



## STUDIES ON GENETIC VARIABILITY AND CHARACTER ASSOCIATION FOR YIELD AND ITS ATTRIBUTES IN BLACKGRAM [*Vigna mungo* (L.) Hepper]

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### ABSTRACT

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An experiment was carried out to estimate the genetic parameters such as variability, heritability and genetic advance, character association and path analysis for eleven quantitative characters viz., days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, hundred seed weight, harvest index, SPAD chlorophyll meter reading, protein content and seed yield per plant in 42 genotypes of blackgram [*Vigna mungo* (L.) Hepper]. The genotypic coefficient of variation for all characters studies were less than the phenotypic coefficient of variation indicating the interaction of genotype with the environment. High heritability coupled with high genetic advance as per cent of mean was observed for days to maturity, number of plant height, number of clusters per plant, number of pods per plant and seed yield per plant. Association studies revealed that, days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant and hundred seed weight showed positive and significant correlation with seed yield per plant both at the genotypic and phenotypic level. Path analysis studies revealed that clusters per plant, pods per plant and 100-seed weight had positive and high direct effects on seed yield per plant.

**KEYWORDS:** Genetic variability, heritability, genetic advance, character association, path analysis.

## INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper], is one of the nutritious pulse crops, popularly known as urdbean. It is an important short duration pulse crop and self pollinated grain legume grown in many parts of India. It is mainly grown for its dry beans that are rich in proteins with high lysine content which is deficient in cereal grains. This crop is grown in cropping systems as a mixed crop, catch crop, sequential crop besides being grown as a sole crop under residual soil moisture conditions after the harvest of rice and also before and after the harvest of other summer crops under semi irrigated and dryland conditions. The productivity of pulse crops is very low as compared to cereals, the reason being growing of the crop in less fertile soil with less inputs and unavailability of cultivars with high yield potential adapted to local conditions. Hence, the selection for yield along with other contributing characters should be taken into account. For improving the seed yield, studies on genetic variability of important traits responsible for increasing the yield is highly necessary. Knowledge on heritability and genetic advance of the character indicate the scope for improvement of a trait through selection. Heritability estimates along with

genetic advance are also helpful in predicting the gain under selection. To accumulate optimum contribution of yield contributing characters, it is essential to know the correlation of various characters along with path coefficients. The objective of the present study was to determine the variability parameters along with correlation and path analysis to understand the mode of inheritance and degree and direction of association of different yield component traits with the seed yield.

## MATERIAL AND METHODS

The present investigation was carried out during *rabi*, 2017 at dry land farm of Regional Agricultural Research Station, Tirupati. The experimental material comprised of 42 blackgram genotypes which were raised in Randomised Block Design, each entry being sown in three Randomised Block Design, each entry being sown in three rows of 4 m length with a spacing of 30 × 10 cm. The package of practices recommended for the crop was followed. Eleven traits viz., days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, hundred seed weight, harvest index, SPAD chlorophyll meter reading, protein content and seed yield per plant were recorded from randomly selected plants in each

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of the genotypes per replication, except days to 50 per cent flowering and days to maturity which were recorded on plot basis. The statistical analysis for variance was worked out according to Panse and Sukhatme (1961). Phenotypic and Genotypic coefficients of variation were calculated based on the method advocated by Burton (1952). Heritability, Genetic advance as per cent of mean and correlation coefficients were estimated as per the formula given by Johnson *et al.* (1955). The path coefficient analysis was worked as suggested by Dewey and Lu (1959).

## RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the genotypes for all the characters studied (Table 1) which gives the evidence of sufficient variability among the genotypes. The estimates of phenotypic coefficient of variation were higher than the genotypic coefficient of variation (Table 2) indicating the influence of environment in governing the characters. Maximum estimate of phenotypic coefficient of variation was registered for seed yield per plant (25.94 %) followed by clusters per plant (25.76 %) and primary branches per plant (25.41) suggesting the presence of sufficient phenotypic variability for these traits. Low estimates of phenotypic coefficient of variation was recorded for days to 50 per cent flowering (7.54) , harvest index (6.07 %) and protein content (5.20 %). These results were in accordance with Kumar *et al.* (2015) for seed yield per plant and Patel *et al.* (2014) for clusters per plant. Quantitative characters are influenced more by the environment, obstructing the transmission of the phenotype observed to the next generation. So, study on the heritable portion of the variability is necessary. Heritability is a good index of characters from parents to off springs and helps as a tool for selection of elite genotypes. In the present study, highest heritability was recorded for days to maturity (99.81 %) followed by days to 50 % flowering (98.72 %), plant height (97.91%), 100 seed weight (90.64 %), harvest index (83.90 %), SPAD chlorophyll meter reading (78.75 %), clusters per plant (67.67 %), pods per plant (67.46 %) and seed yield per plant (63.24 %). High heritability alone is not sufficient enough to exercise selection unless the information is accompanied with substantial amount of genetic

