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Assessment of genetic variability in blackgram (*Vigna mungo*) under rainfed conditions of Jammu and Kashmir

RADHESHYAM KUMAWAT[1], SANJEEV KUMAR[1]*, SUBHASH C KASHYAP[1] and ADITI SINGH[1]

Sher-e-Kashmir University of Agriculture Sciences and Technology, Jammu, Jammu and Kashmir 180 009, India

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Blackgram [*Vigna mungo* (L.) Hepper], is an annual, diploid (2n = 2x = 22) self-pollinating crop with a genome size of about 574 Mbp. It is a significant pulse crop in Asian nations and is indigenous to India. At national level it has been cultivated in almost all agroecological zones. Blackgram a significant pulse crop, plays an important role in the vegetarian Indian diet (Indhu *et al.* 2018). It includes high quantities of protein (25 g), potassium (983 mg), calcium (138 mg), iron (7.57 mg), niacin (1.447 mg), thiamine (0.273 mg) and riboflavin (0.254 mg). Genetic variability is an imperative measure in any successful blackgram breeding programme. Any successful breeding programme must consider the associated inheritance of numerous quantitative features through the assessment of genetic parameters including phenotypic coefficient of variation and genotypic coefficient of variation, heritability, and GAM. Any successful breeding programme must consider the associated inheritance of numerous quantitative features through the assessment of genetic parameters including phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV), heritability and genetic advance percentage of mean (GAM) (Bhagat *et al.* 2023). To enhance seed output and its constituent parts, it was previously needed to investigate the extent and nature of genetic variability in the population prior to initiating any plant breeding programme (Kumar *et al.* 2020). Till date no variety has been released by Sher-e-Kashmir University of Agriculture Sciences and Technology, Jammu, Jammu and Kashmir and this study would help us in developing a base for first new variety of urdbean to Jammu and Kashmir. That's why this study is novel for the release of a new variety. Heritability estimates in addition GAM is more useful as compare to alone value of heritability to predicting the results for selection of the best genotype. In context of these aspects, the current study aims to assess the correlation coefficient (r), genetic variability, heritability (h^2), and genetic advance percent (GAM) of mean in 30 genotypes of blackgram.

A total of 30 assorted genotypes including advanced breeding lines of blackgram placid from G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand; ICAR-Indian Institute of Pulses Research, Kanpur, Uttar Pradesh (AZAD-2); and Punjab Agriculture University, Ludhaina, Punjab (Mash-114) were used in the existing study. The experiments were conducted during rainy (*kharif*) season of 2021 in randomised block design (RBD) at 3 different locations, viz. Pulses Research Sub-Station (PRSS), Samba, Environment (E_1); Environment (E_2) and Environment (E_3) at Advanced Centre for Rainfed Agriculture (ACRA), Rakhdhiansar of Sher-e-Kashmir University of Agriculture Sciences and Technology, Jammu, Jammu and Kashmir. Thirty (30) diverse genotypes of blackgram were evaluated for study of variability, heritability (h^2), genetic advance and correlation (r) in three environments and data for 11 morphological traits namely plant height, days to 50% flowering, number of branches/plant, days to maturity, number of pods/plant, number of seeds/pod, pod length, number of clusters/plant, number of pods/cluster, 1000-seed weight and seed yield/plant were recorded in the field before and after the harvested of research trial at each location (PRSS, Samba and ACRA, Rakhdhiansar of Jammu and Kashmir) during *kharif* 2021.

Mean sum of squares due to genotypes were ascertained significant at 5% and 1% level of significance for all the eleven variables (Table 1). Maximum and minimum days to 50% flowering exhibited by the genotypes PU-15-21 and PU-07-7, respectively across the environments with an average of 48.30 days (Table 2). Ten out of the 30 genotypes demonstrated below-average performance suggesting an early flowering in blackgram. Kumar *et al.* (2020) published similar results with respect to days to 50% flowering. Genotype PU-13-05 exhibited the highest number of branches/plant (8.53), while PU-15-26 least (4.17). Mean performance for DTM ranged from 80.44

[1]Sher-e-Kashmir University of Agriculture Sciences and Technology, Jammu, Jammu and Kashmir. *Corresponding author email: ssalgotra@gmail.com

Table 1 Pooled analysis of variance for 11 quantitative traits

Source of variation	DF	Mean sum of squares										
		PH	DTF	NOBP	DTM	NPPP	NSPP	PL	NCPP	NPPC	1000-SW	SYPP
Replications	2	80.7	24.02	0.38	16.51	12.4	0.74	0.63	1.69	1.17	21.45	2.54
Genotypes	29	181.7**	29.93**	10.10**	30.02**	151.4**	8.07**	4.96**	18.87**	4.29**	65.92**	9.27**
Errors	174	17.2	8.82	0.5	8.31	10.6	0.46	0.44	1.05	0.36	6.91	0.4

** and * indicates levels of significance at 1% and 5%, respectively.

DF, Degree of freedom; PH, Plant height; DTF, Days to 50% flowering; NOBP, Number of branches/plant; DTM, Days to maturity; NPPP, Number of pods/plant; NSPP, Number of seeds/pod; PL, Pod length; NCPP, Number of clusters/plant; NPPC, Number of pods/cluster; 1000-SW, 1000-seed weight (g); SYPP; Seed yield/plant.

