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Variability and association studies in advanced double cross entries of Blackgram (*Vigna mungo* L.)

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Abstract
The aim of this study was to evaluate genetic variability, path and correlation analysis among 187 double cross pyramided lines of blackgram (*Vigna mungo* L.) with a focus on yield and its related traits. The variability analysis found that PCV was greater than GCV for all attributes indicated that notable influence of the environment on these attributes. Variability analysis revealed that the traits seed yield/plant, number of clusters/plant, number of pods/plant, number of seeds/pod and number of branches/plant which exhibited both high heritability and GAM. This suggests that these traits are governed by additive gene action, making them ideal options for selection to enhance yield in blackgram. The results of path and correlation analysis emphasize the significance of traits like the number of clusters/plant, the number of pods/cluster and the number of pods/plant. These traits are identified as primary selection criteria for increasing yield in urdbean.

Keywords: Variability, path analysis, double cross, correlation, Blackgram

Introduction

Leguminous crops, especially pulses that produce edible grains, have seen a resurgence in the past decade as a means to tackle global agricultural challenges. In addition to providing nutritional benefits, legumes play a crucial role in enriching soil fertility (Stagnari *et al.* 2017) [22]. Blackgram (*Vigna mungo* L.), a notable short-duration pulse crop, is widely grown in India. This crop is self-pollinated and a member of the Fabaceae family. India plays a significant role in global pulse production, contributing approximately 25% of the total production, with 33% of the world's pulse acreage and a consumption rate of around 27% (Hadimani *et al.,* 2019) [7]. The states of Uttar Pradesh, Andhra Pradesh and Madhya Pradesh are key contributors to the cultivation of blackgram. In the year 2021-22, blackgram was cultivated across 4.63 million hectares in India, resulting in a total production of 2.78 million tonnes, with an average productivity of approximately 599 kilograms per hectare (Indiastat.com). Despite its potential, blackgram often faces challenges leading to low productivity and yield. These challenges include limited genetic variability in the available genotypes. Variability estimates serve as valuable tools for predicting genetic progress when different levels of selection intensity are applied. When combined with high genetic advance, high heritability estimates provide more trustworthy selection criteria than heritability estimate alone (Johnson *et al.*, 1955) [9]. Evaluating variability in combination with heritability and GAM offers insights into the potential improvement of a trait through selective breeding. Association studies are valuable tools for understanding how different traits influence yield, revealing both positive and negative associations. These studies primarily highlight the relationships between yield and its related traits. Correlation coefficient estimates play a crucial role in identifying and prioritizing traits of substantial significance while excluding those of minimal or negligible importance during the selection process. Path analysis is a valuable complement to correlation studies as it breaks down the correlation coefficients into its distinct indirect and direct effects (Dewey and Lu, 1959) [5]. This helps in understanding the specific contributions of each trait to the overall outcome, providing a more detailed view of trait interactions and their impact on seed yield. Hence, the study was conducted on advanced double cross entries of blackgram to explore genetic variability, path and correlation studies of different characteristics contributing to the yield of blackgram.

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Materials and Methods

The current study was carried out at the National Pulses Research Centre, Vamban, employing a Randomised Block Design with two replications during the season *Rabi* 2022-23. The breeding material comprised of 187 advanced lines obtained through double crosses along with their parents as check varieties. Table 1 provides information about the parentage of these advanced double cross lines. The planting was done with a spacing of 30 x 10 cm. To maintain the crop stand, the prescribed agronomic practises were followed. The data on different biometrical traits *viz.*, days to 50% flowering, plant height (cm), number of branches/plant, number of clusters/plant, number of pods/cluster, number of pods/plant, pod length (cm), number of seeds/pod, hundred seed weight (g), powdery mildew disease score and seed yield/plant (g) were recorded from three randomly selected plants from each entry/replication. The analysis involved using the mean value of three selected plants. The powdery mildew disease scores were assessed on the 60th day after sowing (DAS) using the score chart (Table 6) provided by the All-India Co-ordinated Research Project (AICRP) on MULLaRP (Alice and Nadarajan, 2007) [1]. The Percent Disease Index, as described by Wheeler (1969) [26], was calculated based on the scoring chart, and entries were graded according to their disease index scores. The analysis of variance was carried out following the method outlined by Panse and Sukhatme (1954) [14]. To assess genetic variability, parameters such as the Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were computed in accordance with the recommendations made by Burton (1952) [3], using the results obtained from the analysis of variance. The GCV and PCV estimates were classified based on the criteria provided by Sivasubramanian and Madhavamenon (1973) [20]. For estimating heritability and genetic advance, the methods suggested by Lush (1940) [12] and Johnson *et al.* (1995) [9] were employed, respectively. The heritability values were categorized following the guidelines presented by Robinson *et al.* (1949) [16]. Additionally, the range of genetic advance as a per cent of the mean was categorized as mentioned by Johnson *et al.* (1955) [9]. The analysis of correlations and path coefficients was conducted using the TNAUSTAT software (Manivannan, 2014) [13]. The direct and indirect effects were categorized according to the scale specified by Lenka and Misra (1973) [11].

