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Research Note

Correlation and path coefficient analysis in blackgram [*Vigna mungo* (L.) Hepper]

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Abstract
Fourty five blackgram genotypes were studied including two check varieties (Pratap Urd-1 and PU-31) in randomized block design with three replications to study correlation and path coefficient analysis for 14 traits. Seed yield per plant was positively and significantly correlated with number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, biological yield and harvest index at both phenotypic as well as genotypic level. The positive direct effect on seed yield per plant was exhibited by number of pods per plant, biological yield, harvest index, days to 50 per cent flowering, plant height and number of seeds per pod. Thus, seed yield per plant can be improved by practicing selection for number of pods per plant, biological yield, harvest index, days to 50 per cent flowering, plant height and number of seeds per pod.

Key words
Blackgram, Correlation, Path coefficient analysis.

Blackgram (*Vigna mungo* (L.) Hepper) is an annual leguminous crop belongs to family Fabaceae and sub-family Papilionaceae wih a chromosome number of 2n=22. It is popularly known as “urd bean, urd or mash”, an excellent source of easily digestible good quality proteins. In addition, being an important source of human food and animal feed, it also plays an important role in sustaining soil fertility by improving soil physical properties and fixing atmospheric nitrogen. Being a drought resistant crop, it is suitable for dry land farming and predominantly used as an intercrop with other crops.

Blackgram is the fourth important pulse crop in India which holds about 13 per cent of the total pulse area and contributing about 10 per cent to the total pulse production. In India, blackgram is grown on 44.93 lakh hectares area with a production of 29.26 lakh tonnes and 651 kg/ha productivity (Directorate of Economics and Statistics, 2016-17). It is mostly grown in Andhra Pradesh, Uttar Pradesh, Maharashtra, Madhya Pradesh, Tamil Nadu, Rajasthan, Orissa and Bihar.

The major objective of crop breeding programme is to achieve higher yield. It is a complex character with low heritability and therefore, direct selection for yield to improve it is often not so successful. Therefore, it is advantageous to find out the closely related component traits of yield, so that, suitable selection strategies can be devised to improve yield. Association analysis provides measures of relationship among the traits and serves to assess the opportunity of mutual improvement of two desirable traits by common selection programme (Konda *et al*. 2008). Path analysis provides information about how close the other traits are to the yield. Direct and indirect attribution of component characters towards the yield was analyzed using only the genotypic correlation. Evaluation and exploitation of genotypes for various yield related characters as well as utilizing suitable breeding techniques for the development of improved varieties need to be explored. Therefore, several yield contributing characters *viz*., days to 50 per cent flowering, days to 75 per cent maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, pod length (cm), number of seeds per pod, seed yield per plant (g), biological yield per plant (g), harvest index (%), 100-seed weight (g) and seed protein content (%) were included in the present investigation.

The importance of blackgram as the source of vegetable protein and its role in sustainable agriculture in Indian situation is well known. Though, tremendous progress has been made in achieving quantum jumps in cereal crops, which ushered in an era of green revolution, the gains made in improvement of productivity of pulses in general and blackgram in particular are very less.

Several high yielding and disease resistant cultivars developed through routine breeding approaches have been released in blackgram. Inspite of this, production, area and productivity remained virtually stagnant over the last 20 years in India. Hence, there is vast scope of genetic improvement in blackgram for developing superior high yielding varieties.

In this experiment, 32 genotypes were collected from Pulses Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola2-Maharashtra and 13 genotypes were collected from AICRP on MULLARP, ARS, Agriculture University, Kota. The experiment for the present investigation was carried out on 45 genotypes of blackgram including 2 checks (Pratap Urd-1 and PU-31) sown in randomized block design in 3 replications during *kharif*, 2017 at Instructional Research Farm, Department of Plant Breeding and Genetics, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur. Two rows of each genotype were sown in 3 meter length. The row to row and plant to plant distance was kept at 30 cm and 10 cm, respectively. Data were collected on 14 traits *viz.,* days to 50 per cent flowering, days to 75 per cent maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, pod length (cm), number of seeds per pod, seed yield per plant (g), biological yield per plant (g), harvest index (%), 100-seed weight (g) and seed protein content (%). The observations for the above traits were recorded on randomly selected five competitive plants per plot in each replication except for days to 50 per cent flowering and days to 75 per cent maturity where observations were recorded on whole plot basis.