Table 2 Pooled mean values of genotypes of blackgram

Genotype	PH	DTF	NOBP	DTM	NPPP	NSPP	PL	NCPP	NPPC	1000-SW	SYPP
AZAD-2	54.60	50.78	6.68	85.67	33.31	6.27	4.84	10.39	4.05	47.61	6.51
MASH- 114	61.13	49.78	5.36	85.22	34.43	5.99	5.05	9.97	4.26	40.56	5.97
NU-1	59.78	50.44	4.70	86.34	35.57	5.61	5.10	7.42	4.12	40.85	4.12
PU-07-7	52.34	51.44	6.30	86.45	30.59	5.81	4.31	6.48	3.24	42.65	5.22
PU-10	56.00	47.89	5.79	84.00	32.82	6.28	4.65	6.64	3.83	44.59	6.22
PU-13-05	61.73	49.56	8.53	81.00	35.64	6.79	6.76	8.64	5.67	41.28	8.16
PU-15-2	66.32	49.45	7.88	85.56	42.99	6.99	6.46	10.80	6.20	42.70	8.27
PU-15-21	61.60	44.56	4.81	88.44	30.71	5.98	5.22	9.32	3.78	35.76	4.20
PU-15-23	47.64	47.56	5.13	81.44	39.20	4.98	4.07	10.13	3.68	44.69	5.98
PU-15-26	55.75	45.22	4.17	80.44	40.59	4.85	5.04	9.12	3.83	44.49	5.94
PU-15-28	56.69	50.56	7.50	84.78	41.86	5.98	5.96	9.76	5.42	45.09	6.49
PU-15-29	56.10	46.89	5.51	85.00	36.78	4.77	4.31	8.19	4.74	43.02	4.65
PU-15-30	54.99	45.89	4.67	83.67	32.63	5.54	4.18	8.09	4.07	42.18	6.32
PU-15-31	48.56	47.89	4.68	82.89	36.40	4.57	4.33	7.43	3.79	42.40	6.40
PU-15-32	49.87	44.78	4.68	82.89	36.66	4.82	4.76	8.62	3.87	43.86	5.15
PU-15-34	51.08	46.67	5.97	83.00	36.30	6.07	4.46	6.61	4.24	40.39	5.89
PU-15-35	52.25	46.89	4.72	82.78	42.81	3.74	4.44	9.75	3.77	41.72	6.40
PU-15-40	51.61	48.67	4.43	84.55	38.47	5.21	4.50	8.53	3.53	43.83	5.58
PU-17-4	62.10	50.00	5.20	83.55	37.22	4.49	4.98	8.90	3.35	42.93	5.57
PU-19	59.40	48.56	6.59	82.56	36.24	7.39	6.10	10.54	4.29	42.58	7.79
PU-31	53.26	47.00	6.23	81.22	39.79	6.60	6.21	9.07	4.64	42.39	7.82
PU-35	53.04	49.11	4.91	81.56	38.95	5.26	4.35	10.09	3.91	43.68	6.56
PU-40	57.23	47.89	5.40	84.33	30.15	5.31	4.53	8.36	3.17	44.31	6.11
PU-7	58.71	49.22	5.02	82.56	36.73	4.89	4.44	8.80	3.94	48.48	5.96
PU-8	52.90	49.33	4.81	83.22	38.90	5.67	4.68	10.02	3.90	41.56	7.14
PU-9	56.48	48.78	5.41	82.22	43.87	6.70	5.99	11.27	4.55	43.56	6.13
PU-IPU-2-43	56.93	47.67	4.29	83.11	40.03	3.89	4.92	6.19	4.08	47.92	5.74
PU-KU-99- 21	56.65	47.11	5.25	83.67	32.11	6.14	4.31	10.93	3.28	49.48	6.22
PU-KUG216	62.75	48.67	5.25	85.33	31.66	3.81	4.17	10.50	3.59	44.92	5.37
PU-UPU-97-1	53.56	50.89	5.83	85.00	28.54	4.82	4.95	10.89	3.93	41.79	5.28
Grand Mean	56.03	48.30	5.52	83.75	36.40	5.51	4.94	9.05	4.09	43.38	6.10
Min.	47.64	44.56	4.17	80.44	28.54	3.74	4.07	6.19	3.17	35.76	4.12
Max.	66.32	51.44	8.53	88.44	43.87	7.39	6.76	11.27	6.20	49.48	8.27
SE (m) ±	3.25	1.41	0.53	-	2.54	0.53	0.48	1.25	0.48	2.28	0.57
CD (*P*<0.05)	9.24	4.00	1.51	1.90	7.22	1.51	1.37	-	1.38	-	1.64