Results and Discussion

Variability studies

The results from the Analysis of Variance (ANOVA) revealed significant variations among the double cross entries for all the characteristics under investigation indicating substantial degree of genetic variation present among the experimental material (Table 2). This suggests that there is an ideal chance of identifying genotypes with high yielding potential. These findings were consistent with the findings of Sivakumar *et al.* (2022) [19] and Deekshith *et al.* (2022) [4].

Table 3 displays the mean values for each trait, as well as the variation range and assessments of genetic factors such as PCV, GCV, heritability, and genetic advance per cent of mean. It is also depicted visually in Figures 1 and Figure 2. The calculated PCV values exceeded the GCV values for all the traits studied. This trend was similar across all traits, demonstrating that environment had an impact on these characteristics. These findings align with reports of Gomathi

et al. (2023) [6]. The traits *viz.*, number of branches/plant (20.09), number of clusters/plant (21.45), number of pods/plant (27.21), Powdery mildew disease score (34.12) and seed yield/plant (32.74) exhibited notably high PCV estimates. Among these, the number of pods/plant (24.96), powdery mildew disease score (20.02) and seed yield/plant (31.71) also displayed substantial genotypic coefficient of variation (GCV) estimates. Plant height (11.39, 10.50) and number of seeds/pod (12.78, 11.95) had moderate PCV and GCV estimates. Further, selection of these characteristics would be effective based on the heritable nature of these traits. Number of pods/cluster (15.06, 9.32) and pod length (10.58, 9.25) displayed moderate PCV and low GCV estimates. Low PCV and GCV estimates were recorded for the traits hundred seed weight (6.79, 6.24) and days to 50% flowering (2.07, 2.88). These traits were significantly affected by environmental factors, suggesting that selection for these characters might be ineffective.

Combination of high heritability and high GAM was recorded for number of branches/plant (77.55, 32.10), number of clusters/plant (83.05, 36.69), number of pods/plant (84.18, 47.18), number of seeds/pod (87.42, 23.01) and seed yield/plant (93.79, 63.26). This indicates that the impact of the environment on the expression of these traits is relatively low, and these traits are primarily controlled by additive gene action in their inheritance. Therefore, prioritizing these traits in a breeding program has the potential to improve yield. This observation is similar with the findings reported by Patidar *et al.* (2018) [15] and Blessy *et al.* (2018) [2]. High heritability and moderate GAM were observed for plant height (85.09, 19.96), pod length (76.39, 16.66) and hundred seed weight (84.5, 11.81). These findings align with the results reported by Kumar *et al.* (2015) [10]. Moderate heritability with moderate GAM was noted for number of pods/cluster (38.29, 11.88). Days to 50% flowering (87.52, 5.54) had high heritability with low GAM. This observation aligns with the results reported by Teja *et al.* (2021) [25] and implies that environmental factors play a significant role in influencing the expression of this trait, making selection ineffective.