advance. High heritability coupled with high genetic advance as per cent of mean was recorded for days to maturity, plant height, clusters per plant, pods per plant and seed yield per plant indicating the importance of additive gene action in governing the inheritance of these traits. This suggests that most likely the heritability is due to additive gene effects and hence selection may be effective for these characters. It may be suggested that for additive effects pedigree or modified pedigree method of selection is followed. These results were in agreement with Sharma *et al.* (2006), Rahim *et al.* (2010) and Patidar *et al.* (2018).

Genotypic correlations were higher than the phenotypic correlations (Table 3) for most of the characters which can be explained due to the masking or modifying effects of environment on genetic association between characters. In the present investigation, seed yield per plant recorded high significant and positive association with clusters per plant ( $r_p = 0.709^{**}$  and  $r_g = 0.757^{**}$ ), followed by plant height ( $r_p = 0.466^{**}$  and  $r_g = 0.605^{**}$ ), number of pods per plant ( $r_p = 0.613^{**}$  and  $r_g = 0.572^{**}$ ) and days to maturity ( $r_p = 0.409^{**}$  and  $r_g = 0.515^{**}$ ). These results were in accordance with the findings of Umadevi and Ganesan (2005), Shivade *et al.* (2011) and Mathivathana *et al.* (2015). Hence, these characters can be utilized in indirect selection so as to improve the seed yield per plant. Path coefficient analysis revealed that number of clusters per plant ( $P = 0.4652$  and  $G = 0.6288$ ), pods per plant ( $P = 0.3851$  and  $G = 0.2916$ ) and 100 seed weight ( $P = 0.3734$  and  $G = 0.4221$ ) (Table 4, Fig 1 and Fig 2) showed true relationship with seed yield per plant by plant establishing significant and positive direct effects both at the genotypic and phenotypic level. These results were similar with that of Bharti *et al.* (2014) and Bandi *et al.* (2018). The residual effect was 0.578, indicating that along with the present characters some more characters like pod length, seeds per pod, main stem bearing should be taken into consideration while formulating selection strategies for yield improvement.

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### CONCLUSION

The present investigation registered high heritability along with high genetic advance as per cent of mean for days to maturity, plant height, clusters per plant, pods per plant and seed yield per plant suggesting that these characters should be given top priority for effective selection. Considering the nature and magnitude of character association and their direct and indirect effects it can be concluded that the improvement in seed yield is possible through simultaneous manifestation of clusters per plant, pods per plant and 100-seed weight.

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**Table 1 Analysis of variance for physiological, yield and its component traits in blackgram**

S.No	Characters	Mean sum of squares		
		Replications df: 2	Treatments df: 41	Error df: 82
1	Days to 50 per cent flowering	0.10	23.94**	0.10
2	Days to maturity	0.01	198.93**	0.01
3	Plant height	0.18	191.64**	1.36
4	Primary branches per plant	2.77	0.72**	0.14
5	Clusters per plant	7.68	10.95**	1.50
6	Pods per plant	121.72	148.83**	20.62
7	100 seed weight	0.08	0.58**	0.02
8	Harvest Index	0.26	5.37**	0.29
9	SCMR	14.44	24.71**	2.04
10	Protein per cent	0.07	0.11**	0.04
11	Seed yield per plant	17.29	13.63**	2.21

\*, \*\* Significant at 5 % and 1 % level, respectively

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Table 2. Mean, Range, Coefficient of variation, Heritability and Genetic advance for eleven quantitative characters in Blackgram