PH, Plant height; DTF, Days to 50% flowering; NOBP, Number of branches/plant; DTM, Days to maturity; NPPP, Number of pods/plant; NSPP, Number of seeds/pod; PL, Pod length; NCPP, Number of clusters/plant; NPPC, Number of pods/cluster; 1000-SW, 1000-seed weight (g); SYPP, Seed yield/plant.

to 88.44 days, with poorer performance for 10 genotypes (PU-13-05, PU-15-23, PU-15-26, PU-15-30, PU-15-31, PU-15-32, PU-15-35, PU-9, PU-35), and PU-8, suggesting the early-maturing genotypes. These genotypes are desirable for rainfed conditions due to early maturity. Alike results were also showed by Kumar *et al.* (2021) and Kumar *et al.* (2022) for days to maturity in urdbean and mungbean under rainfed conditions, respectively.

Mean of number of pods/plant ranged from 28.54–43.87 with genotype PU-9 displayed the highest performance, while 15 genotypes revealed greater mean values as compared to the outstanding mean (36.40), aiding in higher-yielding varieties. PU-19 had the greatest number of seeds/pod (7.39). The study found a mean value between 6.19 and11.27 for number of clusters/plant. Genotype PU-9 had the highest mean, while ten genotypes revealed higher means than the average of 9.05. Number of pods/cluster varied from 3.17–6.20. Thousand-seed weight varied among 35.76–49.48 g. The creation of higher yielding cultivars can be helped by greater average performance of 1000 seed weight. Mean value of seed yield/plant revealed that genotype PU-15-2 acquired maximum contribution (8.27 g) while NU-1 was found extremely poor with the lowest contribution (4.12 g). Similar outcomes have been published by Kumar *et al.* (2020) for days to 50% flowering (DTF), plant height (PH), number of branches/plant (NOBP), pod length (PL), number of seeds/pod (NSPP), and seed yield/plant (SYPP).

Present study revealed an important positive correlation of pod length, number of branches/plant, and number of pods/cluster with seed yield/plant indicating their role in developing high-yielding varieties (Fig. 1). Kumar *et al.* (2016) also revealed positive correlation of NOBP and PH with seed yield in lentil. Days to 50% flowering showed highly positive significant correlation with days to maturity. This is helpful in developing early maturing varieties of blackgram. Sridhar *et al.* (2020) in blackgram and Desai *et al.* (2020) in greengram also showed similar results of correlation coefficient in respect of DTF and DTM. All the examined traits had larger phenotypic coefficients of variation than genotypic coefficients of variation (Fig. 2). Similar results were reported by Kumar *et al.* (2017) for plant height, seed yield/plant and 1000 seed weight in chickpea and Kumar *et al.* (2021), Aman *et al.* (2022) and Kumawat *et al.* (2023) for plant height, seed yield/plant and 1000 seed weight in blackgram.

The extent of distinction between GCV and PCV indicates that the environment has played significant part in these traits. Considering the current studies, except for plant height, days to 50% flowering, days to maturity and 1000 seed weight, all the remaining traits had high to modest magnitude of coefficients of variation. Kumar *et al.* (2020) exhibited high PCV for number of branches/plant, pod length and seed yield/plant had a moderate PCV. Characters, viz. number of branches/plant, number of pods/plant, number of seeds/pod, pod length, number of clusters/plant and seed yield/plant demonstrated the potential for direct selection of these variables. In respect of DFL alike outcomes expressed by Hemavathy *et al.* (2015). The magnitude of heritability and

