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CORRELATION AND PATH COEFFICIENT ANALYSIS FOR YIELD AND YIELD COMPONENTS IN BLACKGRAM (*Vigna mungo* (L.) HEPPER)

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ABSTRACT

Eighty genotypes along with two national checks 'T-9' and 'Shekhar-2' were evaluated in Randomized Block Design with three replications. Wide range of variability was observed for quantitative traits. The variability study indicated high to moderate phenotypic and genotypic coefficient of variation accompanied by high heritability and genetic advance as per cent of mean for traits like number of clusters per plant, number of pods per cluster, primary branches per plant, harvest index and seed yield per plant indicating their importance in selection for yield improvement. Seed yield per plant showed strong positive correlation with number of clusters per plant, number of pods per cluster and harvest index, these traits has also showed positive direct effect on seed yield indicated scope for improvement through selection of these traits.

INTRODUCTION

Pulses are the main sources of protein for the predominant vegetarian population of India. Besides they are also used as fodder and concentrate for the cattle. The vital role of pulses in fixation of atmospheric nitrogen needs no emphasis, which in fact is very crucial in light of price hike of nitrogenous fertilizers. As compared to growth in food seed production consequent to Green Revolution, the growth in production of pulses is rather disappointing leading to a raise in the prices of pulses. Like in any other crop the growth in production of pulses is largely determined by growth in area under cultivation or an improvement in the productivity levels or a combination of both. The area and productivity of pulses during the previous decades have been fluctuating and hence, the production has remained almost stagnant.

Blackgram (*Vigna mungo* L. Hepper, 2n=22) is one of the nutritious pulse crop, popularly known as urdbean. It has been identified as a potential crop in most of the countries but its national average is one third of the potential yield (Ghafoor *et al*., 1997). Being short duration crop, it has special advantage of growing during summer (July to October) and spring (April to June) seasons as well as in inter and multiple cropping systems (Zahid *et al*., 1998). Lack of stable varieties for higher yield is a major bottleneck for growing of this crop; hence improvement of blackgram is an important task for pulse breeders.

The knowledge of certain genetic parameters is also essential for proper understanding and their manipulation in any crop improvement programme. Seed yield is the result of the expression and association of several plant growth components. Association studies give an idea about the contribution of different traits towards seed yield and it reveals the type, nature and magnitude of correlation between yield components with yield and among themselves. Selection based on yield components is advantageous if different yield related traits have been well documented (Pohelman, 1995 and Singh *et al.,* 2003). Path analysis identifies the yield components which directly and indirectly influence the yield (Rao *et al.,* 2006). Hence, the present research work was carried out to study the correlation coefficients and path analysis to identify the best traits to be used for future exploitation.

MATERIALS AND METHODS

The experimental material comprised of 82 blackgram genotypes. These genotypes were evaluated in Randomized Complete Block Design with three replications during *Kharif* 2014-15 at Field Experimentation Centre of the Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad (U.P.). The genotypes were sown on 22nd July, 2014. Each plot consisted of 4 rows. Spacing was maintained at 30 X 10cm. The normal recommended agronomic practices were followed to raise the healthy crop. Fertilizers were applied at the rate of 60:40:40 kg of NPK per ha. The full dose of phosphorus and potassium and half dose of nitrogen were applied as basal dose at the time of sowing. The rest of the nitrogen was applied after 30 days of sowing. Ten plants from middle row of each genotype in each replication were randomly taken for recording observations on plant height, primary branches per plant, number of clusters per plant, number of pods per cluster, number of seeds per pod, pod length, 100 seed weight(g), harvest index(%), biological yield per plant and seed yield per pant (g). Whereas, days to 50% flowering and days to maturity were recorded on plot basis. After attaining the physiological maturity, the plots were harvested manually. Mean values of different traits were subjected to Analysis of Variance (Fisher, 1936), Coefficient of Variation (Burton, 1952), Heritability (Burton and Devane, 1953) and Genetic Advance (Johanson *et al*., 1955). The character association was estimated from variance and covariance components as per Al Jibouri *et al.* (1958). While the direct and indirect effects of component traits up on seed yield were measured by path analysis as described by Dewey & Lu (1959).