The phenotypic and genotypic correlation coefficients of all the characters were worked-out as per formula suggested by Al-Jibouri *et al.* (1958). The path coefficient analysis was carried-out as per the method suggested by Dewey and Lu (1959).

The estimates of genotypic and phenotypic correlation coefficients between different characters of blackgram genotypes are presented in Table 1. In the present investigation, the genotypic correlation coefficients were relatively higher than their corresponding phenotypic correlation coefficients for all the characters which indicated inherent association between various characters. This indicates relatively low influence of environment in modifying the total expression of the genotypes, thus altering the phenotypic expression (Reni *et al*. 2013 and Punia *et al*. 2013).

A perusal of Table-1 revealed that seed yield per plant was positively and significantly correlated with number of branches per plant (rp = 0.375**, rg = 0.516**), number of clusters per plant (rp = 0.388**, rg = 0.563**), number of pods per plant (rp = 0.669**, rg = 0.947**), number of pods per cluster (rp = 0.179*, rg = 0.254*), biological yield (rp = 0.586**, rg = 0.730**) and harvest index (rp = 0.628**, rg = 0.557**) at both phenotypic as well as genotypic level. Hemalatha *et al.* (2017) and Sushmitharaj *et al.* (2018) also reported positive significant correlation of seed yield per plant with number of pods per plant. Similarly Gowsalya *et al*. (2016) and Babu *et al*. (2016) also observed similar findings for number of pods per plant, number of clusters per plant and number of branches at both phenotypic and genotypic levels. Hence, the seed yield can be improved if the characters namely number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, biological yield and harvest index were given importance during selection process. It suggested that increase in growth related traits, pod characters and seed characters might contribute to high yields in blackgram. This situation meant to select high yielding genotypes of blackgram, it was essential to consider the above characters with their increasing magnitude. It helped in simultaneous improvement of all the positively correlated characters.

Seed yield per plant was negatively and significantly correlated with seed protein content (rp = -0.236**, rg = -0.414**) at both phenotypic as well as genotypic levels. Similar results were also reported by Konda *et al* (2008).

Days to 50 per cent flowering showed significant correlation in positive direction with pod length (rp = 0.254**, rg = 0.305**) at both phenotypic and genotypic levels. These results are in agreement with the results of Kanta and Verma (2003).

Days to 75 per cent maturity exhibited significant and positive correlation with 100-seed weight (rp = 0.236**, rg = 0.338**) at both phenotypic and genotypic levels.Plant height showed significant and negative correlation with pod length (rp = -0.179*, rg = -0.253*) at both phenotypic and genotypic levels.

Number of branches per plant exhibited significant and positive correlation at both phenotypic and genotypic levels with number of clusters per plant (rp = 0.685**, rg = 0.781**), number of pods per plant (rp = 0.533**, rg = 0.604**) and biological yield (rp = 0.395**, rg = 0.523**). These results were in agreement with Mathivathana *et al*. (2015). Mehra *et al*. (2016) also reported that number of branches per plant were significant and positive correlation with number of pods per plant.

Number of clusters per plant showed significant and positive correlation with number of pods per plant (rp = 0.495**, rg = 0.594**) and biological yield (rp = 0.378**, rg = 0.518**) at both phenotypic and genotypic levels. Mathivathana *et al*. (2015) and Sushmitharaj *et al.* (2018) also reported the same correlation.

Number of pods per plant showed significant and positive correlation with number of pods per cluster (rp = 0.344**, rg = 0.261**), biological yield (rp = 0.525**, rg = 0.740**) and harvest index (rp = 0.292**, rg = 0.452**) at both phenotypic and genotypic levels. Mathivathana *et al*. (2015) also reported that number of pods per plant was having significant positive association with harvest index. Similarly Mehra *et al*. (2016) reported positive association of number of pods per plant with biological yield per plant.

Number of pods per cluster exhibited significant and positive correlation with harvest index (rp = 0.178*, rg = 0.266*) at both phenotypic as well as genotypic level. This result was in accordance with Mathivathana *et al*. (2015).

100-seed weight showed significant and positive correlation with seed protein content (rp = 0.180*, rg = 0.237*) at both phenotypic and genotypic levels.