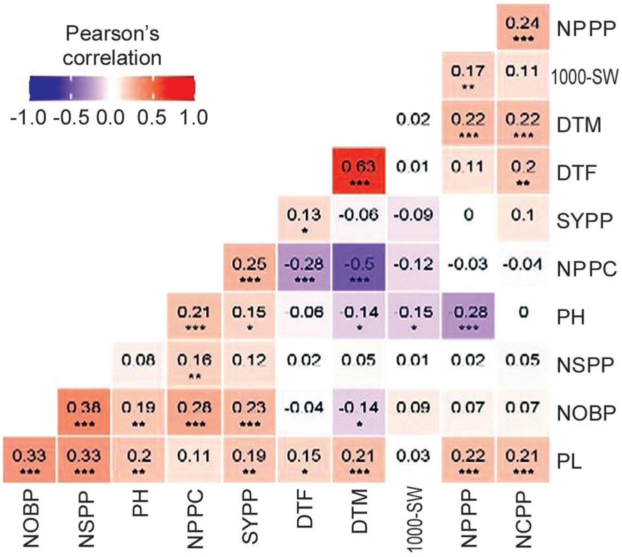
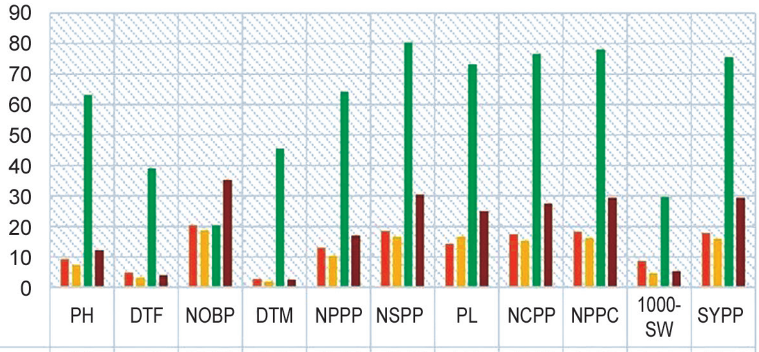


Fig. 1 Correlation coefficient between seed yield/plant and contributing traits.
PH, Plant height; DTF, Days to 50% flowering; DTM, Days to maturity; NPPP, Number of pods/plant; NSPP, Number of seeds/pod; PL, Pod length; NOBP, Number of branches/plant; NCPP, Number of clusters/plant; NPPC, Number of pods/cluster; 1000-SW, 1000-seed weight (g); SYPP; Seed yield/plant.



	PH	DTF	NOBP	DTM	NPPP	NSPP	PL	NCPP	NPPC	1000-SW	SYPP
🟥 PCV (%)	9,2	4,9	20,27	2,73	12,91	18.45	14,2	17,44	18,27	8,63	17,88
🟨 GCV (%)	7,35	3,05	18,6	1,84	10,34	16.52	16,59	15,26	16,13	4,7	15,94
🟩 Heritability (%)	63,17	38,88	20,27	45,38	64,17	80.19	73,22	76,56	78,01	29,61	75,52
🟫 GA (%) as mean	12,08	3,92	35,16	2,55	17,06	30.48	25,03	27,51	29,36	5,26	29,29

Fig. 2 Estimates of genetic variability of blackgram.
PH, Plant height; DTF, Days to 50% flowering; NOBP, Number of branches/plant; DTM, Days to maturity; NPPP, Number of pods/plant; NSPP, Number of seeds/pod; NCPP, Number of clusters/plant; NPPC, Number of pods/cluster; 1000-SW (g), 1000-seed weight (g); SYPP; Seed yield/plant; PCV, Phenotypic coefficient of variation; GCV, Genotypic coefficient of variation; GA, Genetic advance mean.

genetics advance as (%) of mean for 11 variables under study showed in Fig. 2. For the traits, viz. NSPP, PL, NCPP, NPPC, and SYPP, higher h^2(bs) and high genetic advance as (%) of mean were found in the present research utilizing pooled average analysis. Its high heritability and high genetic advance demonstrated that additive gene effects were responsible for the heritability and that phenotypic selection might be successful in the initial generations. Some traits including plant height and number of branches/plant revealed high h^2 with moderate genetic advance as (%) of mean. In this situation, early-stage selection may be advantageous. Kumar and Singh (2017) reported high heritability with high genetic advance for plant height and number of branches/ plant. Low heritability estimates were paired with low genetic advance as per cent mean detected for 1000-seed weight suggested that selection would be ineffectual because environmental factors strongly influenced these variables.

SUMMARY

Analysis of variance for 11 traits under investigation revealed significant variability among the genotypes. This indicated an extensive range of genetic variability existed among the genotypes of blackgram. On the basis of higher mean performance than general mean, genotype PU-19 reported higher seed yield/plant along with higher number of seeds/pod, number of clusters/plant, number of pods/ cluster. Hence, recommended for the enhancement of area under this variety particular in rainfed ecology. On pooled basis seed yield/plant had significant correlation with all yield contributors except plant height. Number of seeds/pod, number of clusters/plant, number of pods/cluster and seed yield/plant signified high heritability as well as high genetic advance as percentage of mean indicated the presence of additive gene action, while plant height and number of pods/ plant exhibited modest heritability as well as modest genetic advance as percentage of mean. Consequently, suggesting the presence of additive gene action and phenotypic selection for such traits may be useful in the future of blackgram improvement programs.

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