RESULTS AND DISCUSSION

The analysis of variance revealed that the mean sum of squares for genotypes was highly significant for all the traits investigated (Table 1). This significance suggested the presence of substantial amount of genetic variability among the blackgram genotypes Pushpa Reni *et al.* (2013) and Vijay Kumar *et al.* (2015).

Table 2, revealed that the estimates of Range, Mean, Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Heritability (broad sense) and Genetic Advance depicted considerable range of variation for all the traits under study indicating enough scope for bringing about improvement in desirable direction through selection breeding.

In general estimates of phenotypic coefficient of variation (PCV) were higher than corresponding genotypic coefficient of variation (GCV). The differences between PCV and GCV were very low for all the traits studied except primary branches per plant, pods per cluster and seeds per pod indicating that these traits were less affected by environmental fluctuations. These results are in agreement with those obtained by Yashoda *et al.* (2016) and Sheetal R. Patel *et al.*(2014). High values of GCV and PCV were observed for clusters per plant (34.81 and 35.27), primary branches per plant (24.66 and 26.28) and pods per cluster (22.38 and 24.41) suggesting possibility of improvement in these traits through direct selection.

The range observed for heritability in broad sense was from 72 to 99 per cent and maximum heritability was recorded for the traits plant height, harvest index followed by seed yield per plant, clusters per plant, biological yield per plant, pod length, primary branches per plant, pods per cluster, days to maturity, 100 seed weight, days to 50% flowering and seeds per pod. These results of heritability indicated that additive gene action was in preponderance for expression of traits. Panigrahi *et al*. (2014) also reported high heritability estimates for plant height, seed yield per plant and clusters per plant which support the present findings.

Genetic advance indicates the possible gains, which can be expected from the traits under investigation. Heritability

Table 1: Analysis of variance for 82 blackgram genotypes

Genotypes	Degree of freedom	Plant height (cm)	Primary Branches per Plant	Days to 50% Flowering	Days to Maturity	Clusters per Plant	Pods per Cluster	Seeds per Pod	Pod Length (cms)	100 Seed Weight (g)	Harvest Index (%)	Biological Yield per Plant (g)	Seed Yield per Plant (g)
Replication	(r-1) = 2	0.71	0.01	17.71	4.5	0.12	0.01	0.01	0.01	0.02	0.15	0.01	0.01
Genotypes	(v-1) = 81	362.93**	1.08**	56.58**	74.44**	24.95**	1.24**	1.07**	0.31**	0.37**	66.67**	7.75**	1.44**
Error	(r-1) (v-1) = 162	0.85	0.04	5.91	4.48	0.21	0.07	0.12	0.01	0.02	0.05	0.1	0.01
S.E.		0.53	0.12	1.4	1.22	0.26	0.15	0.2	0.06	0.09	0.13	0.18	0.07
C.D. 5%		1.49	0.34	3.92	3.41	0.75	0.43	0.56	0.17	0.27	0.38	0.52	0.19
C.D. 1%		1.96	0.46	5.17	4.5	0.99	0.57	0.74	0.23	0.36	0.51	0.69	0.26

** significant at 5% level

Table 2 : Estimates of genetic variability parameters for different quantitative characters in blackgram

