent MDU 1 is a high-yielding variety released for Tamil Nadu, India. However, it is susceptible to bruchid storage pests. The donor parent TU 68 was developed at Bhabha Atomic Research Centre, Trombay, from a cross between *Vigna mungo* and *Vigna mungo var sylvestris*. It has resistance to bruchid pests. Hybridization was made between MDU 1 and TU 68, and two backcrosses were made to the recurrent parent MDU 1 to introgress the bruchid resistance. The BC_2F_4 generation of the cross MDU1xTU68 was evaluated in the field at Tamil Nadu Agricultural University, Coimbatore, during the post-rainy season (December-February) of 2023-2024. All the progenies and parents were grown in two rows of 4 m length with 30 cm x 10 cm spacing. All the recommended agronomic practices were followed. Seed yield per plant was recorded on all plants at the time of harvest. The environmental variance was calculated as the average of the parental variances. Genotypic variance is estimated by subtracting the environmental variance from phenotypic variance. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) suggested by Burton, (1952), heritability, and genetic advance given by Johnson *et al.*, (1995) were estimated. Descriptive statistics were done by using TNAUSTAT (Manivannan, 2014).

Results and Discussion

Mean performance of progenies

Table 1 presents the mean performance and variability parameters of BC_2F_4 progenies for seed yield per plant. The recurrent parent MDU 1 has the highest seed yield per plant (8.9 g) among the parents. The donor parent has a low yield (5.9 g). The seed yield of progenies ranged between 1 g and 17.88 g. However, no progenies had surpassed the parent MDU 1 for seed yield per plant. Among the 24 progenies, 8 progenies, viz., 30-3-1 (7.6 g), 51-6-1 (6.8 g), 74-6-1 (7.1 g), 87-5-1 (7.2 g), 89-5-1 (6.9 g), 95-1-2 (6.9 g), 95-5-2 (7.2 g), and 124-1-1 (6.9 g), recorded on par yield with MDU 1, and the rest of the progenies yielded lower than MDU 1.

Phenotypic and genotypic coefficient of variation

All progenies had a higher PCV than GCV, indicating that the environment has an influence. All progenies showed high PCV and GCV except one progeny, i.e., 55-15-1, which has high PCV and moderate GCV. These results indicate that sufficient variability is present in the progenies. Therefore, directional selection could further enhance the progeny's mean. Many authors, viz., Vinoth and Jayamani, (2014), Baisakh *et al.* (2014), Gowsalya *et al.* (2016), Indhu *et al.* (2018), Sathya *et al.* (2018), Sindhu *et al.* (2023), Gnanasekaran *et al.* (2023), and Gomathi *et al.* (2023) also obtained high PCV and GCV for seed yield per plant in their studies in blackgram. However, there are few studies on moderate PCV and GCV for seed yield (Kumawat *et al.*, 2024), high PCV and moderate GCV for seed yield (Gomathi *et al.*, 2023; Kumar *et al.*, 2015), and moderate PCV and low GCV for seed yield (Konda *et al.*, 2009).

It is well known that only a part of the observed variations, i.e., genetic variation alone, will be transmitted to the next generation. Hence, the knowledge of the heritability of the traits will be essential to know the extent to which traits were transmitted from parents to progenies. Among the 24 progenies, 16 progenies recorded high heritability, 7 progenies had moderate heritability, and 1 progeny (55-15-1) recorded low heritability. Gowsalya *et al.* (2016), Sohel *et al.* (2016), Sowmyasree *et al.* (2018), Sathya *et al.* (2018), Vadivel *et al.* (2019), Gomathi *et al.* (2023) also obtained high heritability for seed yield per plant. Bishnoi *et al.* (2017) and Sushmitharaj *et al.* (2018) reported moderate heritability, while Kumar *et al.* (2015) reported a low heritability for seed yield per plant.