Correlation studies

Correlation coefficients among different characteristics were displayed in Table 4. The seed yield/plant exhibited significant and positive correlation with all characteristics, except powdery mildew score, which shows non-significant association (0.108). These traits include days to 50% flowering (0.181), plant height (0.435), number of branches/plant (0.151), number of clusters/plant (0.827), number of pods/cluster (0.519), number of pods/plant (0.911), pod length (0.415), number of seeds/pod (0.575) and hundred seed weight (0.364). This aligns with the results of prior investigations carried out by Gomathi *et al.* (2023) [6] and Surendhar *et al.* (2023) [23]. This demonstrates that there was a significant association between the mentioned traits and seed yield/plant, indicating that these traits might be taken into account to increase seed yield. The alignment with previous research adds further credibility to these findings.

Among the yield components number of clusters/plant had significant positive correlation with number of pods/plant (0.905). The magnitude of this correlation was the highest among the yield components studied. Number of pods/plant had significant and positive association with all the traits except days to 50% flowering, number of branches/plant and

powdery mildew disease score. These findings closely resemble the research findings reported by Sathees *et al.* (2019) [17] and Sushmitharaj *et al.* (2018) [24]. Hence selection based on number of clusters/plant and number of pods/plant would be effective to improve the yield. The powdery mildew disease score showed significant positive associations with the number of branches/plant (0.299), the number of pods/cluster (0.239), and the number of seeds/pod (0.243). However, for remaining traits powdery mildew disease score had negligible associations.

Path analysis

Path analysis dissects the correlation coefficients to provide insights into the specific contributions of independent factors to yield. In this study, seed yield/plant was treated as the dependent variable, while the other traits were regarded as independent variables. Direct and indirect effects between yield and other yield related characters as revealed by the path analysis were tabulated in the table 5.

Number of pods/plant exhibited a high positive direct effect on seed yield, with a coefficient of 0.758. This suggests that there is significant potential for enhancing seed yield through the selection of this trait. The importance of this feature for yield improvement was further supported by Gomathi *et al.* (2023) [6], who also showed a comparable high positive direct effect of number of pods/plant on seed yield/plant in their study. Moderate positive direct effect was recorded for the trait number of seeds/pod (0.286). The traits days to 50% flowering, plant height, number of branches/plant, number of clusters/plant, pod length, powdery mildew disease score and hundred seed weight were found to have negligible direct effects on seed yield/plant.

Among the yield components, number of clusters/plant (0.686) and number of pods/cluster (0.360) had high positive indirect effect through number of pods/plant on seed yield/plant. Sathya *et al.* (2018) [18] and Sowmyasree *et al.* (2018) [21] also documented a significant positive indirect effect on the number of clusters/plant through the number of pods/plant on seed yield/plant. This suggests that the number of pods/plant may indirectly influence the seed yield, as supported by their research findings. The traits *viz.*, plant height (0.284), pod length (0.265), number of seeds/pod (0.277) and hundred seed weight (0.254) had moderate positive indirect effect on seed yield through number of pods/plant. Days to 50% flowering had low positive indirect effect *via* number of pods/plant (0.109) on seed yield.

Table 1: Genetic materials used in the investigation (Parentage details of the double cross pyramided entries)