S.No.	Traits	Range	Mean	Coefficient of variation		Heritability (%)	Genetic advance (as % of mean)
				GCV%	PCV%		
1.	Plant height (cm)	38.97-83.56	59.35**	18.51	18.58	99	38
2.	Primary branches per plant	1.26-4.56	2.38**	24.66	26.28	88	47.66
3.	Days to 50% flowering	32.00-57.00	44.52**	9.23	10.73	74	16.37
4.	Days to maturity	57.00-79.00	66.92**	7.22	7.88	84	13.61
5.	Clusters per plant	3.47-17.93	8.25**	34.81	35.27	97	70.78
6.	Pods per cluster	1.18-4.51	2.79**	22.38	24.41	84	42.26
7.	Seeds per pod	4.13-7.20	5.80**	9.69	11.42	72	16.94
8.	Pod length (cm)	3.33-4.79	3.99**	7.93	8.4	89	15.43
9.	100 Seed weight (g)	2.81-4.67	3.72**	9.18	10.25	80	16.94
10.	Harvest Index (%)	12.47-38.67	25.56**	18.44	18.46	99	37.93
11.	Biological yield per plant	10.17-25.74	16.18**	9.87	10.07	96	19.93
12.	Seed yield per plant (g)	2.23-5.91	4.10**	16.89	17.15	97	34.25

** Significant at 5% level

Table 3 : Phenotypic (P) and genotypic (G) correlation coefficients of different traits in blackgram

Traits		PH	PB	DF	DM	CP	PC	SP	PL	HSW	HI	BY	SY
PH	P	1	0.2509***	0.2694***	0.4773***	-0.1186	0.1280*	0.1067	0.1863**	0.1229	-0.1049	0.0904	-0.1076
	G	1	0.2682***	0.3137***	0.5212***	-0.1208	0.1421*	0.1264*	0.1995**	0.1391*	-0.1046	0.0939	-0.1084
PB	P		1	0.0987	0.2584***	0.088	0.1298*	0.1826**	-0.0182	0.1537*	-0.1115	-0.0911	-0.1908**
	G		1	0.1111	0.2818***	0.0954	0.1614*	0.1825**	-0.0312	0.1604*	-0.1181	-0.0954	-0.2040**
DF	P			1	0.6854***	-0.0852	0.1358*	0.0053	0.0007	0.1490*	-0.0357	0.0239	-0.0495
	G			1	0.7322***	-0.104	0.1597*	-0.0324	-0.0126	0.1840**	-0.0394	0.0247	-0.0547
DM	P				1	0.0459	0.3063***	0.0623	0.0378	0.1748**	0.0033	0.061	-0.0179
	G				1	0.0525	0.3649***	0.0618	0.0416	0.1851**	0.0054	0.0844	-0.0086
CP	P					1	0.3028***	0.0535	-0.0687	0.1397*	0.3357***	-0.0861	0.3200***
	G					1	0.3261***	0.0546	-0.0682	0.1712**	0.3399***	-0.091	0.3287***
PC	P						1	0.0432	0.0184	0.2286***	0.1460*	-0.0321	0.1203*
	G						1	0.0597	0.0245	0.3104***	0.1621*	-0.0356	0.1354*
SP	P							1	0.4048***	0.0938	-0.1441*	0.0312	-0.1528*
	G							1	0.4761	0.067	-0.1699**	0.04	-0.1832**
PL	P								1	0.1730**	-0.1950**	-0.0076	-0.2286***
	G								1	0.2120***	-0.2071**	-0.0073	-0.2453***
HSW	P									1	0.0279	0.021	0.0334
	G									1	0.0329	0.0304	0.0422
HI	P										1	-0.4475***	0.9125***
	G										1	-0.4605***	0.9233***
BY	P											1	-0.0803
	G											1	-0.1137
SY	P												1
	G												1

*, ** and *** Significant at 5%, 1% and 0.1% level respectively;PH- **Plant height (cm),** PB**- Primary Branches per Plant,** DF**-Days to 50% flowering,** DM- **Days to maturity**, CP- **Clusters per Plant**, PC- **Pods per cluster**, SP- **Seeds per Pod**, PL- **Pod Length**, HSW- **Hundred Seed Weight**, HI- **Harvest Index** and BY- **Biological Yield per Plant** and SY- **Seed Yield per Plant**.

