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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

Genetic variability and correlations among 82 genotypes of blackgram was assessed for twelve quantitative traits. These genotypes along with two national checks 'T-9' and 'Shekhar-2' were evaluated Field Experimentation Centre of Genetics and Plant Breeding, SHUATS, Prayagraj, Uttar Pradesh, India. 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 percent of mean for traits like number of clusters/plant, number of pods/cluster, primary branches/plant, harvest index and seed yield/plant indicating their importance in selection for yield improvement. Seed yield/ plant showed strong positive correlation with number of clusters/plant, number of pods/cluster and harvest index, these traits has also showed positive direct effect on seed yield indicated scope for improvement through selection of these traits.

Keywords: Blackgram, correlation and path analysis

1. 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 crops 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) [5]. 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. 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.

Seed yield is the result of the expression and association of several plant growth components. Association studies gives 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 [15] and Singh, *et al.*, 2003) [20]. Path analysis identifies the yield components which directly and indirectly influence the yield (Rao, *et al.*, 2006) [18]. 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.

2. 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* at Field Experimentation Centre of the Department of Genetics and Plant Breeding,

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Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (U.P.). 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/ 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/plant, number of clusters/plant, number of pods/cluster, number of seeds/pod, pod length, 100 seed weight (g), harvest index (%), biological yield/plant and seed yield/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) [4]. The character association was estimated from variance and covariance components as per Al Jibouri, *et al.*, (1958) [1]. While the direct and indirect effects of component traits up on seed yield were measured by path analysis as described by Dewey & Lu, (1959) [3].

3. 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 reported by Pushpa Reni, *et al.*, (2013) [17] and Vijay Kumar, *et al.*, (2015) [22].

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. 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/plant ($p=0.3200^{***}$, $g=0.3287^{***}$), pods/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/plant. Similar kind of significant positive association of clusters/plant, pods/ cluster and harvest index with seed yield was reported earlier in blackgram by Chauhan, *et al.*, (2007) [2] and Isha Parveen, *et al.*, (2011) [8].

On contrary, seed yield showed significant negative association with pod length ($p= -0.2286^{***}$, $g= -0.2453^{***}$), seeds/pod ($p= -0.1528^*$, $g= -0.1832^{**}$) and primary branches/plant ($p= -0.1908^{**}$, $g= -0.2040^{**}$) which reveals that selection for these traits forms a setback in further increase of seed yield. Mishra, (1983) [11], Natarajaratnam, *et al.*, (1985) [13] and Rozina Gul, *et al.*, (2008) [19] also reported that pod length and seeds/pod had negative correlation with seed yield/plant.

Similarly, plant height showed significant positive association with pod length ($p=0.1863^{**}$, $g=0.1995^{**}$), pods/cluster

($p=0.1280^*$, $g=0.1421^*$), seeds/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/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/pod, 100-seed weight and days to maturity was reported earlier by Isha Parveen, *et al.*, (2011) [8] and Jyothsna, *et al.*, (2016) [9], with pods/cluster by Kanimoli, *et al.*, (2015) [10], with days to flowering by Pushpa Reni, *et al.*, (2013) [17] and Vijay Kumar, *et al.*, (2014) [23].

Clusters/plant exhibited highly significant positive association with pods/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/cluster, hundred seed weight and harvest index in a linear fashion. Similar kind of significant positive association of clusters/plant with pods/cluster was reported earlier by Gopi Krishnan, *et al.*, (2002) [6] and Kanimoli, *et al.*, (2015) [10] while with hundred seed weight was reported by Panigrahi, *et al.*, (2014) [14] and with harvest index was reported by Isha Parveen, *et al.*, (2011) [8] and Vijay Kumar, *et al.*, (2014) [23] 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/plant was shown by harvest index (0.9233), followed by clusters/plant (0.3287), pods/cluster (0.1354) and hundred seed weight (0.0422) (Table 2). 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) [8] and Vijay Kumar, *et al.*, (2014) [23].

On contrary, pod length recorded negative direct effect on seed yield followed by number of seeds/pod, primary branches/plant, plant height and biological yield. These results were in accordance with the reports of Pooran Chand, *et al.*, (2002) [16] and Sunil Kumar, *et al.*, (2003) [21] for days to 50% flowering, Nagarjuna Sagar, *et al.*, (2001) [12] and Chauhan, *et al.*, (2007) [2] for number of primary branches and pods/cluster and Govindaraj, *et al.*, (2001) [7] for pod length.

4. Conclusion

Out of twelve quantitative characters, three characters *viz.*, cluster/plant, pods/cluster and harvest index were highly significant and positively correlated with seed yield at both phenotypic and genotypic level.

Pod length having negative direct effect on seed yield, influenced the seed yield through its high positive indirect effects via clusters/plant and primary branches/plant and registered positive association with seed yield and seeds/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/cluster, pod length, and clusters/plant to register positive association with seed yield/plant. Hence, these traits could be utilized in direct selection so as to improve the seed yield in blackgram.

