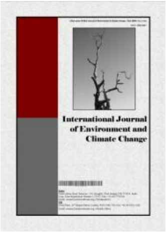

International Journal of Environment and Climate Change

12(11): 344-351, 2022; Article no.IJECC.89458
ISSN: 2581-8627
(Past name: British Journal of Environment & Climate Change, Past ISSN: 2231–4784)

Correlation and Path Coefficient Analysis for Yield and Yield Attributing Traits in Blackgram (*Vigna mungo*. (L) Hepper)

M. Priyanka [a*], K. Rukmini Devi [b], K. Parimala [c] and Ch. Anuradha [d]

[a] *Department of Genetics and Plant Breeding, Professor Jayashankar Telangana State Agricultural University, Agricultural College, Rajendranagar, Hyderabad, Telangana, India.*
[b] *Department of Genetics and Plant Breeding, Professor Jayashankar Telangana State Agricultural University, Agricultural Research Station, Madhira, Telangana, India.*
[c] *Department of Genetics and Plant Breeding, Professor Jayashankar Telangana State Agricultural University, Seed Research and Technology Center, Rajendranagar, Hyderabad, Telangana, India.*
[d] *Department of Biotechnology, Professor Jayashankar Telangana State Agricultural University, Agricultural College, Rajendranagar, Hyderabad, Telangana, India.*

Authors' contributions

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

Article Information

DOI: 10.9734/IJECC/2022/v12i1130980

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/89458

Original Research Article

Received 06 May 2022
Accepted 11 July 2022
Published 13 July 2022

ABSTRACT

The present research work was conducted at Agricultural Research Station (ARS), Madhira during *Rabi* 2022 to assess the correlation and path coefficient analysis among yield contributing traits in 35 blackgram genotypes. Correlation analysis has revealed that Plant height, number of seeds pod^{-1}, 100 seed weight, harvest index and biological yield was positively correlated with seed yield per plant. The path coefficient analysis recorded that, days to 50 percent flowering, plant height, number of clusters per plant, number of seeds per pod, 100 seed weight, biological yield and harvest index had direct positive effect on yield. Blackgram seed yield can be significantly improved with the selection of plants with more number of seeds per pod, 100 seed weight, biological yield and harvest index in the segregating generations as these traits were positively associated with the seed yield per plant.

**Corresponding author: E-mail: mujjapriyanka@gmail.com;*

Keywords: Correlation; path coefficient analysis; blackgram.

1. INTRODUCTION

Blackgram (*Vigna mungo* (L.) Hepper) is one of the most important legume crop among the pulses which belongs to the family Leguminaceae and sub family Papilionaceae with a chromosome number of 2n=22. It is commonly referred to as "urd bean, urd, or mash," and it is a great source of quickly digestible, high-quality protein. Majority of blackgram is used in the preparation of dal, curries, soups, desserts, and snacks. Urdbean's nutritional benefit comes from its high and easily digestible protein content. It is commonly utilised as an intercrop in rice or wheat because it improves soil nitrogen status (Parashar, 2006) [1].

Selection of promising plants is important in any crop breeding programme. Hence, Information on the contribution of several characteristics to seed yield is provided through an association study. The complicated attribute of seed yield is controlled by a variety of constituent variables. A quick and efficient breeding programme for improving yield will be created using the interactions between yield and its component attributes. The strength and direction of a link between a character and yield are shown by studies on correlation values. The yield components that have both direct and indirect influence on the yield are identified using path analysis. In order to identify the most promising blackgram genotypes, this study intends to compare the relationships between seed yield and its related components in 35 different blackgram genotypes.

2. MATERIALS AND METHODS

This experiment has thirty five genotypes of black gram, which included six lines, four testers, one check and twenty four hybrids developed through Line × Tester mating design. The research place was geographically located at about 16.9244° North latitude and 80.3666° East longitude. All the thirty five genotypes were raised in randomised complete block design with three replications at Agricultural Research Station, Madhira. The sowing was done with a spacing of 30 cm between the rows and 10 cm between the plants. All the remaining practices were done according to the recommendations to get a good yield. The observations were recorded based on five randomly selected plants for eleven characters viz., days to 50 percent flowering, days to maturity, plant height, number of clusters per plant, number of pods per plant, pod length, number of seeds per plant, 100 seed weight, biological yield, harvest index and seed yield. Genotypic and phenotypic correlation between eleven quantitative characters were estimated according to Panse and Sukhatme [2], whereas path coefficient analysis was done by the method suggested by Dewey and Lu [3].

