



CHARACTER ASSOCIATION AND PATH ANALYSIS FOR SEED YIELD & ITS COMPONENTS IN BLACK GRAM [*VIGNA MUNGO* (L.) HEPPEL]

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Abstract

The experimental material was consisting of 40 Black gram genotypes, check as T-9. The experiment was laid out in Randomised Complete Block Design with 3 replications. The observations were logged on five randomly taken plants to each treatment and replication for 13 quantitative characters viz. days to 50% flowering, days to 50% pod setting, plant height, number of primary branches per plant, clusters per plant, pods per plant, pod length, seeds per pod, days to maturity, seed index, biological yield, harvest index and seed yield to estimate the variability, heritability and genetic advance as % mean, character association and path analysis. High heritability along with high Genetic advance as % mean was observed for harvest index and seed yield per plant represents simple selection is effective to improve these characters. The correlations revealed that primary branches, pods per plant, seed index and harvest index have the significant positive association with the seed yield per plant at both genotypic and phenotypic levels. The path analysis revealed that the primary branches, pods per plant, harvest index had shown the true relationship with seed yield by establishing the positive correlations and direct effects at both genotypic and phenotypic levels, while clusters per plant genotypic levels and seed index at phenotypic levels.

Key words : Black gram, genetic variability, correlation, path analysis.

Introduction

Pulses are the chief source of protein, high in fibre content than cereals and offer a plentiful quantity of vitamins and minerals. Around the world, pulses are cultivated in more than 171 countries. With an area of 72.3 million ha and production has 64.4 million tonnes with the productivity of 890 Kg/ha. Among various pulses grown Black gram (*Vigna mungo* L. Hepper.) is the important pulse crop in India with high price among the pulses. Black gram is the best source of protein, fat and carbohydrates and also contains iron, folic acid, calcium, magnesium and folate support blood circulation improves cardiovascular health (Ipga.co.in). To improve the productivity of such an important crop through Breeding requires the knowledge of genetic variability of important traits of seed yield, heritability along with the genetic advance as percent mean provides an opportunity for simple selection of the trait. Being the seed yield as the complex character the improvement of this particular character requires a knowledge of other yield contributing characters (Singh and Singh). The estimates of the

correlation coefficient indicate the interrelationship among the characters whereas the path analysis splits the correlations into direct and indirect effects which allow us to understand the cause and effect of related characters (Wright, 1921). The present study was aimed to assess the variability, heritability, genetic advance, correlation coefficients and path analysis for finding the optimal selection criteria to improve the seed yield of the Black gram.

Materials and Methods

The present investigation was carried out at the Field Experimentation Centre, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, U.P. (India) during *Kharif*-2016. The experimental materials consist of 40 genotypes obtained from IIPR, Kanpur, Dept. of GPB, SHUATS. The experiment was laid out in Randomised Complete Block Design with 3 replications. The genotypes were sown by hand dibbling in each plot by imposing randomisation in each replication along with check T-9. Each plot has 4 rows with the spacing of row to row 30

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cm and plant to plant 10 cm. The fertiliser dose of 20:40:40 kg of NPK/ha is applied as Nitrogen as two splits, phosphorus and potassium as basal dose. All recommended package of practices were followed during the cropping period to raise a good crop. The observations were recorded in each plot and replication by taking 5 plants randomly for 13 quantitative characters *viz.* days to 50% flowering, days to 50% pod setting, plant height, number of primary branches per plant, clusters per plant, pods per plant, pod length, seeds per pod, days to maturity, seed index, biological yield, harvest index and seed yield. The data was subjected to the statistical analysis the correlation coefficients are estimated as suggested by Al Jibouri *et al.* (1958) and the path analysis was calculated as suggested by Dewey and Lu (1959).

Results and Discussion

The analysis of variance revealed highly significant to significant differences among the genotypes for all the thirteen characters studied (table 1). In the present study, variation among the characters are estimated by Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV). The PCV was slightly higher than the GCV for few characters indicates the interaction of genotypes with the environment (Table 2). High GCV and PCV were recorded for harvest index (29.45 and 29.98) followed by a number of primary branches per plant (25.85 and 33.56) and seed yield /plant (20.39 and 29.98).

