Correlation and Path Analysis for Yield and Yield Contributing Traits in Advance Generation of Blackgram (*Vigna mungo* (L.) Hepper)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

Despite being a short-duration legume crop with excellent nutritional value, blackgram is rarely grown extensively because of various obstacles. In light of this, the research sought to understand the nature and strength of the relationship between yield and related qualities for efficient production, with the goal of developing blackgram genotypes with greater adaptability, genetic variability, and high yielding potential. Fifty one genotypes derived from seventeen inter-varietal

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crosses with variable plant and pod characteristics were evaluated in Randomized Complete Block Design with three replications during *kharif* 2018 at Palampur. Significant differences were observed among all genotypes for all the characters. Seed yield per plant showed positive association towards plant height, pods per plant, biological yield per plant and harvest index. The positive association was mainly due to direct effects of these traits with seed yield per plant and also indirectly contributed for positive association with other traits. Therefore, these traits provide an important criterion of selection procedures for achieving enhanced performance of blackgram genotypes for higher yield.

1. INTRODUCTION

Leguminous blackgram (*Vigna mungo*) is thought to have its origin in Indian-subcontinent, belongs to the Fabaceae family, specifically falling under the sub-family Papilionaceae and possesses a chromosomal count of 2n=22 [1]. According to Bhareti et al. [2], it is thought that its ancestor was *V. mungo* var. *silvestris*, with its primary & secondary centres of origin being in Central Asia and India, respectively. It is a good source of protein, oil, fibre, carbohydrates, ash, amino acids, vitamins as well as crucial minerals i.e. phosphorus and iron [3]. The crop thrives in challenging weather conditions and enhances soil fertility by effectively fixing atmospheric nitrogen. It is cultivated using a variety of agricultural practises under varied agro-ecological conditions and cropping systems [4]. Despite this fact, it also identified as a promising crop in a number of nations, systematic research data on crop development utilising biometrical techniques are not yet accessible [5]. In order to describe the accuracy of phenotypic values, the estimate of heredity serves as a forecasting tool [6]. Correlations, although useful in evaluating the amount & direction of character connections, might be deceptive if a high correlation between two traits results from indirect effects [7]. Earlier researchers used path analysis to determine the effect of some other trait on yield in blackgram by dividing genotypic correlations into direct and indirect effects of the traits. In this view, four varieties that were suggested for cultivation in Himachal Pradesh were employed with 51 F_5 progenies, produced through seventeen inter-varietal crosses using the pedigree method of selection to study the inter-relationship for yield contributing traits.

2. MATERIALS AND METHODS

This study was undertaken at Experimental Farm of Department of Genetics and Plant Breeding, CSK HPKV, Palampur situated at altitude of about 1300m *amsl* (above mean sea level) with 32°6' N latitude, 76°3' E longitude referring the mid-hill zone-II and characterized by sub-temperate climate along with heavy rainfalls (2500 mm per annum). The experimental field's soil had a clay loam texture and a pH of 5.7. The experimental material comprised of 51 genotypes derived from 17 inter-varietal crosses followed by pedigree selection along with four recommended varieties *viz.,* Palampur-93, Him Mash-1, HPBU-111 and UG-218. These 55 genotypes (Table 1) were evaluated during *kharif* 2018 in Randomized Complete Block Design (RCBD) implemented using three replications. Each genotype was planted in paired rows, each measuring 1 meter in length and spaced at 30 centimetres, with an intra-plant distance of 10 centimetres. The crop was cultivated under rainfed conditions and all recommended agronomic practices were followed to ensure optimal growth and yield. Observations were recorded on ten randomly selected plants in each replication for all the genotypes for twelve quantitative traits *viz.*, days to 50% flowering, days to 75% maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g), harvest index (%) and protein content (%). Nitrogen content was estimated using Micro-Kjeldhal method (AOAC 1965) and the crude protein content was determined by multiplying the nitrogen percentage by 6.25 and expressed as a percentage. Analysis of variance was performed following the approach outlined by Panse and Sukhatme (1967). Data observed for correlation coefficient values (r) were calculated at genotypic and phenotypic levels using the formula proposed by Al- Jibouri et al. [8] and path analysis was performed following the procedure of Dewey and Lu [7] using OP-STAT software.