Sl. No	Characters	Mean	Range		Variance		Coefficient of variation		Heritability (Broad Sense) (%)	Genetic Advance (GA)	Genetic Advance as Per cent of mean (%)
			Min	Max	Genotypic	Phenotypic	Genotypic (%)	Phenotypic (%)			
1	Days to 50 per cent flowering	37.60	33.00	45.00	7.94	8.05	7.50	7.54	98.72	5.77	15.34
2	Days to maturity	74.16	65.00	90.00	66.27	66.39	10.97	10.99	99.81	16.73	22.57
3	Plant height (cm)	22.23	11.10	55.63	63.43	64.78	35.82	36.20	97.91	16.23	73.02
4	Primary branches per plant (no.)	2.25	1.00	3.00	0.19	0.33	19.45	25.41	58.62	0.69	30.68
5	Clusters per plant (no.)	8.37	5.33	12.66	3.17	4.65	21.19	25.76	67.67	3.01	35.91
6	Pods per plant (no.)	31.85	13.67	45.33	42.74	63.36	20.53	24.99	67.46	11.06	34.73
7	100 seed weight (g)	5.13	4.13	6.20	0.19	0.21	8.27	8.68	90.64	0.83	16.21
8	Harvest Index (%)	36.56	30.00	39.33	4.13	4.93	5.56	6.07	83.90	3.83	10.49
9	SCMR	39.75	34.60	44.93	7.56	9.60	6.92	7.79	78.75	5.03	12.64
10	Protein content (%)	21.55	17.80	25.33	0.02	0.06	3.10	5.20	35.68	0.18	3.82
11	Seed yield per plant (g)	9.45	5.23	13.99	3.80	6.01	20.63	25.94	63.24	3.19	33.80

Table 3. Phenotypic ( $r_p$ ) and Genotypic ( $r_g$ ) correlation coefficients among eleven yield attributing characters in blackgram

Characters		Days to maturity	Plant height	Branches per plant	Clusters per plant	Pods per plant	100 seed weight	Harvest index	SCMR	Protein content (%)	Seed yld per plant
Days to 50 per cent flowering	rp	0.695**	0.579**	0.329**	0.255**	0.143	0.427**	0.096	0.056	0.131	0.345**
	rg	0.700**	0.588**	0.429**	0.310**	0.166	0.451**	0.103	0.068	0.221*	0.426**
Days to maturity	rp		0.644**	0.313**	0.294**	0.099	0.622**	0.034	-0.081	0.200*	0.409**
	rg		0.651**	0.411**	0.357**	0.122	0.652**	0.147	-0.092	0.336**	0.515**
Plant height (cm)	rp			0.249**	0.471**	0.335**	0.594**	-0.016	0.087	0.100	0.466**
	rg			0.327**	0.565**	0.418**	0.621**	-0.026	0.085	0.185	0.605**
Primary branches per plant (no.)	rp				0.371**	0.360**	-0.015	0.185**	0.166	-0.061	0.286**
	rg				0.605**	0.567**	-0.040	0.237**	0.256**	-0.375**	0.528**
Clusters per plant (no.)	rp					0.737**	0.100	0.153	0.238**	-0.144	0.709**
	rg					0.711**	0.121	0.228*	0.322**	-0.151*	0.757**
Pods per plant (no.)	rp						-0.123	0.143	0.219*	-0.196*	0.613**
	rg						-0.141	0.211*	0.291**	-0.258**	0.572**
100 seed weight (g)	rp							-0.020	-0.177*	0.179*	0.347**
	rg							0.006	-0.238**	0.325**	0.418**
Harvest index (%)	rp								-0.001	-0.268**	0.079
	rg								-0.014	-0.402**	0.151
SCMR	rp									-0.223*	0.024
	rg									-0.304**	-0.042
Protein content (%)	rp										-0.069
	rg										0.002

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Table 4 Direct and indirect effects of yield component characters on seed yield in blackgram