3. RESULTS AND DISCUSSION

Knowing the degree of genetic linkage between various features that influence yield is helpful in determining the genotypes that are most desired because yield is a dependent trait with a complex inheritance pattern due to its polygenic nature. Estimates of phenotypic and genotypic correlations therefore offer understanding of how the environment affects hereditary expression.

The phenotypic and genotypic correlation coefficients among yield and yield components i.e., days to 50 percent flowering, days to maturity, plant height, number of clusters per plant, number of per pods plant, pod length, number of seeds per plant, 100 seed weight, biological yield, harvest index and seed yield were assessed and the results have been presented in Table 1.

The results indicated that the genotype correlation coefficients were consistently greater than the phenotype correlation coefficients for all the characters under investigation demonstrating that the association between yield and yield component traits was mainly attributed to the genetic factors.

Seed yield per plant exhibited positive significant correlation with plant height, number of seeds pod^{-1}, 100 seed weight, biological yield and Harvest index both at phenotypic and genotypic levels. Similar results were given by Konda et al. [4] and Narayanan et al. [5] for seeds per pod and 100 seed weight, Parveen et al. [6] for harvest index, [7], Saran et al. [8] and Tank and Sharma [9] for biological yield and harvest index. Hence, the seed yield can be improved if the characters namely number of seeds pod-1, 100 seed weight, biological yield and harvest index were given importance during selection process. It suggested that increase in growth related traits, number of seeds pod-1 and 100 seed weight might contribute to increase in yields in blackgram.

Table 1. Phenotypic and Genotypic correlation coefficient analysis for yield and yield attributes in blackgram

Character		DFF	DM	PH	CPP	PPP	PL	SPP	100SW	BY	HI	SYP
DFF	**P**	1.000	-0.0441	0.1381	-0.3377**	-0.1181	0.3190**	-0.0852	0.0936	-0.1007	0.1386	0.0491
	G	1.000	-0.0467	0.1450	-0.6749	-0.2029	0.4354	-0.1111	0.1226	-0.1256	0.1769	0.0629
DM	**P**		1.000	-0.2133*	-0.1282	0.0797	-0.2561**	-0.0200	-0.0640	0.0090	-0.1468	-0.1121
	G		1.000	-0.3002	-0.1341	0.0341	-0.3774	0.0060	-0.0999	0.0276	-0.1860	-0.1368
PH	**P**			1.000	0.0811	0.3386**	0.4463**	0.2645**	0.1913	0.1552	0.3760**	0.4063*
	G			1.000	0.0292	0.4173	0.7015	0.3604	0.2021	0.1730	0.3987	0.4282
CPP	**P**				1.000	0.1366	-0.0406	-0.0464	-0.0118	0.1510	0.0703	0.1376
	G				1.000	0.3087	-0.1359	-0.0521	-0.0302	0.2628	0.1465	0.2477
PPP	**P**					1.000	0.2205*	0.1446	0.1869	0.1476	0.0921	0.1606
	G					1.000	0.2148	0.3522	0.2074	0.2121	0.1132	0.2117
PL	**P**						1.000	0.1201	0.0591	-0.1644	0.1682	0.0351
	G						1.000	0.1751	0.0374	-0.2392	0.2249	0.0341
SPP	**P**							1.000	0.1425	0.2348*	0.4613**	0.4956**
	G							1.000	0.1681	0.3767	0.6862	0.7428
100SW	**P**								1.000	0.3248**	0.4465**	0.5322**
	G								1.000	0.3755	0.4961	0.5896
BY	**P**									1.000	0.0351	0.6106**
	G									1.000	0.0594	0.6278
HI	**P**										1.000	0.8085**
	G										1.000	0.8105
SYP	**P**											1.000
	G											1.000