Table 1. Details of genotypes of blackgram used in the present study

Code	Pedigree	Genotype	Source
1.	TU-94-2 X Palampur-93	GPB/15-21-P-5-2-10	CSK HPAU, Palampur
2.	TU-94-2 X Palampur-93	GPB/15-21-P-2-1-8	CSK HPAU, Palampur
3.	TU-94-2 X Palampur-93	GPB/15-21-P-4-8-9	CSK HPAU, Palampur
4.	DU-1 X Palampur-93	GPB/15-06-P-2-8-2	CSK HPAU, Palampur
5.	DU-1 X Palampur-93	GPB/15-06-P-6-4-17	CSK HPAU, Palampur
6.	DU-1 X Palampur-93	GPB/15-06-P-1-10-4	CSK HPAU, Palampur
7.	COBG-653 X HPBU-111	GPB/15-04-P-3-5-12	CSK HPAU, Palampur
8.	COBG-653 X HPBU-111	GPB/15-04-P-4-6-3	CSK HPAU, Palampur
9.	COBG-653 X HPBU-111	GPB/15-04-P-5-9-9	CSK HPAU, Palampur
10.	DU-1 X Him Mash-1	GPB/15-02-P-2-4-8	CSK HPAU, Palampur
11.	DU-1 X Him Mash-1	GPB/15-02-P-3-10-10	CSK HPAU, Palampur
12.	DU-1 X Him Mash-1	GPB/15-02-P-5-9-1	CSK HPAU, Palampur
13.	TU-17-4 X Palampur-93	GPB/15-15-P-3-3-8	CSK HPAU, Palampur
14.	TU-17-4 X Palampur-93	GPB/15-15-P-2-6-4	CSK HPAU, Palampur
15.	TU-17-4 X Palampur-93	GPB/15-15-P-4-9-11	CSK HPAU, Palampur
16.	HPBU-124 X HPBU-111	GPB/15-13-P-1-5-7	CSK HPAU, Palampur
17.	HPBU-124 X HPBU-111	GPB/15-13-P-4-9-10	CSK HPAU, Palampur
18.	HPBU-124 X HPBU-111	GPB/15-13-P-6-4-5	CSK HPAU, Palampur
19.	KU-216 X Him Mash-1	GPB/15-07-P-5-7-10	CSK HPAU, Palampur
20.	KU-216 X Him Mash-1	GPB/15-07-P-2-1-13	CSK HPAU, Palampur
21.	KU-216 X Him Mash-1	GPB/15-07-P-4-3-9	CSK HPAU, Palampur
22.	KU-553 X Him Mash-1	GPB/15-10-P-2-10-1	CSK HPAU, Palampur
23.	KU-553 X Him Mash-1	GPB/15-10-P-3-9-1	CSK HPAU, Palampur
24.	KU-553 X Him Mash-1	GPB/15-10-P-4-9-8	CSK HPAU, Palampur
25.	COBG-653 X Palampur-93	GPB/15-01-P-6-1-8	CSK HPAU, Palampur
26.	COBG-653 X Palampur-93	GPB/15-01-P-5-4-11	CSK HPAU, Palampur
27.	COBG-653 X Palampur-93	GPB/15-01-P-4-4-17	CSK HPAU, Palampur
28.	KU-553 X HPBU-111	GPB/15-03-P-5-5-8	CSK HPAU, Palampur
29.	KU-553 X HPBU-111	GPB/15-03-P-1-10-2	CSK HPAU, Palampur
30.	KU-553 X HPBU-111	GPB/15-03-P-6-1-11	CSK HPAU, Palampur
31.	IPU-05-13 X Palampur-93	GPB/15-09-P-4-7-10	CSK HPAU, Palampur
32.	IPU-05-13 X Palampur-93	GPB/15-09-P-5-5-1	CSK HPAU, Palampur
33.	IPU-05-13 X Palampur-93	GPB/15-09-P-1-2-5	CSK HPAU, Palampur
34.	IPU-02-33 X Palampur-93	GPB/15-08-P-5-3-4	CSK HPAU, Palampur
35.	IPU-02-33 X Palampur-93	GPB/15-08-P-1-5-11	CSK HPAU, Palampur
36.	IPU-02-33 X Palampur-93	GPB/15-08-P-4-9-16	CSK HPAU, Palampur
37.	KU-553 X Palampur-93	GPB/15-05-P-3-9-8	CSK HPAU, Palampur
38.	KU-553 X Palampur-93	GPB/15-05-P-5-4-12	CSK HPAU, Palampur
39.	KU-553 X Palampur-93	GPB/15-05-P-6-8-4	CSK HPAU, Palampur
40.	TU-17-4 X Him Mash-1	GPB/15-19-P-4-9-11	CSK HPAU, Palampur
41.	TU-17-4 X Him Mash-1	GPB/15-19-P-2-10-1	CSK HPAU, Palampur
42.	TU-17-4 X Him Mash-1	GPB/15-19-P-6-6-7	CSK HPAU, Palampur
43.	HPBU-126 X HPBU-111	GPB/15-12-P-1-7-10	CSK HPAU, Palampur
44.	HPBU-126 X HPBU-111	GPB/15-12-P-6-3-15	CSK HPAU, Palampur
45.	HPBU-126 X HPBU-111	GPB/15-12-P-4-4-11	CSK HPAU, Palampur
46.	KUG-540 X Palampur-93	GPB/15-14-P-5-8-7	CSK HPAU, Palampur
47.	KUG-540 X Palampur-93	GPB/15-14-P-2-10-2	CSK HPAU, Palampur
48.	KUG-540 X Palampur-93	GPB/15-14-P-1-4-9	CSK HPAU, Palampur
49.	HPBU-126 X Palampur-93	GPB/15-16-P-2-4-7	CSK HPAU, Palampur
50.	HPBU-126 X Palampur-93	GPB/15-16-P-4-3-11	CSK HPAU, Palampur
51.	HPBU-126 X Palampur-93	GPB/15-16-P-1-7-1	CSK HPAU, Palampur
52.	Palampur-93	Pure line selection from local material of Himachal Pradesh by CSKHPAU, Palampur	
53.	Him Mash-1	Pure line selection from local material of Himachal	

