Original Research Article

CORRELATION AND PATH COEFFICIENT ANALYSIS FOR YIELD AND YIELD ATTRIBUTING TRAITS IN BLACKGRAM (*Vigna mungo*. (L) Hepper)

ABSTRACT

The present research work was carried out at Agricultural Research Station, Madhira during *Rabi* 2021 to assess the correlation and path coefficient analysis among yield attributes in 35 blackgram genotypes. Correlation analysis revealed that seed yield was positively correlated with plant height, number of seeds pod^{-1}, 100 seed weight, biological yield and harvest index. The path coefficient analysis showed that, days to 50 percent flowering, plant height, number of clusters plant^{-1}, number of seeds pod^{-1},100 seed weight, biological yield and harvest index had positive direct effect on yield. Blackgram seed yield can be significantly improved with the selection of plants with more number of seeds pod^{-1},100 seed weight, biological yield and harvest index in the segregating populations as these traits were positively associated with the seed yield.

Key words: 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 a dry-season intercrop in rice or wheat because it improves soil nitrogen status. (Parashar, 2006) [1].

In any crop breeding, selection of promising plant is important. An association study gives information about the contribution of different characters towards seed yield. Seed yield is a complex trait and is influenced by number of component traits. The study on inter-relationship between the component traits and seed yield will formulate an effective and viable breeding programme for improvement of yield in a short time. Studies on correlation values indicate the intensity and direction of association of a character with yield. Path analysis identifies the yield components with direct and indirect influence on the yield. As a result, this study aims to determine the relationship between seed yield and its related components among thirty five distinct blackgram genotypes in order to find the most promising ones.

2. MATERIAL AND METHODS

This experiment consisted of thirty five genotypes of black gram, which included six lines, four testers and twenty four hybrids developed through Line × Tester mating design. The place is geographically located at about 16.9244° North latitude and 80.3666° East longitude. All the thirty five genotypes were raised in randomised block design with three replications at Agricultural Research Station, Madhira. The sowing was taken up with a spacing of 30 cm between the rows and 10 cm between the plants. The recommended agronomical and plant protection practices were followed 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 plant^{-1}, number of pods plant^{-1}, pod length (cm), number of seeds plant^{-1}, 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 (1978) [2], whereas path coefficient analysis was done by the method suggested by Dewey and Lu (1959) [3].

3. RESULTS AND DISCUSSION

As yield is a dependent trait with a complex inheritance pattern due to its polygenic nature, knowledge of the extent of genetic association between different characters that contribute to yield is useful in identifying the most desirable genotypes. As a result, estimates of phenotypic and genotypic correlations provide insight into how the environment influences heredity 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 plant^{-1}, number of pods plant^{-1}, pod length (cm), number of seeds plant^{-1}, 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 genotypic correlation coefficients were consistently greater than the phenotypic correlation coefficients for all the characters under investigation demonstrating that the association between yield and its component traits was mainly attributed to the genetic factors.

Seed yield plant^{-1} exhibited positive and 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.

Days to 50 percent flowering, number of clusters plant^{-1}, number of pods plant^{-1} 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 negative and non-significant association among the traits had a complex linkage relation among the pair of combinations and had a weak association with yield.

Interrelationships among yield attributing traits revealed that days to 50 percent flowering was significantly and positively correlated with pod length, positive and non-significant correlation with plant height, 100 seed weight and harvest index, negative and significant correlation with clusters plant^{-1} and negative and non-significant correlation with days to maturity, pods plant^{-1} 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 plant^{-1}, pod length, seeds pod^{-1} and harvest index at both phenotypic and genotypic levels which were similar with the findings of Vijay Kumar et al. [13] for pods plant^{-1}, pod length, seeds pod^{-1}, Shalini and Lal [14] , Parveen, et al. [6] and Jyothsna, et al. [15] for pod length and seeds pod^{-1} and Sridhar et al. [16] for pods plant^{-1}.

Number of seeds pod^{-1} and 100 seed weight showed positive and significant correlation with biological yield and harvest index.

Number of cluster plant^{-1} was positively correlated with pods plant^{-1}, biological yield and harvest index but negatively correlated with pod length, seeds pod^{-1} and 100 seed weight. These results were in accordance with Vijay kumar et al. [17] for number of pods plant^{-1} and Bandi et al. [11] for pod length and 100 seed weight.

Pods plant^{-1} and pod length was positively correlated with seeds pod^{-1}, 100 seed weight and harvest index. Bandi et al. [11] also revealed similar results for pod length.