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Table 1: Analysis of variance for 82 blackgram genotypes

Genotypes	Degree of freedom	Plant height (cm)	Primary Branches/Plant	Days to 50% Flowering	Days to Maturity	Clusters/Plant	Pods/Cluster	Seeds/Pod	Pod Length (cm)	100 Seed Weight (g)	Harvest Index (%)	Biological Yield/Plant (g)	Seed Yield/Plant (g)
Replication	2	0.71	0.01	17.71	4.50	0.12	0.01	0.01	0.01	0.02	0.15	0.01	0.01
Genotypes	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	162	0.85	0.04	5.91	4.48	0.21	0.07	0.12	0.01	0.02	0.05	0.10	0.01
S.E.		0.53	0.12	1.40	1.22	0.26	0.15	0.20	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

* Significant at 5% level

Table 2: Estimation of direct and indirect effect between yield and its related traits at genotypic level

S. No	Traits	PH	PB	DF	DM	CP	PC	SP	PL	HSW	HI	BY	SY
1.	PH	0.0004	0.0001	0.0001	0.0002	-0.0001	0.0001	0.0001	0.0001	0.0001	0.0000	0.0000	-0.1084
2.	PB	-0.0066	-0.0246	-0.0027	-0.0069	-0.0023	-0.0040	-0.0045	0.0008	-0.0039	0.0029	0.0023	-0.2040
3.	DF	0.0061	0.0022	0.0196	0.0143	-0.0020	0.0031	-0.0006	-0.0002	-0.0036	-0.0008	0.0005	-0.0547
4.	DM	-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.	CP	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.	PC	-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.	SP	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.	PL	-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.	HSW	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.	HI	-0.1153	-0.1303	-0.0434	0.0060	0.3748	0.1787	-0.1873	-0.2284	0.0363	1.1027	-0.5078	0.9233
11.	BY	0.0370	-0.0376	0.0097	0.0333	-0.0359	-0.0141	0.0158	-0.0029	0.0120	-0.1816	0.3943	-0.1137

PH- Plant height (cm), PB- Primary Branches/Plant, DF-Days to 50% flowering, DM- Days to maturity, CP- Clusters/Plant, PC- Pods/cluster, SP- Seeds/Pod, PL- Pod Length, HSW- Hundred Seed Weight, HI- Harvest Index and BY- Biological Yield/Plant and SY- Seed Yield/Plant.

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

Traits		PH	PB	DF	DM	CP	PC	SP	PL	HSW	HI	BY	SY
PH	P	1.0000	0.2509***	0.2694***	0.4773***	-0.1186	0.1280*	0.1067	0.1863**	0.1229	-0.1049	0.0904	-0.1076
	G	1.0000	0.2682***	0.3137***	0.5212***	-0.1208	0.1421*	0.1264*	0.1995**	0.1391*	-0.1046	0.0939	-0.1084
PB	P		1.0000	0.0987	0.2584***	0.0880	0.1298*	0.1826**	-0.0182	0.1537*	-0.1115	-0.0911	-0.1908**
	G		1.0000	0.1111	0.2818***	0.0954	0.1614*	0.1825**	-0.0312	0.1604*	-0.1181	-0.0954	-0.2040**
DF	P			1.0000	0.6854***	-0.0852	0.1358*	0.0053	0.0007	0.1490*	-0.0357	0.0239	-0.0495
	G			1.0000	0.7322***	-0.1040	0.1597*	-0.0324	-0.0126	0.1840**	-0.0394	0.0247	-0.0547
DM	P				1.0000	0.0459	0.3063***	0.0623	0.0378	0.1748**	0.0033	0.0610	-0.0179
	G				1.0000	0.0525	0.3649***	0.0618	0.0416	0.1851**	0.0054	0.0844	-0.0086
CP	P					1.0000	0.3028***	0.0535	-0.0687	0.1397*	0.3357***	-0.0861	0.3200***
	G					1.0000	0.3261***	0.0546	-0.0682	0.1712**	0.3399***	-0.0910	0.3287***
PC	P						1.0000	0.0432	0.0184	0.2286***	0.1460*	-0.0321	0.1203*
	G						1.0000	0.0597	0.0245	0.3104***	0.1621*	-0.0356	0.1354*
SP	P							1.0000	0.4048***	0.0938	-0.1441*	0.0312	-0.1528*
	G							1.0000	0.4761	0.0670	-0.1699**	0.0400	-0.1832**
PL	P								1.0000	0.1730**	-0.1950**	-0.0076	-0.2286***
	G								1.0000	0.2120***	-0.2071**	-0.0073	-0.2453***
HSW	P									1.0000	0.0279	0.0210	0.0334
	G									1.0000	0.0329	0.0304	0.0422
HI	P										1.0000	-0.4475***	0.9125***
	G										1.0000	-0.4605***	0.9233***
BY	P											1.0000	-0.0803
	G											1.0000	-0.1137
SY	P												1.0000
	G												1.0000

* ** and *** Significant at 5%, 1% and 0.1% level respectively

PH- Plant height (cm), PB- Primary Branches/Plant, DF-Days to 50% flowering, DM- Days to maturity, CP- Clusters/Plant, PC- Pods/cluster, SP- Seeds/Pod, PL- Pod Length, HSW- Hundred Seed Weight, HI- Harvest Index and BY- Biological Yield/Plant and SY- Seed Yield/Plant.

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