Code	Pedigree	Genotype	Source
		Pradesh by CSKHPAU, Palampur	
54.	HPBU-111	Pure line selection from local material of Himachal Pradesh by CSKHPAU, Palampur	
55.	UG-218	Pure line selection from local material of Himachal Pradesh by CSKHPAU, Palampur	

3. RESULTS AND DISCUSSION

In order to determine the effectiveness of selection, genetic variability is a fundamental prerequisite in crop development programme. Its presence is essential for both broad adaptability & resistance to biotic/abiotic factors. Analysis of variance revealed that the mean sum of squares resulting from genotypes were significantly different for all of the characteristics, indicating that the existing material had enough genetic variation to allow for the selection of superior genotypes with desirable characteristics.

3.1 Range and Mean

The observation for morphological and yield traits expressed that days to 50% flowering varied from 43.00 - 49.66 days with mean of 46.19 days, days to 75% maturity varied from 72.66 - 80.00 days with mean of 76.39 days, plant height varied from 15.10 - 24.92 cm with mean of 19.54 cm, branches per plant vary from 1.85 -3.10 cm with average of 2.56 cm, pods per plant vary from 11.53 - 18.92 with mean of 14.52, pod length varied from 4.05 - 4.78 cm with mean of 4.41 cm. seeds per pod varied from 4.00 - 5.66 with mean of 4.93, biological yield per plant ranged from 9.72 - 19.48 g with mean of 13.60 g. Seed yield per plant varied from 2.38 - 3.94 g with mean of 3.08 g and the harvest index ranged between 18.49 - 32.68% with mean value of 22.79%. In case of quality traits, 100-seed weight varied from 3.66 - 5.30 g with mean of 4.58 g and protein content varied from 19.20 - 24.50% with mean of 22.18%.

3.2 Correlation Coefficient Analysis

Comprehending the nature and extent of the association between traits is essential for steering the mean population under investigation in the intended direction. Understanding the relationships between key characteristics serves as the foundation for designing breeding programmes that are more effective. Additionally, it assists in simultaneously enhancing multiple characters [9]. In this regard, number of pods per plant followed by plant height, biological yield per plant and harvest index demonstrated significant and positive correlations with seed yield per plant (Table 3) at genotypic (G) and phenotypic (P) levels. Days to 50% flowering and protein content were both negatively correlated with seed yield per plant at the genotypic level, indicating that early selection should be done with caution. Prior studies [10,11], that emphasised a focus on these features also revealed substantial and favourable associations for the majority of these traits, with varying magnitudes in varied breeding material.