Characters		Days to 50 % flowering	Days to maturity	Plant height	Branches per plant	Clusters per plant	Pods per plant	100 seed weight	HI	SCMR	Protein content (%)	Seed yield per plant
Days to 50 per cent flowering	P	<b>0.0940</b>	0.0442	-0.1033	0.0021	0.1188	0.0546	0.1536	-0.0073	-0.0054	-0.0059	<b>0.3455**</b>
	G	<b>0.1256</b>	-0.0011	-0.1151	0.0374	0.1895	0.0484	0.1838	-0.0127	-0.0172	-0.0120	<b>0.4266**</b>
Days to maturity	P	0.0654	<b>0.0636</b>	-0.1148	0.0020	0.1366	0.0379	0.2301	-0.0101	0.0078	-0.0087	<b>0.4097**</b>
	G	0.0880	<b>-0.0061</b>	-0.1275	0.0358	0.2246	0.0355	0.2730	-0.0181	0.0233	-0.0176	<b>0.5153**</b>
Plant height (cm)	P	0.0545	0.041	<b>-0.1782</b>	0.0016	0.2190	0.1277	0.2118	0.0012	-0.0084	-0.0043	<b>0.4658**</b>
	G	0.0739	-0.001	<b>-0.1958</b>	0.0285	0.3551	0.1219	0.2509	0.0032	-0.0215	-0.0097	<b>0.6054**</b>
Primary branches per plant (no.)	P	0.0309	0.0199	-0.0444	<b>0.0063</b>	0.1726	0.1374	-0.0100	-0.0140	-0.0160	0.0027	<b>0.2855**</b>
	G	0.0539	-0.0007	-0.0639	<b>0.0872</b>	0.3806	0.1652	-0.0196	-0.0292	-0.0650	0.0197	<b>0.5281**</b>
Clusters per plant (no.)	P	0.0240	0.0187	-0.0839	0.0023	<b>0.4652</b>	0.2810	0.0302	-0.0115	-0.0230	0.0063	<b>0.7092**</b>
	G	0.0379	-0.0006	-0.1106	0.0528	<b>0.6288</b>	0.2073	0.0431	-0.0282	-0.0818	0.0079	<b>0.7567**</b>
Pods per plant (no.)	P	0.0135	0.0063	-0.0597	0.0023	0.3426	<b>0.3851</b>	-0.0502	-0.0108	-0.0211	0.0085	<b>0.6129**</b>
	G	0.0209	-0.0002	-0.0819	0.0494	0.4471	<b>0.2916</b>	-0.0684	-0.0261	-0.0740	0.0136	<b>0.5720**</b>
100 seed weight (g)	P	0.0387	0.0392	-0.1011	-0.0002	0.0376	-0.0513	<b>0.3734</b>	0.0007	0.0180	-0.0078	<b>0.3473**</b>
	G	0.0547	-0.0010	-0.1164	-0.0041	0.0642	-0.0472	<b>0.4221</b>	-0.0017	0.0648	-0.0172	<b>0.4182**</b>
Harvest Index (%)	P	0.0090	0.0085	0.0029	0.0012	0.0710	0.0547	-0.0037	<b>-0.0756</b>	0.0001	0.0116	<b>0.0796</b>
	G	0.0129	-0.0002	0.0051	0.0207	0.1435	0.0616	0.0059	<b>-0.1234</b>	0.0035	0.0211	<b>0.1506</b>
SCMR	P	0.0053	-0.0051	-0.0155	0.0010	0.1108	0.0837	-0.0697	0.0001	<b>-0.0964</b>	0.0097	<b>0.0238</b>
	G	0.0085	0.0001	-0.0166	0.0223	0.2025	0.0849	-0.1077	0.0017	<b>-0.2540</b>	0.0160	<b>-0.0422</b>
Protein content (%)	P	0.0129	0.0127	-0.0178	-0.0004	-0.0670	-0.0751	0.0667	0.0202	0.0215	<b>-0.0434</b>	<b>-0.0697</b>
	G	0.0288	-0.0005	-0.0363	-0.0327	-0.0950	-0.0752	0.1383	0.0495	0.0773	<b>-0.0525</b>	<b>0.0015</b>