Table 1 : Analysis of variance for seed yield & its contributing characters in Black gram genotypes (Mean squares).

Source of variation	d.f.	Days to 50% flowering	Days to 50% pod setting	Plant height (cm)	Primary branches /plant	Clusters /plant	Pods/ plant	Pod length (cm)	Seeds /pod	Days to maturity	Seed index (gm)	Biological yield (gm)	Harvest index (%)	Seed yield/ plant (gm)
Replications	2	0.006	1.225	3.284	0.098	0.183	0.974	0.004	0.094	0.408	0.249	0.514	0.72	0.576
Genotypes	39	14.169**	4.971**	138.228**	1.249**	1.158**	22.692**	0.368**	1.145**	10.016*	0.946**	275.042**	75.883**	9.372**
Error	78	2.753	1.909	2.397	0.239	0.506	0.717	0.001	0.161	5.571	0.374	0.465	0.9	0.218

**Significant at 1% level and *Significant at 5% level.

Table 2 : Estimates of variability, heritability and genetic advance as per cent of mean for seed yield and yield components in Black gram genotypes.

S.no.	Characters	Range		Grand Mean	Genotypic coefficient of variance (GCV)	Phenotypic coefficient of variance (PCV)	Heritability (in broad sense) (%)	Genetic advance as percent mean
		Minimum	Maximum					
1.	Days to 50% flowering	46.33	56.67	48.94	3.98	5.23	58.02	6.25
2.	Days to 50% pod setting	56.00	61.33	58.30	1.73	2.9313.13	34.84	2.10
3.	Height of genotypes	37.64	63.02	52.58	12.79	13.13	94.97	25.69
4.	Number of primary branches	1.27	3.33	2.27	25.85	33.56	59.32	41.02
5.	Cluster/plant	3.67	7.33	5.23	8.95	16.32	30.08	10.11
6.	Pods/plant	17.25	28.67	23.98	11.28	11.82	91.08	22.18
7.	Length of pods	3.43	4.94	4.26	8.19	8.24	98.84	16.78
8.	Seeds/pod	3.70	6.30	5.10	1.79	13.72	67.06	18.95
9.	Days to maturity	64.67	72.33	67.82	11.31	3.91	21.01	1.69
10.	Seed index	3.00	5.68	3.86	17.90	19.46	33.79	13.53
11.	Biological yield	33.07	68.90	53.43	29.45	17.95	99.49	36.79
12.	Harvest index %	8.41	28.62	16.97	20.39	29.98	96.52	59.61
13.	Seed yield/plant	4.77	11.63	8.56	20.39	21.11	93.33	40.59

Table 3 : Genotypic and phenotypic correlation coefficients of Black gram genotypes.

Characters	Days to 50% flowering	Days to 50% pod setting	Plant height (cm)	Primary branches /plant	Clusters /plant	Pods/ plant	Pod length (cm)	Seeds/ pod	Days to maturity	Seed index (gm)	Biological yield (gm)	Harvest index (%)	Seed yield /plant (gm)
Days to 50% flowering	G	1											
	P	1											
Days to 50% pod setting	G	0.371**	1										
	P	0.379**	1										
Plant height (cm)	G	0.238**	0.207*	1									
	P	0.12	0.078	1									
Primary branches/plant	G	0.155	0.202*	0.468**	1								
	P	0.085	0.054	0.376**	1								
Clusters/ plant	G	0.236**	0.319**	-0.278**	-0.14	1							
	P	-0.026	-0.138	-0.086	-0.066	1							
Pods/ plant	G	-0.265**	-0.138**	0.167	0.045	-0.17	1						
	P	-0.153	-0.158	0.147	0.028	-0.082	1						
Pod length (cm)	G	-0.162	-0.053	0.195*	0.103	-0.426**	0.129*	1					
	P	-0.137	-0.054	0.191*	0.09	-0.211*	0.207*	1					
Seeds/ pod	G	-0.329**	-0.108	0.07	0.220*	0.343**	0.265**	0.442**	1				
	P	-0.186*	-0.029	0.051	0.092	0.067	0.231*	0.361**	1				
Days to maturity	G	-0.213**	0.237**	0.162	-0.16	-0.089	0.069	-0.206*	1				
	P	0.274**	0.317**	0.031	0.008	-0.162	0.017	-0.067	1				
Seed index (gm)	G	0.244**	-0.388**	-0.190*	0.178	0.646**	0.084	0.116	0.272**	1			
	P	0.11	-0.059	-0.123	0.082	0.089	0.071	0.065	0.157	-0.214*	1		
Biological yield (gm)	G	0.246**	-0.04	0.049	-0.097	0.239**	-0.224*	-0.045	0.196*	0.012	1		
	P	0.186*	-0.006	0.05	-0.066	0.148	-0.214*	-0.043	0.085	0.006	1		
Harvest index (%)	G	-0.207*	-0.169	-0.009	0.220*	0.338**	-0.121	0.208*	-0.399**	0.453**	-0.577**	1	
	P	-0.142	-0.7	-0.013	0.151	0.148	0.358**	-0.125	-0.163	0.250**	-0.570**	1	
Seed yield/ plant (gm)	G	-0.137	-0.291**	0.06	0.343**	0.202*	-0.326**	0.071	-0.264**	0.447**	0.021	0.638**	1
	P	-0.096	-0.14	0.062	0.245**	0.062	-0.320**	0.034	-0.107	0.237**	0.016	0.651**	1