Plant height had a positive and significant correlation with branches per plant, pods per plant, pod length, seeds per pod and biological yield per plant and significantly negatively associated with harvest index at the genotypic level while positively associated with pods per plant and biological yield per plant at the phenotypic level. These results were in agreement with the findings of Singh et al. [12]. At the genotypic level, pods per plant are considerably and positively connected with pod length, seeds per pod, biological yield per plant and significantly negatively linked with protein content, whereas pod length correlated significantly positive with seeds per pod at both levels. Biological yield per plant was considerably and negatively connected with harvest index at both levels, whereas harvest index demonstrated strong negative connection with 100-seed weight and protein content at genotypic level. Chauhan et al. [13] also revealed negative association of harvest index with 100-seed weight in blackgram.

3.3 Direct and Indirect Effects of Different Traits on Seed Yield

Instead of showing cause and effect link, correlation analysis simply depicts the overall influence of a certain characteristic on yield, subsequently, it shows the association pattern of component attributes with yield. In these situations, path coefficient analysis [14,7] is crucial for separating the correlation into indirect & direct effects of a particular causative component. Consequently, path analysis is employed to evaluate the cause-effect relationship as well as to make effective choices.

Table 2. Estimates of phenotypic and genotypic correlation coefficient among various yield and morphological traits in urdbean

Traits		Days to 75% maturity	Plant Height (cm)	Branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	Biological yield per plant (g)	Harvest index (%)	100-seed weight (g)	Protein content (%)	Seed yield per plant (g)
Days to 50% flowering	P	0.903*	0.005	0.001	0.003	-0.186*	-0.123	0.065	-0.069	-0.033	0.126	0.020
	G	1.003*	-0.201*	-0.268*	-0.279*	-0.637*	-0.176*	-0.087	-0.113	-0.203*	0.165*	-0.230*
Days to 75% maturity	P		0.063	0.031	0.057	-0.173*	-0.066	0.120	-0.094	0.005	0.038	0.065
	G		-0.077	-0.551*	-0.173*	-0.711*	-0.188*	0.025	-0.167*	-0.088	0.090	-0.150
Plant Height (cm)	P			0.037	0.919*	-0.045	0.028	0.909*	-0.036	-0.031	-0.018	0.859*
	G			0.348*	0.870*	0.324*	0.193*	0.825*	-0.191*	-0.051	-0.130	0.738*
Branches per plant	P				0.018	0.118	0.102	0.023	0.079	-0.079	-0.005	0.061
	G				0.331*	0.050	0.391*	0.063	0.385*	-0.092	0.175*	0.412*
Pods per plant	P					-0.036	0.012	0.890*	0.147	0.021	-0.081	0.944*
	G					0.470*	0.166*	0.780*	0.057	-0.041	-0.297*	0.896*
Pod length (cm)	P						0.347*	-0.057	0.006	0.139	-0.119	-0.035
	G						1.023*	0.016	0.253*	0.304*	-0.138	0.320*
Seeds per pod	P							-0.011	0.035	0.064	-0.068	0.019
	G							0.079	0.034	0.113	-0.113	0.139
Biological yield per plant (g)	P								-0.237*	-0.021	-0.056	0.824*
	G								-0.518*	0.031	-0.216*	0.585*
Harvest index (%)	P									-0.006	-0.130	0.339*
	G									-0.164*	-0.200*	0.386*
100-seed weight (g)	P										0.043	-0.007
	G										0.127	-0.129
Protein content (%)	P											-0.147
	G											-0.453*

*P<.05

Table 3. Estimates of direct and indirect effects on seed yield at phenotypic level and genotypic level for different traits in urdbean