estimates along with genetic advance are normally more useful in predicting the gain under selection than heritability estimates alone (Johnson *et al.*1955). High heritability accompanied with high genetic advance as percent of mean for all the traits except days to maturity, pod length, seeds per pod and days to 50% flowering. It indicates that most likely the heritability may be due to additive gene effect and selection may be effective in early segregating generation for these traits. Similar findings have been reported for number of clusters per plant by Panigrahi *et al.* (2014), primary branches per plant and plant height by Awnindra K Singh *et al.* (2014), pods per cluster by Veeramani *et al.* (2005), harvest index by Ghafoor *et al.* (1997) and seed yield per plant by Sateesh Babu *et al.* (2016) and Patel *et al.* (2014). Presence of high genetic advance as % of mean (70.78 %) for clusters per plant indicated that it is governed by additive gene action and selection would be more effective in such cases as earlier reported by Panigrahi *et al.* (2014).

Correlation among different traits is generally due to the presence of linkage and pleotropic effect of different genes. Environment plays an important role in the development of phenotypic correlation (Ali *et al.*, 2009). In general genotypic correlations were higher than their corresponding phenotypic correlation in all the cases, thereby suggesting strong inherent association between various traits at genetic level. The inter character correlation at phenotypic and genotypic level among twelve traits studied are present in Table-3 it was one of the major objectives of this study.

A perusal of results revealed that high significant and positive correlation of seed yield was seen with cluster per plant (p = 0.3200, g = 0.3287***), pods per cluster (p = 0.1203, g = 0.1354*) and harvest index (p = 0.9125, g = 9233***), indicating increase in any of above character would lead to increase in seed yield. Hence, these traits could be utilized in indirect selection so as to improve the seed yield per plant. Similar kind of significant positive association of clusters per plant, pods per cluster and harvest index with seed yield was reported earlier in blackgram by Chauhan *et al.* (2007),

Table 4 : Estimation of direct and indirect effect between yield and its related traits at genotypic level

S. No	Traits	Plant height (cm)	Primary Branches per Plant	Days to 50% flowering	Days to maturity	Clusters per Plant	Pods per Cluster	Seeds per Pod	Pod Length	Hundred Seed	Harvest Index Weight	Biological Yield per Plant	Seed Yield per Plant
1	Plant height	0.0004	0.0001	0.0001	0.0002	-0.0001	0.0001	0.0001	0.0001	0.0001	0	0	-0.1084
2	Primary Branches per Plant	-0.0066	-0.0246	-0.0027	-0.0069	-0.0023	-0.004	-0.0045	0.0008	-0.0039	0.0029	0.0023	-0.204
3	Days to 50% flowering	0.0061	0.0022	0.0196	0.0143	-0.002	0.0031	-0.0006	-0.0002	-0.0036	-0.0008	0.0005	-0.0547
4	Days to maturity	-0.0275	-0.0148	-0.0386	-0.0527	-0.0028	-0.0192	-0.0033	-0.0022	-0.0098	-0.0003	-0.0044	-0.0086
5	Clusters per Plant	0.0003	-0.0002	0.0003	-0.0001	-0.0025	-0.0008	-0.0001	0.0002	-0.0004	-0.0008	0.0002	0.3287
6	Pods per Cluster	-0.0017	-0.0019	-0.0019	-0.0043	-0.0039	-0.0119	-0.0007	-0.0003	-0.0037	-0.0019	0.0004	0.1354
7	Seeds per Pod	0.0006	0.0009	-0.0002	0.0003	0.0003	0.0003	0.0049	0.0023	0.0003	-0.0008	0.0002	-0.1832
8	Pod Length	-0.0034	0.0005	0.0002	-0.0007	0.0012	-0.0004	-0.0081	-0.0171	-0.0036	0.0035	0.0001	-0.2453
9	Hundred Seed Weight	0.0016	0.0018	0.0021	0.0021	0.0019	0.0035	0.0008	0.0024	0.0113	0.0004	0.0003	0.0422
10	Harvest Index	-0.1153	-0.1303	-0.0434	0.006	0.3748	0.1787	-0.1873	-0.2284	0.0363	1.1027	-0.5078	0.9233
11	Biological Yield per Plant	0.037	-0.0376	0.0097	0.0333	-0.0359	-0.0141	0.0158	-0.0029	0.012	-0.1816	0.3943	-0.1137