S. No.	Parentage	No. of Entries	Entries
1	(ADT 3 x TU 68) x (VBN 4 x LBG 17)	35	VBG 22 -251, VBG 22 -255, VBG 22 -256, VBG 22 -257, VBG 22 -260, VBG 22 -264, VBG 22 -275, VBG 22 -277, VBG 22 -284, VBG 22 -288, VBG 22 -290, VBG 22 -291, VBG 22 -293, VBG 22 -295, VBG 22 -296, VBG 22 -301, VBG 22 -304, VBG 22 -305, VBG 22 -306, VBG 22 -308, VBG 22 -309, VBG 22 -310, VBG 22 -312, VBG 22 -313, VBG 22 -314, VBG 22 -315, VBG 22 -316, VBG 22 -317, VBG 22 -318, VBG 22 -319, VBG 22 -320, VBG 22 -322, VBG 22 -323, VBG 22 -325 and VBG 22 -326
2	(MDU 1 x TU 68) x (VBN 4 x LBG 17)	58	VBG 22 -328, VBG 22 -330, VBG 22 -331, VBG 22 -333, VBG 22 -335, VBG 22 -336, VBG 22 -337, VBG 22 -338, VBG 22 -339, VBG 22 -340, VBG 22 -341, VBG 22 -342, VBG 22 -343, VBG 22 -344, VBG 22 -345, VBG 22 -346, VBG 22 -347, VBG 22 -348, VBG 22 -349, VBG 22 -350, VBG 22 -351, VBG 22 -353, VBG 22 -354, VBG 22 -355, VBG 22 -356, VBG 22 -357, VBG 22 -358, VBG 22 -359, VBG 22 -360, VBG 22 -362, VBG 22 -363, VBG 22 -364, VBG 22 -366, VBG 22 -367, VBG 22 -368, VBG 22 -371, VBG 22 -372, VBG 22 -373, VBG 22 -374, VBG 22 -375, VBG 22 -376, VBG 22 -377, VBG 22 -378, VBG 22 -379, VBG 22 -380, VBG 22 -381, VBG 22 -382, VBG 22 -383, VBG 22 -385, VBG 22 -390, VBG 22 -394, VBG 22 -396, VBG 22 -401, VBG 22 -402, VBG 22 -403, VBG 22 -404, VBG 22 -405 and VBG 22 -406
3	(MDU 1 x MASH 1008) x (VBN 4 x LBG 17)	42	VBG 22 -408, VBG 22 -410, VBG 22 -411, VBG 22 -413, VBG 22 -416, VBG 22 -417, VBG 22 -418, VBG 22 -420, VBG 22 -421, VBG 22 -422, VBG 22 -423, VBG 22 -424, VBG 22 -425, VBG 22 -426, VBG 22 -427, VBG 22 -428, VBG 22 -429, VBG 22 -430, VBG 22 -431, VBG 22 -432, VBG 22 -433, VBG 22 -434, VBG 22 -436, VBG 22 -438, VBG 22 -439, VBG 22 -440, VBG 22 -441, VBG 22 -442, VBG 22 -443, VBG 22 -444, VBG 22 -446, VBG 22 -447, VBG 22 -448, VBG 22 -449, VBG 22 -450, VBG 22 -451, VBG 22 -452, VBG 22 -526, VBG 22 -527, VBG 22 -528, VBG 22 -529 and VBG 22 -530
4	(MDU 1 x MASH 1008) x (ADT 5 x TU 68)	25	VBG 22 -454, VBG 22 -455, VBG 22 -456, VBG 22 -457, VBG 22 -458, VBG 22 -459, VBG 22 -460, VBG 22 -462, VBG 22 -463, VBG 22 -467, VBG 22 -468, VBG 22 -469, VBG 22 -471, VBG 22 -472, VBG 22 -473, VBG 22 -474, VBG 22 -475, VBG 22 -476, VBG 22 -477, VBG 22 -479, VBG 22 -480, VBG 22 -481, VBG 22 -482, VBG 22 -483 and VBG 22 -484
5	(VBN 4 x CO 5) x (MDU 1 x TU 68)	27	VBG 22 -486, VBG 22 -488, VBG 22 -489, VBG 22 -490, VBG 22 -491, VBG 22 -493, VBG 22 -494, VBG 22 -495, VBG 22 -496, VBG 22 -497, VBG 22 -498, VBG 22 -499, VBG 22 -500, VBG 22 -501, VBG 22 -502, VBG 22 -503, VBG 22 -505, VBG 22 -506, VBG 22 -508, VBG 22 -509, VBG 22 -510, VBG 22 -511, VBG 22 -514, VBG 22 -516, VBG 22 -523, VBG 22 -524 and VBG 22 -525

Table 2: Analysis of variance (ANOVA) for various characteristics of advanced double cross entries of blackgram

Source of Variation	DF	Mean sum of squares										
		Days to 50% flowering	Plant height (cm)	Number of branches/ plant	Number of clusters /plant	Number of pods/cluster	Number of pods/plant	Pod length (cm)	Number of seeds/pod	Hundred seed weight (g)	Powdery mildew disease score	Seed yield /plant (g)
Replication	1	0.21	0.38	0.005	0.33	0.13	3.55	0.003	0.002	0.002	1.41	0.07
Treatment	186	2.93*	32.41*	0.40*	3.91*	0.16*	28.81*	0.33*	0.99*	0.11 *	0.51*	1.66*
Error	186	0.19	2.61	0.05	0.36	0.07	2.47	0.04	0.06	0.01	0.25	0.05