\*, \*\* Significant at 5 % and 1 % level, respectively

Residual effect: Phenotypic = 0.578

Genotypic = 0.457



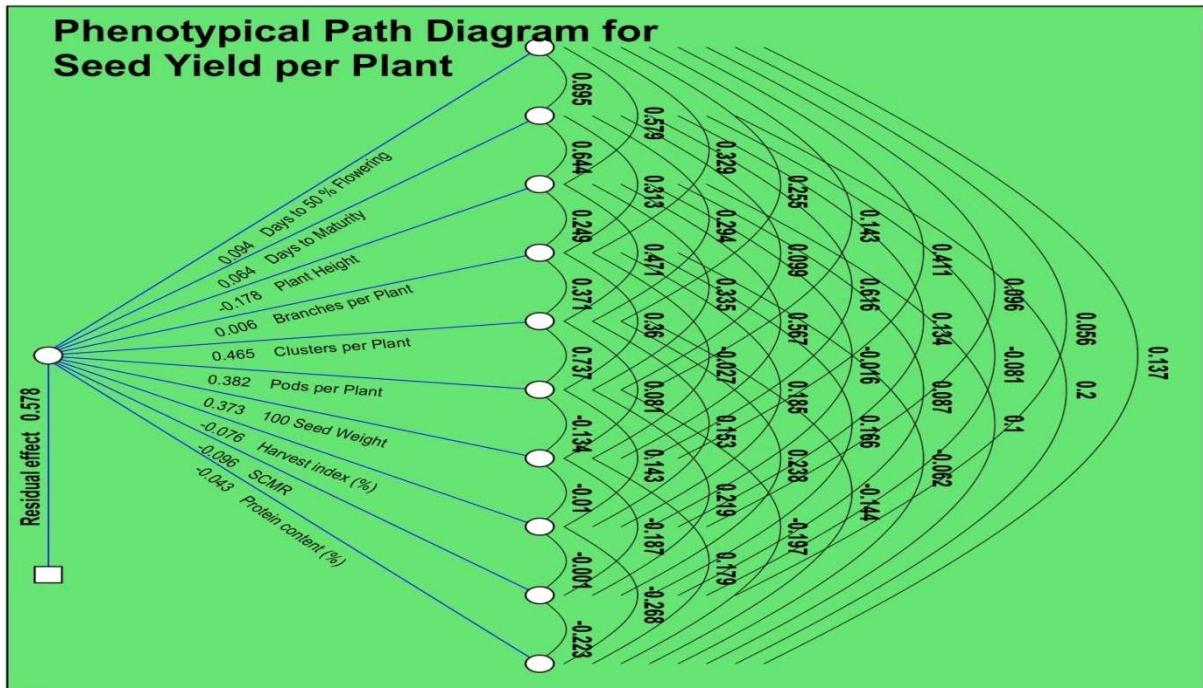


Fig 1. Phenotypic path diagram of seed yield and yield components in blackgram

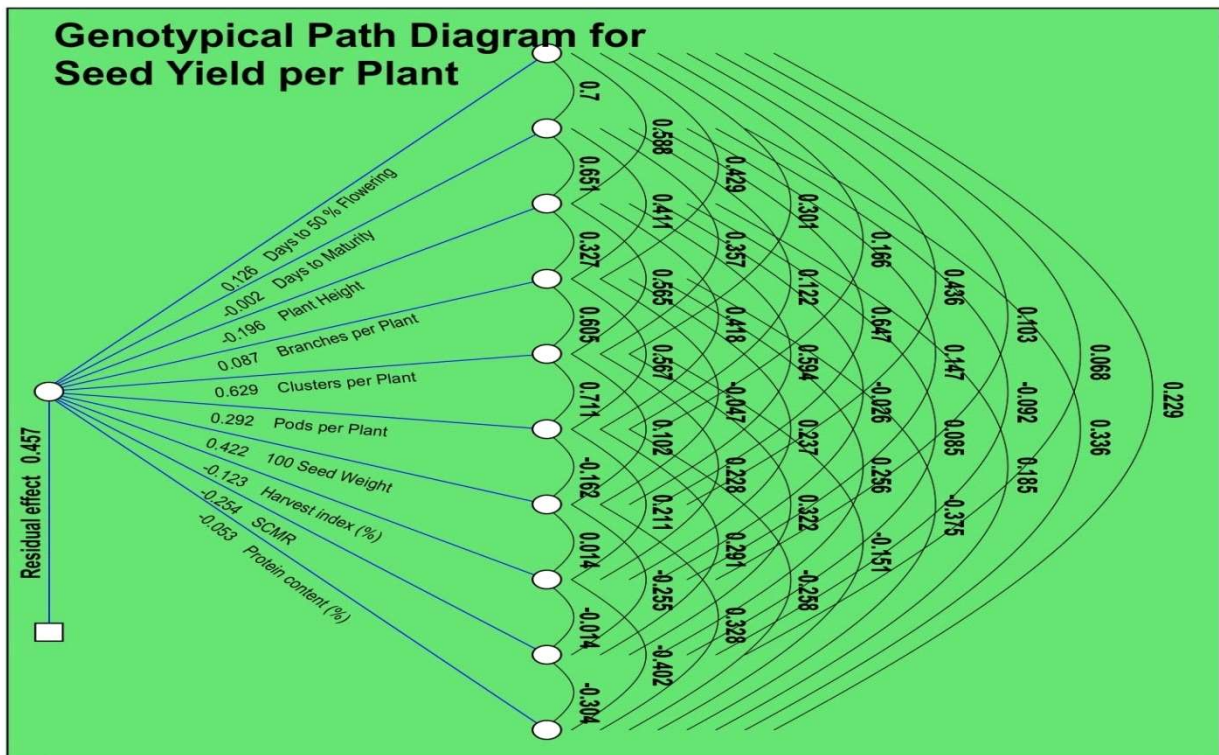


Fig 2. Genotypic path diagram of seed yield and yield components in blackgram