When more number of variables was considered in correlation, the association becomes more complex and does not have meaningful interpretation. Hence, genotypic correlation partitioned into direct and indirect effects to specify the cause and their relative importance (Table-2). The highest positive direct effect on seed yield per plant was exhibited by number of pods per plant (0.732) followed by biological yield (0.354), harvest index (0.240), days to 50 per cent flowering (0.096), plant height (0.080) and number of seeds per pod (0.054). Reni *et al.* 2013 revealed that the highest positive direct effect on seed yield per plant was recorded by number of pods per plant and days to 50 per cent flowering. Panigrahi *et al*. (2014) also showed that days to 50 per cent flowering and number of pods per plant showed positive direct effect with seed yield per plant. Similarly Mehra *et al*. (2016) reported that biological yield per plant exhibited highest positive direct effect on seed yield. Likewise Patidar and Sharma (2017) reported that number of pods per plant, biological yield per plant and plant height exerted high positive direct association with seed yield.

The negative direct effect on seed yield was exhibited by number of pods per cluster (-0.171) followed by number of branches per plant (-0.135), seed protein content (-0.098), number of clusters per plant (-0.092), days to 75 per cent maturity (-0.059), pod length and 100- seed weight (-0.050). Punia *et al.* (2013) reported that days to 75 per cent maturity and 100- seed weight exerted negative direct effect on seed yield per plant. Panigrahi *et al*. (2014) observed that pod length expressed negative direct effect on seed yield per plant. The negative direct effect indicated that these characters had low association and selection based on these characters would not be effective.

The number of pods per plant exhibited highest positive indirect effect on seed yield per plant via biological yield (0.542), number of branches per plant (0.442), number of clusters per plant (0.435), harvest index (0.331) and number of pods per cluster (0.191). The remaining estimates of the indirect effect in the present study were too low to be negligible importance. The component of residual effect of path analysis was 0.0093, low residual effect indicated that number of characters for path analysis were adequate and appropriate.

From the correlation study it can be concluded that the seed yield can be improved if the characters namely number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, biological yield and harvest index were given importance during selection process. Since, seed yield per plant was positively and significantly correlated with these traits.

Further, path coefficient analysis revealed that selection based on number of pods per plant, biological yield, harvest index, days to 50 per cent flowering, plant height and number of seeds per pod could help in genetic improvement of seed yield per plant in blackgram genotypes, because these characters had positive direct effect on seed yield per plant.

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Table 1. Estimates of phenotypic and genotypic correlation coefficient of various characters of blackgram [*Vigna mungo* (L.) Hepper]

Character		Days to 50 % flowering	Days to 75 % maturity	Plant height (cm)	No. of branches per plant	No. of clusters per plant	No. of pods per plant	No. of pods per cluster	Pod length (cm)	No. of seeds per pod	Biological yield (g)	Harvest index (%)	100-seed weight (g)	Seed protein content (%)	Seed yield per plant (g)
Days to 50 % flowering	P	1.000	0.032	-0.143	-0.039	-0.109	0.015	0.150	0.254**	-0.010	-0.113	0.128	-0.150	0.054	0.020
	G	1.000	0.161	-0.294	-0.078	-0.061	0.032	0.125	0.305**	-0.005	-0.176	0.306	-0.202	0.025	0.084
Days to 75 % maturity	P		1.000	-0.179*	-0.226**	-0.073	-0.037	0.037	0.119	-0.159	-0.029	-0.080	0.236**	0.142	-0.083
	G		1.000	-0.253*	-0.321**	-0.086	-0.027	0.077	0.166	-0.318	-0.142	-0.068	0.338**	0.238	-0.178
Plant height (cm)	P			1.000	-0.060	0.039	-0.054	-0.100	-0.170*	-0.024	-0.002	0.135	0.070	-0.064	0.102
	G			1.000	-0.076	0.045	-0.066	-0.134	-0.243*	0.017	0.025	0.099	0.085	-0.054	0.094
No. of branches per plant	P				1.000	0.685**	0.533**	-0.283**	-0.100	0.107	0.395**	0.064	0.045	0.062	0.375**
	G				1.000	0.781**	0.604**	-0.377**	-0.107	0.136	0.523	0.108	0.042	0.101	0.516**
No. of clusters per plant	P					1.000	0.495**	-0.627**	-0.016	0.124	0.378**	0.092	0.069	0.052	0.388**
	G					1.000	0.594**	-0.608**	-0.051	0.126	0.518**	0.162	0.078	0.083	0.563**
No. of pods per plant	P						1.000	0.344**	-0.049	0.057	0.525**	0.292**	0.099	-0.148	0.669**
	G						1.000	0.261**	-0.091	0.125	0.740**	0.452**	0.121	-0.213	0.947**
No. of pods per cluster	P							1.000	-0.019	-0.060	0.044	0.178*	-0.002	-0.202*	0.179*
	G							1.000	-0.012	0.012	0.092	0.266*	0.008	-0.333*	0.254*
Pod length (cm)	P								1.000	0.151	-0.189*	0.005	0.038	0.172*	-0.143
	G								1.000	0.197	-0.256*	-0.005	0.063	0.241*	-0.204
No. of seeds per pod	P									1.000	0.021	0.066	0.136	-0.107	0.077
	G									1.000	0.035	0.217	0.177	-0.166	0.195
Biological yield (g	P										1.000	-0.251**	0.091	-0.036	0.586**
	G										1.000	-0.156**	0.119	-0.039	0.730**
Harvest index (%)	P											1.000	-0.148	-0.260**	0.628**
	G											1.000	-0.187	-0.555**	0.557**
100-seed weight (g	P												1.000	0.180*	-0.044
	G												1.000	0.237*	-0.028
Seed protein content (%)	P													1.000	-0.2361**
	G													1.000	-0.4142**
Seed yield per plant (g)	P														1.000
	G														1.000