* - Significant at 5% level

Table 3: Variability estimates for the entries of blackgram

Characters	Mean	Range	PCV (%)	GCV (%)	h²(%)	GAM (%)
Days to 50% flowering	40.62	37.00 to 45.00	3.07	2.88	87.52	5.54
Plant height (cm)	36.67	26.92 to 46.17	11.39	10.5	85.09	19.96
Number of branches/plant	2.35	1.17 to 3.33	20.09	17.7	77.55	32.10
Number of clusters/plant	6.83	4.67 to 11.50	21.45	19.54	83.05	36.69
Number of pods/cluster	2.29	1.85 to 3.32	15.06	9.32	38.29	11.88
Number of pods/plant	14.69	8.00 to 26.00	27.21	24.96	84.18	47.18
Pod length (cm)	4.14	3.19 to 5.50	10.58	9.25	76.39	16.66
Number of seeds/pod	5.74	4.33 to 7.07	12.78	11.95	87.42	23.01
Hundred seed weight (g)	3.76	3.33 to 4.49	6.79	6.24	84.5	11.81
Powdery mildew disease score	1.81	1.00 to 3.50	34.12	20.02	34.41	24.19
Seed yield/plant (g)	2.86	1.47 to 5.76	32.74	31.71	93.79	63.26

Table 4: Correlation coefficients of seed yield and related traits in blackgram

Characters	DFF	PH (cm)	NOBPP	NOCPP	NOPPC	NOPPP	PL (cm)	NOSPP	HSW (g)	PM Score	SYPP (g)
DFF	1	0.226*	0.165*	0.136	0.047	0.143	0.092	0.188*	0.218*	0.030	0.181*
PH (cm)		1	0.439*	0.379*	0.325*	0.374*	0.366*	0.435*	0.402*	0.109	0.435*
NOBPP			1	0.042	0.292*	0.065	0.132	0.261*	0.028	0.299*	0.151*
NOCPP				1	0.291*	0.905*	0.344*	0.355*	0.310*	0.020	0.827*
NOPPC					1	0.475*	0.438*	0.326*	0.240*	0.239*	0.519*
NOPPP						1	0.350*	0.365*	0.335*	0.077	0.911*
PL (cm)							1	0.490*	0.383*	-0.001	0.415*
NOSPP								1	0.308*	0.243*	0.575*
HSW (g)									1	-0.098	0.364*
PM score										1	0.108
DFF											1

*- significant at 5% level

DFF - Days to 50% flowering; PH (cm) - Plant height (cm); NOBPP - Number of branches/plant; NOCPP - Number of clusters/plant; NOPPC - Number of pods/cluster; NOPPP - Number of pods/plant; PL (cm) - Pod length (cm); NOSPP - Number of seeds/pod; HSW (g) - Hundred seed weight (g); PM score – Powdery mildew disease score; SYPP (g) - Seed yield/plant (g)

Table 5: Genotypic path analysis displaying direct and indirect effect of various characteristics with seed yield/plant (g)

Characters	DFF	PH (cm)	NOBPP	NOCPP	NOPPC	NOPPP	PL (cm)	NOSPP	HSW (g)	PM Score	SYPP (g)
DFF	0.014	-0.001	0.003	0.004	0.003	0.109	-0.004	0.054	0.001	-0.001	0.181
PH (cm)	0.003	-0.004	0.009	0.011	0.026	0.284	-0.014	0.125	0.001	-0.005	0.435
NOBPP	0.002	-0.002	0.020	0.001	0.023	0.050	-0.005	0.075	0.000	-0.013	0.151
NOCPP	0.002	-0.001	0.001	0.028	0.023	0.686	-0.013	0.102	0.001	-0.001	0.827
NOPPC	0.001	-0.001	0.006	0.008	0.078	0.360	-0.017	0.093	0.001	-0.011	0.519
NOPPP	0.002	-0.001	0.001	0.026	0.037	0.758	-0.013	0.104	0.001	-0.004	0.911
PL (cm)	0.001	-0.001	0.003	0.010	0.034	0.265	-0.038	0.140	0.001	0.000	0.415
NOSPP	0.003	-0.002	0.005	0.010	0.026	0.277	-0.019	0.286	0.001	-0.011	0.575
HSW (g)	0.003	-0.001	0.001	0.009	0.019	0.254	-0.015	0.088	0.003	0.004	0.364
PM score	0.000	0.000	0.006	0.001	0.019	0.059	0.000	0.070	0.000	-0.045	0.108