G = Genotypic correlation coefficient. P = Phenotypic correlation coefficient. *Significant at 5% level, **Significant at 1% level.

Table 4 : Path coefficients of yield and yield components of Black gram genotypes.

Characters	Days to 50% flowering	Days to 50% flowering pod setting	Plant height (cm)	Primary branches /plant	Clusters /plant	Pods/ plant	Pod length (cm)	Seeds/ pod	Days to maturity	Seed index (gm)	Biological yield (gm)	Harvest index (%)	Correlations with yield per plant
Days to 50% flowering	G	-0.22136	0.00599	0.06128	-0.05222	0.01469	0.11274	0.02117	-0.02926	0.11591	-0.13096	-0.137	
	P	-0.11293	0.00278	0.01381	0.0053	0.03808	0.00975	0.00281	0.00492	0.11177	-0.12659	-0.096	
Days to 50% pod setting	G	-0.08206	0.00522	0.09002	0.08284	0.00483	0.03696	-0.02354	0.04638	-0.00166	-0.10659	-0.291**	
	P	-0.04279	-0.06435	0.00181	0.0088	0.02237	0.01488	0.00151	0.00326	-0.00264	-0.00355	-0.06209	-0.14
Plant height(cm)	G	-0.05262	0.02522	0.20884	-0.07217	0.03297	-0.01746	-0.0239	-0.01606	0.02277	0.02293	-0.00578	0.06
	P	-0.01356	0.02313	0.06118	0.01751	0.0208	-0.05287	-0.00265	0.00032	-0.00551	0.03028	-0.01141	0.062
Primary branches/plant	G	-0.0343	0.0118	0.44623	-0.03629	0.0089	-0.00927	-0.0753	0.01586	-0.02129	-0.0458	0.1389	0.343**
	P	-0.00957	-0.00348	0.16289	0.01339	0.004	-0.02495	-0.00482	0.00008	0.00368	-0.03958	0.13445	0.245**
Clusters/ plant	G	-0.05229	-0.08959	-0.06242	0.25945	-0.03351	0.0385	-0.11744	0.0169	-0.07733	0.11287	0.21365	0.202*
	P	0.00294	0.00886	-0.01019	-0.2035	-0.01167	0.05863	-0.00349	-0.00167	0.00396	0.08869	0.13206	0.062
Pods/ plant	G	0.0587	0.08929	0.00422	-0.04415	0.19693	-0.01984	-0.09094	0.00889	-0.01007	-0.10588	0.24137	0.349**
	P	0.01727	0.01017	0.0034	0.01678	0.14155	-0.05733	-0.0121	0.00018	0.00319	-0.12884	0.31895	0.318**
Pod length(cm)	G	0.03597	0.015	0.00487	-0.11049	0.04322	-0.0904	-0.15134	-0.00682	-0.01385	-0.02116	-0.0765	-0.326**
	P	0.01551	0.00345	0.00441	0.04303	0.02927	-0.27732	-0.01888	0.00012	0.00291	-0.0261	-0.11106	-0.320**
Seeds/ pod	G	0.07284	0.03027	0.00176	0.08893	0.05227	-0.03993	-0.34262	0.02042	-0.03257	-0.01004	0.13164	0.071
	P	0.02106	0.00186	0.00117	-0.01359	0.03276	-0.10012	-0.0523	-0.00069	0.00701	-0.00665	0.12867	0.034
Days to maturity	G	0.04718	-0.06649	0.00408	-0.04413	-0.01762	-0.0062	0.07044	-0.09933	0.07866	0.09253	-0.25181	-0.264**
	P	-0.0309	-0.0204	0.00072	0.03296	0.00243	-0.00329	0.00353	0.01028	-0.00956	0.05089	-0.14496	-0.107
Seed index(gm)	G	-0.05412	0.10874	-0.0048	0.07938	0.16764	-0.01047	-0.09324	0.06528	-0.11968	0.00543	0.2864	0.447**
	P	-0.01244	0.00381	-0.00285	0.01341	-0.01806	-0.01806	-0.00821	-0.0022	0.04466	0.00389	0.2234	0.237**
Biological yield(gm)	G	-0.05435	0.00099	0.00122	-0.04329	0.06203	-0.04417	0.00729	-0.01947	-0.00138	0.47206	-0.36408	0.021
	P	-0.02099	0.00038	0.00117	-0.01073	-0.03002	0.01204	0.00058	0.00087	0.00029	0.60119	-0.50886	0.016
Harvest index (%)	G	0.0459	0.04736	-0.00023	0.09815	0.08777	0.01095	-0.07142	0.0396	-0.05427	-0.27215	0.63154	0.638**
	P	0.01603	0.00448	-0.0003	0.02455	-0.03013	0.03453	-0.00754	-0.00167	0.01118	-0.34296	0.892	0.651**