Genetic advance as a percent of the mean (GAM) is useful in evaluating the expected response to selection in improving traits. All progenies recorded high GAM except 55-15-1, which showed moderate GAM. Sowmini *et al.* (2013), Hasan *et al.* (2017), Anusha *et al.* (2020), and Punithavathy *et al.* (2023) also got high GAM for seed yield per plant in their studies. Konda *et al.* (2009) and Kumar *et al.* (2015) reported moderate GAM, while Karthik *et al.* (2022) had low GAM for seed yield per plant. High heritability, coupled with high GAM, indicated the presence of additive gene action. Hence, selection for seed yield per plant in the promising progenies will be rewarding to further improve the seed yield in the progenies.

Conclusion

This study revealed the presence of significant genetic variability for the trait seed yield per plant in the BC_2F_4 population, indicating the opportunities for improvement through selective breeding. Eight progenies were identified with on-par mean seed yield per plant of MDU 1. All these progenies also had high GCV, heritability, and GAM, indicating the presence of additive gene action. Hence, selection could be practiced in these progenies to further improve the mean seed yield plant. Promising progenies could be tested for bruchid resistance to release as a bruchid-resistant black gram variety.

Table 1 : Variability parameters of BC$_2$F$_4$ progenies of cross MDU 1 x TU 68 for seed yield per plant (g)

Genotypes	**Mean**	**MIN**	**MAX**	**PCV (%)**	**GCV (%)**	**h^2**	**GAM (%)**
30-3-1	7.6^{a}	1.52	17.16	53.07	48.44	83.3	91.09
51-6-1	6.8^{a}	1.25	12.32	52.88	46.99	79.0	86.02
53-6-1	5.6^{*}	1.07	12.31	74.94	69.03	84.8	130.98
54-6-1	5.4^{*}	1.70	9.96	50.89	40.79	64.3	67.36
55-15-1	3.3^{*}	1.26	6.08	52.89	19.00	12.9	14.06
60-8-1	4.5^{*}	1.17	8.39	53.94	39.74	54.3	60.33
61-13-1	4.1^{*}	1.25	8.07	50.10	29.92	35.7	36.80
64-10-1	5.7^{*}	1.33	13.53	50.14	41.16	67.4	69.62
65-13-1	6.2^{*}	1.38	9.96	43.46	34.36	62.5	55.98
69-10-1	6.7^{*}	2.68	10.66	32.06	20.68	41.6	27.49
72-12-1	5.9^{*}	1.71	12.01	54.19	46.33	73.1	81.60
74-6-1	7.1^{a}	1.19	15.29	56.15	51.07	82.7	95.71
87-5-1	7.2^{a}	1.09	13.76	54.77	49.72	82.4	92.97
89-5-1	6.9^{a}	1.25	12.72	53.44	47.76	79.9	87.93
95-1-2	6.9^{a}	1.20	17.88	59.10	54.07	83.7	101.91
95-2-4	6.6^{*}	1.47	14.80	51.31	44.91	76.6	80.98
95-3-5	4.8^{*}	1.73	10.64	51.83	38.57	55.4	59.13
95-5-2	7.2^{a}	2.79	17.38	51.34	45.90	80.0	84.56
95-7-1	5.1^{*}	1.41	9.87	46.22	32.95	50.8	48.39
98-4-1	4.9^{*}	2.08	10.54	48.38	34.96	52.2	52.03
99-4-1	5.6^{*}	1.00	13.10	55.94	47.69	72.7	83.74
109-6-1	5.4^{*}	1.25	11.36	49.70	39.42	62.9	64.41
112-2-1	5.0^{*}	1.69	10.12	43.22	27.89	41.6	37.07
124-1-1	6.9^{a}	1.26	11.61	43.57	36.56	70.4	63.19
Parents:							
MDU 1(P1)	8.9	-	-	-	-	-	-
TU 68 (P2)	5.9	-	-	-	-	-	-

*-significantly different from MDU 1 at (P=0.05); a- on par with MDU 1

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Authors' contributions : PM carried out experimentation and drafted the manuscript and MN planned, supervised, and edited the manuscript. All authors were involved in planning and provided critical feedback on the manuscript. All authors read and approved the final manuscript.

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