Traits		Days to 50% flowering	Days to 75% maturity	Plant Height (cm)	Branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	Biological yield per plant (g)	Harvest index (%)	100-seed weight (g)	Protein content (%)	Correlation with seed yield per plant (g)
Days to 50% flowering	P	**-0.009**	0.016	0.000	0.000	0.000	-0.002	0.000	0.055	-0.036	0.000	-0.003	0.021
	G	**-0.195**	0.151	-0.031	0.006	-0.005	0.031	-0.010	-0.076	-0.099	0.004	-0.007	-0.230*
Days to 75% maturity	P	-0.008	**0.018**	0.003	0.000	0.004	-0.002	0.000	0.102	-0.050	0.000	0.000	0.065
	G	-0.196	**0.151**	-0.012	0.012	-0.003	0.035	-0.011	0.022	-0.146	0.001	-0.004	-0.150
Plant Height (cm)	P	0.000	0.001	**0.042**	0.000	0.067	0.000	0.000	0.769	-0.019	0.000	0.000	0.859*
	G	0.039	-0.012	**0.155**	-0.008	0.015	-0.016	0.011	0.713	-0.167	0.001	0.006	0.738*
Branches per plant	P	0.000	0.000	0.002	**-0.004**	0.001	0.001	0.000	0.019	0.042	0.000	0.000	0.061
	G	0.052	-0.083	0.054	**-0.022**	0.006	-0.002	0.023	0.055	0.336	0.002	-0.008	0.412*
Pods per plant	P	0.000	0.001	0.038	0.000	**0.072**	0.000	0.000	0.753	0.078	0.000	0.002	0.944*
	G	0.054	-0.026	0.135	-0.007	**0.018**	-0.023	0.010	0.673	0.050	0.000	0.013	0.896*
Pod length (cm)	P	0.002	-0.003	-0.002	0.000	-0.003	**0.012**	0.000	-0.048	0.003	0.002	0.003	-0.035
	G	0.124	-0.107	0.050	-0.001	0.008	**-0.050**	0.059	0.014	0.220	-0.006	0.006	0.320*
Seeds per pod	P	0.001	-0.001	0.001	0.000	0.000	0.004	**0.001**	-0.009	0.019	0.000	0.002	0.019
	G	0.034	-0.028	0.030	-0.009	0.003	-0.049	**0.058**	0.068	0.030	-0.002	0.005	0.139
Biological yield per plant (g)	P	0.000	0.002	0.038	0.000	0.064	0.000	0.000	**0.846**	-0.126	0.000	0.001	0.824*
	G	0.017	0.004	0.128	-0.001	0.013	0.000	0.005	**0.863**	-0.452	0.000	0.009	0.585*
Harvest index (%)	P	0.000	-0.001	-0.002	0.000	0.010	0.000	0.000	-0.201	**0.530**	0.000	0.003	0.339*
	G	0.022	-0.025	-0.030	-0.009	0.001	-0.012	0.002	-0.447	**0.872**	0.003	0.009	0.386*
100-seed weight (g)	P	0.000	0.000	-0.001	0.000	0.001	0.002	0.000	-0.017	-0.003	**0.012**	-0.001	-0.007
	G	0.040	-0.013	-0.008	0.002	0.000	-0.015	0.007	0.027	-0.143	**-0.020**	-0.006	-0.129
Protein content (%)	P	-0.001	0.000	0.000	0.000	-0.005	-0.001	0.000	-0.047	-0.069	0.000	**-0.024**	-0.147
	G	-0.032	0.014	-0.020	-0.004	-0.005	0.007	-0.007	-0.187	-0.174	-0.002	**-0.043**	-0.453*

P<.05, Residual effect: Phenotypic-0.015, Genotypic-0.001

In the current investigation, biological yield per plant had the most positive direct impacts, followed by harvest index, pods per plant, plant height, days to 75% maturity and seeds per pod with seed yield per plant at both levels (Table 3). Similar findings also reported by Tambe et al. [15] and Arya et al. [16] in blackgram, suggesting direct selection of attributes to enhance seed yield per plant. Days to 50% flowering, branches per plant and protein content showed substantial direct negative impacts at both levels, suggesting a weak connection between these variables and the futility of selection based on these characteristics.

The link between seed yield per plant and plant height, seed yield per plant and pod length, seed yield per plant and pods per plant, at both levels, was mostly caused by the favourable indirect influence from biological yield per plant, which was followed by days to 75% maturity and branches per plant for seed yield per plant. In a similar manner, harvest index had a negative indirect influence on seed yield per plant via biological yield per plant, indicating that both variables are negatively connected with one another but positively correlated with seed yield per plant and their direct selection would be desired for yield enhancement.

Therefore, the minimal unexplained variation, indicated by the low residual effect at both phenotypic and genotypic levels (P: 0.015; G: 0.001) for seed yield per plant, suggests that the 12 traits considered in this study predominantly contribute to the observed variation in the dependent variable [17,18].