Table 2. Phenotypic and genotypic path coefficients for yield and attributing traits in blackgram

Character		DFF	DM	PH	CPP	PPP	PL	SPP	100SW	BY	HI	SYP
DFF	**P**	0.0063	0.0003	-0.0009	0.0021	0.0007	-0.0020	0.0005	-0.0006	0.0006	-0.0009	0.0491
	G	0.0416	-0.0019	0.0060	-0.0281	-0.0084	0.0181	-0.0046	0.0051	-0.0052	0.0074	0.0629
DM	**P**	0.0000	-0.0003	0.0001	0.0000	0.0000	0.0001	0.0000	0.0000	0.0000	0.0000	-0.1121
	G	0.0009	-0.0196	0.0059	0.0026	-0.0007	0.0074	-0.0001	0.0020	-0.0005	0.0036	-0.1368
PH	**P**	0.0043	-0.0067	0.0313	0.0025	0.0106	0.0140	0.0083	0.0060	0.0049	0.0118	0.4063
	G	0.0129	-0.0266	0.0887	0.0026	0.0370	0.0622	0.0320	0.0179	0.0154	0.0354	0.4282
CPP	**P**	0.0041	0.0016	-0.0010	-0.0123	-0.0017	0.0005	0.0006	0.0001	-0.0019	-0.0009	0.1376
	G	0.0127	-0.0025	0.0005	0.0187	0.0058	-0.0025	-0.0010	-0.0006	0.0049	0.0027	0.2477
PPP	**P**	0.0001	-0.0001	-0.0004	-0.0002	-0.0011	-0.0002	-0.0002	-0.0002	-0.0002	-0.0001	0.1606
	G	0.0026	-0.0004	-0.0055	-0.0040	-0.0131	-0.0028	-0.0046	-0.0027	-0.0028	-0.0015	0.2117
PL	**P**	-0.0038	0.0030	-0.0053	0.0005	-0.0026	-0.0119	-0.0014	-0.0007	0.0020	-0.0020	0.0351
	G	-0.0391	0.0339	-0.0630	0.0122	-0.0193	-0.0898	-0.0157	-0.0034	0.0215	-0.0202	0.0341
SPP	**P**	0.0011	0.0003	-0.0035	0.0006	-0.0019	-0.0016	-0.0131	-0.0019	-0.0031	-0.0060	0.4956
	G	-0.0045	0.0002	0.0145	-0.0021	0.0141	0.0070	0.0402	0.0068	0.0151	0.0276	0.7428
100SW	**P**	-0.0014	0.0009	-0.0028	0.0002	-0.0027	-0.0009	-0.0021	-0.0145	-0.0047	-0.0065	0.5322
	G	0.0008	-0.0006	0.0013	-0.0002	0.0013	0.0002	0.0011	0.0064	0.0024	0.0032	0.5896
BY	**P**	-0.0589	0.0052	0.0908	0.0883	0.0863	-0.0962	0.1374	0.1900	0.5851	0.0206	0.6106
	G	-0.0671	0.0148	0.0924	0.1404	0.1133	-0.1278	0.2012	0.2006	0.5342	0.0317	0.6278
HI	**P**	0.1098	-0.1163	0.2980	0.0557	0.0730	0.1333	0.3655	0.3538	0.0278	0.79253	0.8085
	G	0.1274	-0.1340	0.2873	0.1056	0.0816	0.1621	0.4944	0.3575	0.0428	0.7206	0.8105

Days to 50 percent flowering, number of clusters plant-1, number of pods per plant and pod length showed positive and non-significant correlation with seed yield plant-1 both at phenotypic and genotypic correlation coefficient levels which were similar with the findings of Shivade et al. [10] for number of clusters, number of pods and pod length. It shows that these traits have weak association with yield. The other trait i.e., days to maturity exhibited non-significant and negative correlation with seed yield per plant at both phenotypic and genotypic levels. These results were in accordance with Bandi et al. [11] and Punia et al. [12]. The weak correlation between the characteristics' negative and non-significant associations with yield was caused by a complex linkage relationship between the two combinations.