Veeranjaneyulu *et al.* (2007) and Isha Parveen *et al.* (2011). On contrary, seed yield showed significant negative association with pod length (p=-0.2286, g=-0.2453***) Mishra (1983) and Natarajaratnam *et al.* (1985), seeds per pod (p=-0.1528, g=-0.1832**) Rozina Gul *et al.* (2008) and Natarajaratnam *et al.* (1985) and primary branches per plant (p=-0.1908, g=-0.2040**) which reveals that selection for these traits forms a setback in further increase of seed yield.

Similarly, plant height showed significant positive association with pod length (p=0.1863, g=0.1995**), pods per cluster (p=0.1280, g=0.1421*), seeds per pod (p=0.1067, g=0.1264*), hundred seed weight (p=0.1229, g=0.1391*), days to flowering (p=0.2694, g=0.3137***) and days to maturity (p=0.4773, g=0.5212***). It indicates that selection of the tall plants could result in attaining more number of pods per cluster having longer pods with more number of seeds, increased seed weight and also increase in days to flowering and maturity. Similar kind of significant positive association of plant height with pod length, seeds per pod, 100-seed weight and days to maturity was reported earlier by Jyothsna *et al.* (2016) and Isha Parveen *et al.* (2011), with pods per cluster by Kanimoli *et al.* (2015), with days to flowering by Vijay Kumar *et al.* (2014) and Pushpa Reni *et al.* (2013).

Clusters per plant exhibited highly significant positive association with pods per cluster (p=0.3028, g=0.3261***), hundred seed weight (p=0.1397, g=0.1712**) and harvest index (p=0.3357, g=0.3399***) which indicated that selection of the plants with more number of clusters may increase the number of pods per cluster, hundred seed weight and harvest index in a linear fashion. Similar kind of significant positive association of clusters per plant with pods per cluster was reported earlier by Gopi Krishnan *et al.*(2002) and Kanimoli *et al.* (2015) while with hundred seed weight was reported by Panigrahi *et al.* (2014) and with harvest index was reported by Isha Parveen *et al.* (2011) and Vijay Kumar *et al.* (2014) and corroborates the results of present study.

The path coefficient analysis furnishing the cause and effect of different yield components would provide better index for selection rather than mere correlation coefficients. The results on path coefficient analysis at genotypic level indicated that the highest positive direct effect on seed yield per plant was shown by harvest index (0.9233), followed by clusters per plant (0.3287), pods per cluster (0.1354) and hundred seed weight (0.0422)(Table 4). Hence selection based on these traits would be effective in increasing the seed yield. These positive direct effects observed with seed yield were in accordance with the reports of Isha Parveen *et al.* (2011) and Vijay Kumar *et al.* (2014).

On contrary, pod length recorded negative direct effect on seed yield followed by number of seeds per pod, primary branches per plant, plant height and biological yield. These results were in accordance with the reports of Pooran Chand and Rabhunandha Rao (2002) and Sunil Kumar *et al.*, (2003) for days to 50% flowering, Nagarjunasagar and Reddi Sekhar (2001) and Chauhan *et al.* (2007) for number of primary branches and pods per cluster and Govindaraj and Subramanian (2001) for pod length.

Though, pod length had negative direct effect on seed yield but, it influenced the seed yield through its high positive indirect effects via clusters per plant and primary branches per plant and registered positive association with seed yield and seeds per pod influenced the seed yield through its high positive indirect effects via pod length. Whereas 100-seed weight influenced the seed yield through its high positive indirect effects via pods per cluster, pod length, days to 50% flowering, days to maturity and clusters per plant to register positive association with seed yield per plant. Hence for increasing the seed yield, direct selection based on these traits would be rewarding.

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