4. CONCLUSION

Generally, genotypic correlation exhibited a greater magnitude than the phenotypic correlation across all traits, signifying an inherent association among the various traits. It was found that seed yield per plant showed positive correlation with plant height, pods per plant, biological yield per plant and harvest index at both phenotypic and genotypic level. Results of the path analysis revealed that biological yield per plant had the highest and most favourable direct impacts followed by harvest index, pods per plant, plant height, days to 75% maturity and seeds per pod on seed yield per plant. Therefore, in order to increase seed yield, focus may be laid on these traits. Harvest index and biological yield per plant were observed as good selection indices because of their higher direct contribution toward seed yield per plant.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Dana S. Genomic relationship in the genus Vigna and its implications in the breeding programme. Breeding methods for improvement of pulse crops. 1980;31:357-367.
2. Bhareti P, Singh DP, Khulbe RK. Genetic variability and association analysis of advanced lines and cultivars following intervarietal and interspecific crosses in blackgram. Crop Improvement. 2011;38:67-70.
3. Sohel MH, Miah MR, Mohiuddin SJ, Islam AKMS, Rahman MM and Haque MA. Correlation and path coefficient analysis of Blackgram (*Vigna mungo* (L.) Hepper). Journal of Bioscience and Agriculture Research. 2016;7:621-629.
4. Gupta S, Gupta SR, Dikshit HK, Singh RA. Variability and its characterization in Indian collections of blackgram [Vigna mungo (L.) Hepper]. Plant Genetic Resources Newsletter. 2001;127:20-24.
5. Ghafoor AZ, Ahmad N, Hashmi I, Bashirm M. Genetic diversity based on agronomic traits and SDS-PAGE markersin relation to geographic pattern of blackgram [*Vigna mungo*(L.) Hepper]. Journal of Genetics and Breeding. 2003;57:5-14.
6. Unche PB, MB Misal, SB Borgaonkar, GV Godhawale, BD Chavan and DR Sawant. Genetic variability studies in sweet sorghum (*Sorghum bicolor* L. Moench). Int. J. Plant Sci. 2008;3:16–18.
7. Dewey DR, Lu KH. A correlation and path analysis of components of crested wheat grass seed production. Agronomy Journal. 1959;51:513-518.
8. Al-jibouri HA, Miller PA, Robinson HP. Genotypic and environment variance and covariance in upland cotton cross of interspecific origin. Agronomy Journal. 1958;50:633-636.
9. Falconer DS. Introduction to quantitative genetics, 2nd Edition, Longman Group Limited, Longman House, Harrow, England. 1981;350.

10. Sathees N, Shoba D, Saravanan S, Kumari SMP, Pillai MA. Studies on genetic variability, association and path coefficient analysis in black gram [*Vigna mungo* (L.) Hepper]. International Journal of Current Microbiology and Applied Sciences. 2019;8:1892-1899.

11. Vadivel K, Manivannan N, Mahalingam A, Satya VK, Vanniarajan C, Saminathan VR. Correlation analysis for yield, yield components and MYMV disease scores in blackgram [*Vigna mungo* (L.) Hepper]. Electronic Journal of Plant Breeding. 2019;10:712-716.

12. Singh M, Swarup I, Billore M, Chaudhari PR. Association analysis of yield and yield attributing characters in blackgram [*Vigna mungo* (L.) Hepper]. Agricultural Science Digest. 2016;36:83-87.

13. Chauhan S, Patial R, Mittal RK, Sood VK. Correlation and path analysis for yield and its related traits in F_3 generation of blackgram [*Vigna mungo* (L.) Hepper]. The Bioscan. 2017;12 71-76.

14. Wright S. Correlation and causation. Journal of Agricultural Research. 1921;20:577-587.

15. Tambe RA, Lal GM, Ramteke PW. Correlation and path analysis for yield and yield components in blackgram [*Vigna mungo* (L.) Hepper]. International Journal of Current Microbiology and Applied Sciences. 2018;7:2074-2084.

16. Arya P, Lal GM, Lal SS. Correlation and path analysis for yield and yield components in blackgram (*Vigna mungo* (L.) hepper). International Journal of Advanced Biological Research. 2017;7:382-386.

17. A.O.A.C. Official methods of analysis of the association of official analytical chemists. 11th Edition. Washington, D.C; 1965.

18. Panse VG, Sukhatme PV. Statistical methods for agricultural workers 2nd edition ICAR New Delhi. 1984;381.

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