Table 2. Genotypic path matrix for seed yield per plant (g) in blackgram [*Vigna mungo* (L.) Hepper]

Character	Days to 50 per cent flowering	Days to 75 per cent maturity	Plant height (cm)	No. of branches per plant	No. of clusters per plant	No. of pods/ per plant	No. of pods per cluster	Pod length (cm)	No. of seeds per pod	Biological yield (g)	Harvest index (%)	100-seed weight (g)	Seed protein content (%)	Seed yield per plant (g)
Days to 50 per cent flowering	**0.096**	0.015	-0.028	-0.007	-0.006	0.003	0.012	0.029	0.000	-0.017	0.029	-0.019	0.002	**0.084**
Days to 75 per cent maturity	-0.009	**-0.059**	0.015	0.019	0.005	0.002	-0.005	-0.010	0.019	0.008	0.004	-0.020	-0.014	**-0.178**
Plant height (cm)	-0.024	-0.020	**0.080**	-0.006	0.004	-0.005	-0.011	-0.019	0.001	0.002	0.008	0.007	-0.004	**0.094**
No. of branches per plant	0.011	0.043	0.010	**-0.135**	-0.106	-0.082	0.051	0.014	-0.018	-0.071	-0.015	-0.006	-0.014	**0.516****
No. of clusters per plant	0.006	0.008	-0.004	-0.072	**-0.092**	-0.055	0.056	0.005	-0.012	-0.048	-0.015	-0.007	-0.008	**0.563****
No. of pods/ per plant	0.024	-0.020	-0.048	0.442	0.435	**0.732**	0.191	-0.067	0.092	0.542	0.331	0.088	-0.156	**0.947****
No. of pods per cluster	-0.021	-0.013	0.023	0.064	0.104	-0.045	**-0.171**	0.002	-0.002	-0.016	-0.045	-0.001	0.057	**0.254***
Pod length (cm)	-0.015	-0.008	0.012	0.005	0.003	0.005	0.001	**-0.050**	-0.010	0.013	0.000	-0.003	-0.012	**-0.204**
No. of seeds per pod	0.000	-0.017	0.001	0.007	0.007	0.007	0.001	0.011	**0.054**	0.002	0.012	0.010	-0.009	**0.195**
Biological yield (g)	-0.062	-0.050	0.009	0.185	0.183	0.262	0.033	-0.091	0.013	**0.354**	-0.055	0.042	-0.014	**0.730****
Harvest index (%)	0.073	-0.016	0.024	0.026	0.039	0.108	0.064	-0.001	0.052	-0.037	**0.240**	-0.045	-0.133	**0.557****
100-seed weight (g)	0.010	-0.017	-0.004	-0.002	-0.004	-0.006	0.000	-0.003	-0.009	-0.006	0.009	**-0.050**	-0.012	**-0.028**
Seed protein content (%)	-0.002	-0.023	0.005	-0.010	-0.008	0.021	0.033	-0.024	0.016	0.004	0.054	-0.023	**-0.098**	**-0.414****

R square = 1.0093 and Residual effect =SQRT(1- 1.0093)