Residue = 0.311

DFF - Days to 50% flowering; PH (cm) - Plant height (cm); NOBPP - Number of branches/plant; NOCPP - Number of clusters/plant; NOPPC - Number of pods/cluster; NOPPP - Number of pods/plant; PL (cm) - Pod length (cm); NOSPP - Number of seeds/pod; HSW (g) - Hundred seed weight (g); PM score – Powdery mildew disease score; SYPP (g) - Seed yield/plant (g)

Table 6: Disease score chart for powdery mildew given by AICRP MULLaRP

| Grade	Description	Reaction
0	Plants that do not have infection for the disease	Free (F)
1	Plants showing traces to 10% infection on leaves, stems free from disease.	Resistant (R)
2	Slight infection with thin coating of powdery growth on leaves covering 10.1 - 25% leaf area, slight infection on stem and pods usually free.	Moderately Resistant (MR)
3	Dense powdery coating on leaves covering 25.1-50% leaf area, moderate infection on pods.	Moderately Susceptible (MS)
4	Dense powdery coating covering 50.1-75% area, stems heavily and pods moderately infected. Infected portion turns greyish.	Susceptible (S)
5	Severe infection with dense powdery growth covering 75% area of the whole plant including pods, stems etc. resulting in premature defoliation and drying.	Highly Susceptible (HS)
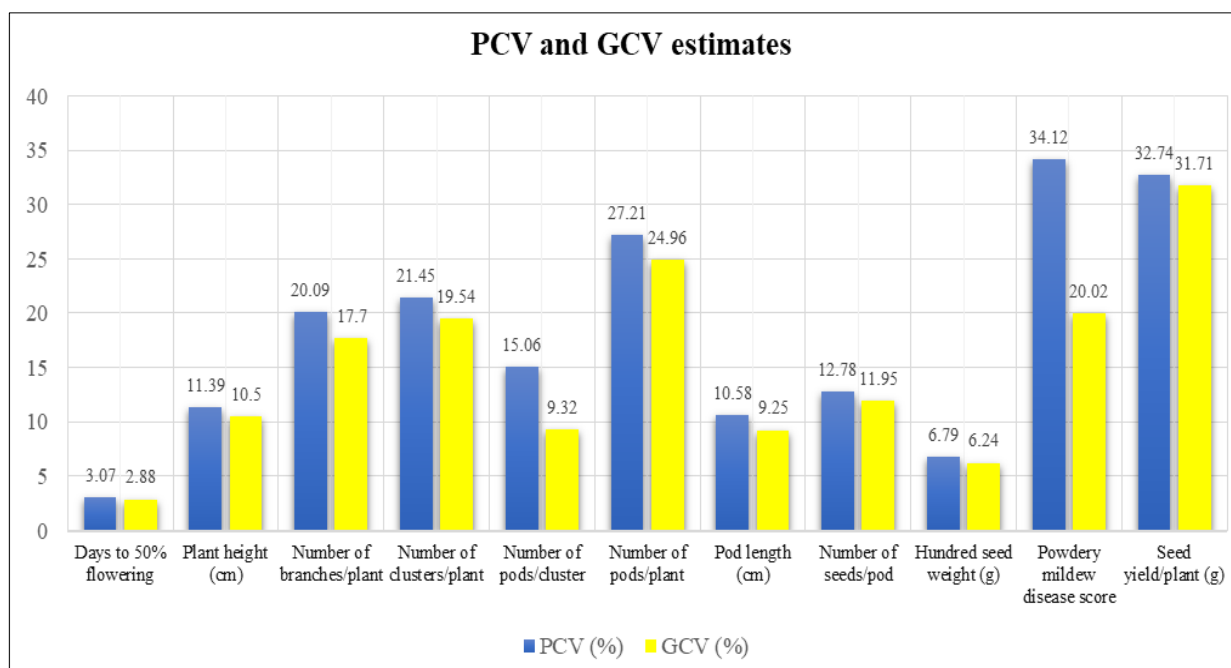
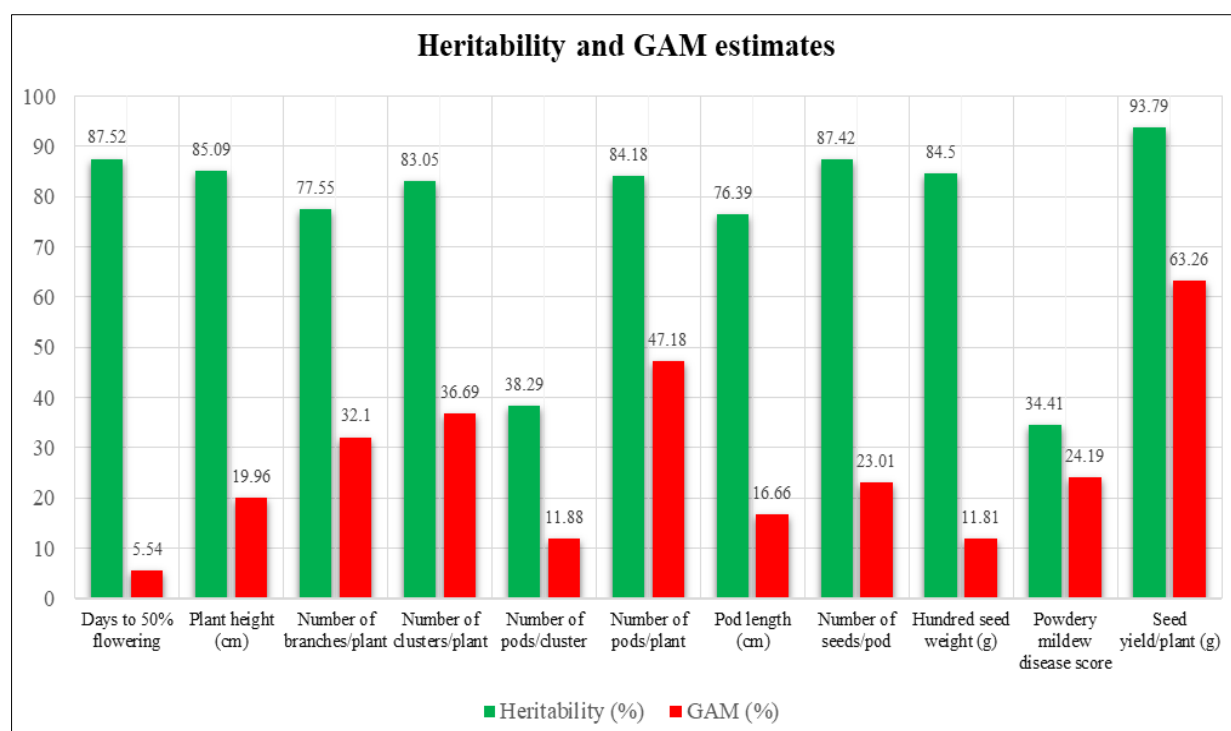**Fig 1:** PCV and GCV estimates for yield and related characteristics

Fig 2: Heritability and GAM estimates for yield and related characteristics

Conclusion

In this study, the variability analysis revealed that seed yield/plant, number of clusters/plant, number of pods/plant, number of seeds/pod and number of branches/plant displayed both high heritability and high GAM. This suggests that these traits are governed by additive gene action. Consequently, selection of these traits holds the potential to enhance yield in blackgram. The results of path and correlation analysis suggest that particular attention should be directed towards the number of clusters/plant, the number of pods/cluster and the number of pods/plant. These traits can therefore be viewed as the main selection factors for increasing yield in blackgram.

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