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 is 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 is 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 pod^{-1} (0.0402), number of clusters plant^{-1} (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 plant^{-1}, number of clusters plant^{-1}, 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 plant^{-1} (-0.0131). These results were in accordance with Panigrahi et al. [20] for pod length. The negative direct effect indicated that these characters had low association and selection based on these characters would not be effective.

The residual effect permits precise explanation about the pattern of interaction of other possible components of yield i.e., residual effect measures the role of the possible independent variables which were not included in the study on the dependent variable. In the present study, the residual effect at genotypic level was 0.0702 indicating that the characters included in the present investigation are contributing more than 92.98 per cent of variability pertaining the dependent variable i.e., grain yield plant^{-1}.

CONCLUSION:

Correlation and Path analysis studies revealed that the important yield attributing traits like harvest index, biological yield, 100 seed weight, number of seeds pod^{-1} 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 plant yield. Hence, these traits should be given the top priority while developing the superior hybrids in blackgram.

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Table 1. Phenotypic and Genotypic correlation coefficients for yield and yield attributing traits

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

Character		DFF	DM	PH	CPP	PPP	PL	SPP	100SW	BY	HI	SYP

Table 2. Phenotypic and Genotypic Path coefficients for yield and yield attributing traits

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

Residual effect: 0.078

Figures in bold are direct effects

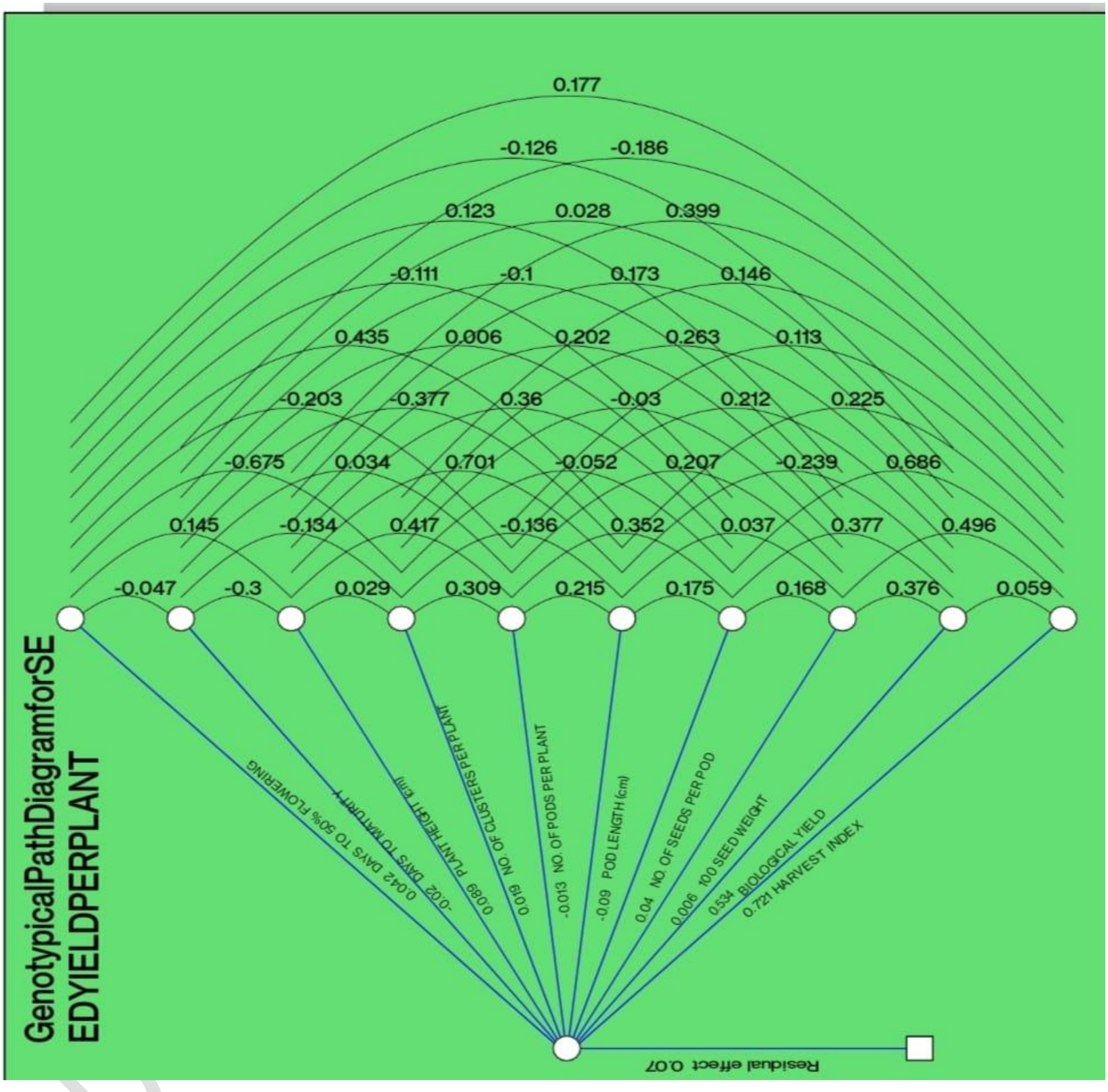

Fig 1: Genotypical Path diagram for seed yield per plant

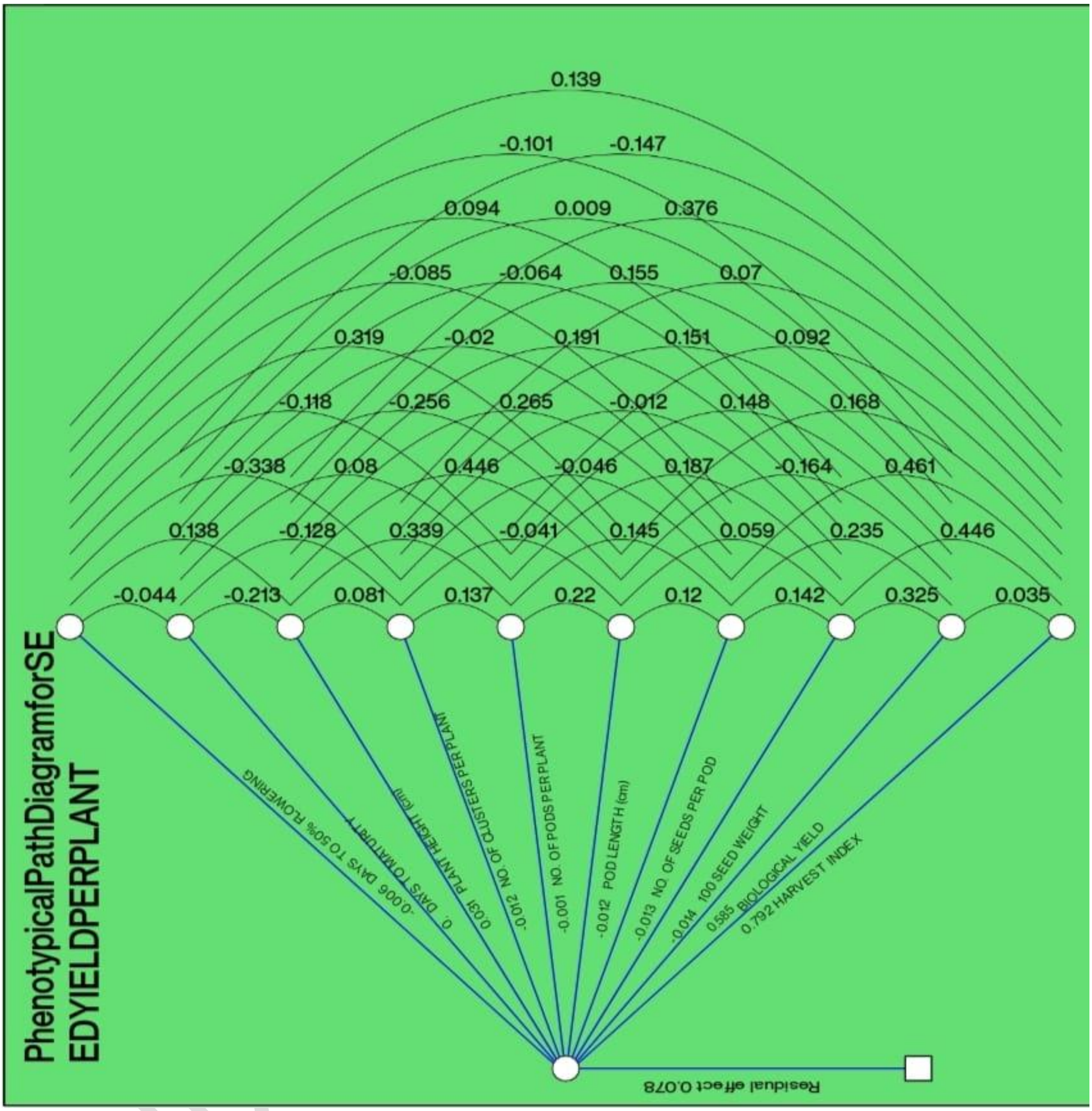

Fig 2: Phenotypical Path diagram for seed yield per plant