Interrelationships among yield attributing traits revealed that days to 50 percent flowering has positive significant correlation with pod length, positive and non-significant correlation with plant height, 100 seed weight and harvest index, negative and significant correlation with clusters per plant and negative and non-significant correlation with days to maturity, pods per plant and Biological yield. These results were in accordance with Bandi et al. [11] for clusters per plant.

Plant height exhibited positive and significant relationship with pods per plant, pod length, seeds per pod and harvest index at both phenotypic and genotypic levels which were similar with the findings of Vijay Kumar et al. [13] for pods per plant, pod length, seeds per pod, Shalini and Lal [14], Parveen, et al. [6] and Jyothsna, et al. [15] for pod length and seeds per pod and Sridhar et al. [16] for pods per plant.

Number of seeds per pod and 100 seed weight showed positive significant correlation with biological yield and harvest index.

Number of cluster per plant was positively correlated with pods per plant, biological yield and harvest index but negatively correlated with pod length, seeds per pod and 100 seed weight. These results were in accordance with Vijay kumar et al. [17] for number of pods per plant and Bandi et al. [11] for pod length and 100 seed weight.

Pods per plant and pod length was positively correlated with seeds per pod, 100 seed weight and harvest index. Bandi et al. [11] also revealed similar results for pod length.

3.1 Path Coefficient Analysis

Simple correlation does not reflect the underlying association of the features to yield, and hence does not explain the cause and effect relationship between the various yield parameters and, ultimately, yield. By splitting the correlation coefficients into direct and indirect effects, the route analysis technique gives information on the true contribution of independent factors on yield.

If the correlation coefficient was positive yet the direct effect is negative, it is because of the indirect effects that generate the positive correlation, which should be prioritised during the selection process. If the correlation coefficient was negative but the direct effect is positive, a constraint must be applied to eliminate the undesirable indirect effects, allowing direct effects to be used.

The path coefficient analysis estimated were shown in Table 2. Path analysis revealed positive direct effects was high for harvest index (0.7206), biological yield (0.5342), plant height (0.0887), days to 50 percent flowering (0.0416), number of seeds per pod (0.0402), number of clusters per plant (0.0187) and 100 seed weight (0.0064). These characters also had strong positive association with grain yield, suggesting that increase in number of seeds per plant, number of clusters per plant, 100 seed weight and plant height would improve the grain yield of blackgram. These findings are similar with Mehra et al. [18] for biological yield, Patidar and Sharma [19] for biological yield and plant height.

The negative direct effect on seed yield was exhibited by pod length (-0.0898), days to maturity (-0.0196) and number of pods per plant (-0.0131). These results were in accordance with Panigrahi et al. [20] for pod length. A selection strategy based on these characters would not be successful, As the negative direct effect, has showed that they had little relationship.

The residual effect assesses the influence of potential independent variables that were not included in the study on the dependent variable, allowing accurate explanation of the pattern of interaction of other possible yield components. According to the current study residual effect at the genotypic level was 0.0702, the features included in the investigation are responsible for more than 92.98% of the variability pertaining to the dependent variable, grain yield per plant. The relation between seed yield with other characters is depicted digrametically both genotypically and phenotypically in Figs. 1 and 2.