Bold are direct effects, G: Genotypic path coefficient, Residual effects (G):0.22149 P: Phenotypic path coefficient, (P): 0.22016

Estimates of heritability is a good index for predicting the transmission of characters from parents to their offspring (Falconer, 1981). High heritability (broad sense) was recorded for characters *i.e.*, biological yield per plant (99.49%), followed by length of pods (98.84%), harvest index (96.52%) plant height (94.97%), seed yield per plant (91.08%), pods per plant (91.08%) seeds per pod (67.06%). High heritability alone may not lead to valid conclusions unless it is accompanied with the Genetic advance as percent mean (Johnson and Robinson, 1955). High heritability coupled with high genetic advance as percent of the mean was recorded for harvest index and biological yield per plant. These findings are in accordance with Chauhan *et al.* (2007) and Veenjaneyulu *et al.* (2007).

The genotypic and phenotypic correlation coefficients were computed among 13 characters (table 3). The primary branches per plant, pods per plant, seed index and harvest index showed highly significant positive association with seed yield at both genotypic and phenotypic levels, while clusters per plant showing significant at genotypic level with seed yield. Therefore, these characters appeared as greatest important associates of seed yield per plant and have also been observed by preceding workers (Kumar *et al.*, 2005; Kumar *et al.*, 2008; Sharma *et al.*, 2005; Issacs *et al.*, 2000; Katna and Verma, 2001).

The correlation values provided only nature and degree of relationship of yield contributing characters on seed yield. Path coefficient analysis is a statistical technique to split the observed correlation coefficients into direct and indirect effects of independent variables on the dependent variable. In the present study, path coefficient analysis was carried out using genotypic and phenotypic correlation matrix of 13 characters (table 4). Path analysis revealed that primary branches per plant, pods per plant, plant height, biological yield and harvest index showing the direct positive effect on seed yield at genotypic and phenotypic levels, while clusters per pod at the genotypic level and days to maturity, seed index at the phenotypic level having positive direct effect on seed yield. These results were in accordance with the findings of Usharani *et al.* (1981), Venkateswarlu (2001) and kanimoli *et al.* (2015). By considering the nature and extent of correlation coefficients and their direct and indirect effects it can be concluded that improvement of Black gram seed yield is brought through simultaneous selection primary branches per plant, clusters per plant, biological yield and harvest index.

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