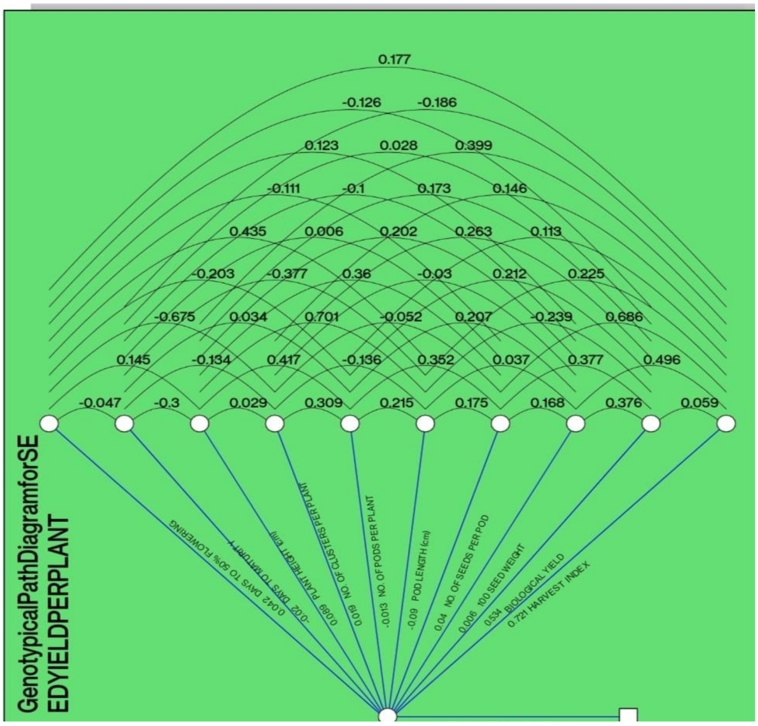

Fig. 1. Genotypical path diagram for seed yield per plant

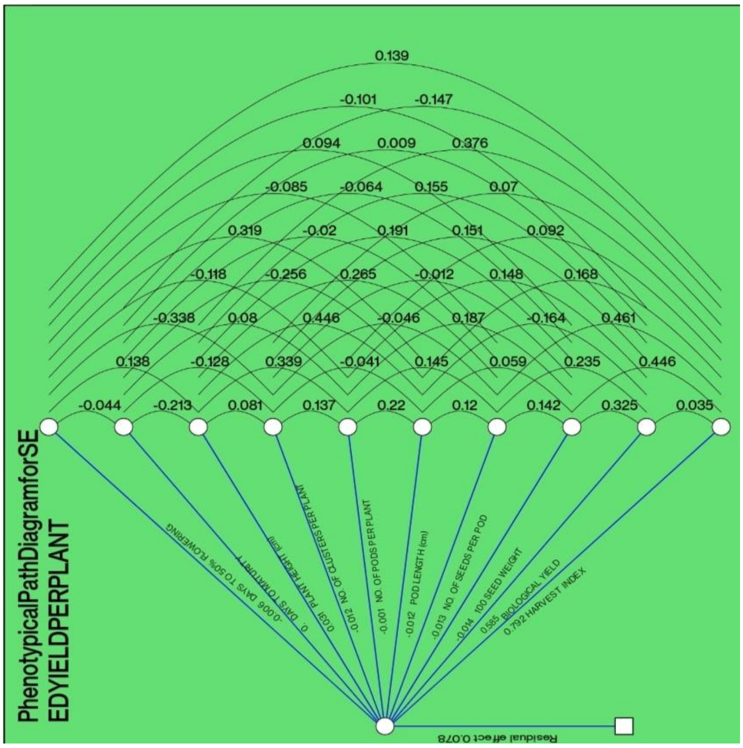

Fig. 2. Phenotypical path diagram for seed yield per plant

4. CONCLUSION

Correlation and Path analysis studies revealed that the important yield attributing traits like harvest index, biological yield, 100 seed weight, number of seeds per pod and plant height exhibited a highly significant correlation values both at phenotypic and genotypic levels. Further, the same traits also exhibited a higher values of direct effects on single yield per plant. Hence, these traits should be given the top priority while developing the superior hybrids in blackgram.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Parashar SMP. Postharvest profile of black gram. MRPC-71, Ministry of Agriculture. Directorate of marketing and inspection, India; 2006.
2. Panse VG, Sukhatme PV. Statistical methods of Agricultural workers. Indian council of Agricultural Research, New Delhi. 1964;359-361.
3. Dewey DR, Lu KH. A correlation and path analysis of components of crested wheatgrass seed production. Agronomy Journal. 1959;51(9):515-518.
4. Konda CR, Salimath PM, Mishra MN. Correlation and path coefficient analysis in blackgram [*Vigna mungo* (L.) Hepper]. Legume Research-An International Journal. 2008;31(3):202-205.
5. Narayanan M, Pillai MA, Shoba D, Pushpam AK. Genetic variability, correlation, path coefficient analysis for yield and yield components in F4 progenies of KKM 1 x VBN 6 in black gram (*Vigna mungo* L. Hepper). The Pharma Innovation Journal. 2021;10(11):1248-1253.
6. Parveen SI, Sekhar MR, Reddy DM, Sudhakar P. Correlation and path coefficient analysis for yield and yield components in blackgram (*Vigna mungo* (L.) Hepper). International Journal of Applied Biology and Pharmaceutical Technology. 2011;2(3):619-625.
7. Teja MKV, Lal GM. Study of genetic variability and character association for yield and yield related traits in f3 generation of blackgram (*Vigna mungo* (L.) Hepper). International Journal of Environment, Agriculture and Biotechnology. 2021;6:3.
8. Saran R, Sharma PP, Dashora A. Correlation and path coefficient analysis for seed yield and its attributing traits in blackgram [*Vigna mungo* (L.) Hepper]. Legume Research-An International Journal. 2020;1:4.
9. Tank HK, Sharma PP. The Correlation and path coefficient analysis in blackgram [*Vigna mungo* (L.) Hepper]. Electronic Journal of Plant Breeding. 2019;10(3):1333-1338.
10. Shivade HA, Rewale AP, Patil SB. Correlation and path analysis for yield and yield components in black gram [*Vigna mungo* (L.) Hepper]. Legume Research-An International Journal. 2011;34(3):178-183.
11. Bandi HRK, Rao KN, Krishna KV, Srinivasulu K. Correlation and path-coefficient estimates of yield and yield component traits in rice fallow blackgram [*Vigna mungo* (L.) Hepper]. International Journal of Current Microbiology and Applied Sciences. 2018;7(3):3304-3309.
12. Punia SS, Gautam NK, Baldeva R, Preeti V, Meenakshi D, Jain NK. Genetic variability and correlation studies in urdbean (*Vigna mungo* (L.) Hepper). Legume Research. 2014;37(6):580-584.
13. Vijay Kumar G, Vanaja M, Sathish P, Vagheera P, Shishodia SS, Abdul Razak. Correlation and path analysis of seed yield and yield contributing components of blackgram (*Vigna mungo* L. Hepper) under rainfed condition from Andhra Pradesh, India. International Journal of Applied Biology and Pharmaceutical Technology. 2014;5(3):137-140.
14. Shalini CH, Lal G. Correlation and path coefficient analysis for yield and yield components in blackgram (*Vigna mungo* (L.) Hepper). The Pharma Innovation Journal. 2019;8(6):65-68.
15. Jyothsna S, Patro TSSK, Ashok S, Sandhya Rani Y, Neeraja B. Character association and Path analysis of Seed Yield and its Yield Components in Black gram (*Vigna mungo* (L.) Hepper). International Journal of Theoretical & Applied Sciences. 2016;8(1):12-16.
16. Sridhar V, Prasad BV, Shivani D, Rao SS. Studies on genetic correlation and path coefficient analysis of blackgram (*Vigna mungo* [L.] Hepper) genotypes under

rainfed situations. International Journal of Chemical Studies. 2020;8(1):1244-1247.

17. Vijay Kumar G, Vanaja M, Sathish P, Vagheera P, Jyothi Lakhsmi N. Correlation analysis for quantitative traits in blackgram (*Vigna mungo* (L.) Hepper) in different seasons. International Journal of Scientific and Research Publications. 2015;5(4):1-10.
18. Mehra R, Tikle AN, Saxena A, Munjal A, Rekhakhandia, Singh M. Correlation, path coefficient and genetic diversity in black gram [*Vigna mungo* (L.) Hepper]. International Research Journal of Plant Science. 2016;7(1):001-011.
19. Patidar M, Sharma H. Correlation and path coefficient studies in Blackgram (*Vigna mungo* (L.) Hepper). Journal of Pharmacognosy and Phytochemistry. 2017;6(4):1626-1628.
20. Panigrahi KK, Mohanty A, Pradhan J, Das TR, Baisakh B. Estimation of Combining Ability in Black Gram (*Vigna mungo* (L.) Hepper) for Yield and its Attributing Traits Using the Diallel Crossing Method. Electronic Journal of Plant Breeding. 2015; 6(3):651-657.

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/89458