Correlation and path analysis for yield and yield contributing traits in blackgram (Vigna mungo (L.) Hepper)

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***Abstract*—The present research aims to determine variability, heritability, genetic advance. Correlation, path analysis in eight genotypes of blackgram. At the School of Agricultural Sciences G H Raisoni University, Saikheda, the experiment was implemented using a randomized block design with three replications during kharif season (2024). Observation was recorded for nine different traits, which included days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, pod length (cm), 100 seed weight (g), seed yield per plant (g).Correlation analysis among the yield and its contributing characters revealed that the genotypic correlation coefficients in most of the cases were higher than their phenotypic correlation coefficients indicating the association was largely due to genetic reasons. Seed yield per plant had a highly significant and positive correlation with the number of primary branches per plant, number of pods per plant,100-seeds weight and plant height at both genotypic and phenotypic levels indicating that these attributes were more influencing the seed yield and therefore these were important characters for bringing genetic improvement of seed yield. The genotypic path coefficient analysis revealed that plant height, number of primary branches per plant, number of pods per plant, 100-seeds weight and number of seeds per pod expressed positive and higher direct effect on seed yield per plant. The residual effect was found to be 0.0953 at genotypic path coefficient analysis. The phenotypic path coefficient analysis revealed that plant height, number of primary branches per plant, number of pods per plant, 100-seeds weight and number of seeds per pod exhibited high and positive direct effects on seed yield per plant. Whereas, negative direct effect on seed yield per plant were contributed through days to maturity and plant height at phenotypic level. The residual effect was found to be 0.0225 at phenotypic path coefficient analysis.**

***Index Terms*—Blackgram, Correlation analysis, path analysis, seed yield**

I. INTRODUCTION

As stated by Bhareti et al. (2011), blackgram (*Vigna mungo* (L.) Hepper), frequently referred to as urd, mashbean, urdbean is 4th most significant pulses within India. An affiliate belonging to Fabaceae and subfamily Faboideae. A significant diploid grain legume that self-pollinates (Naga et al., 2006), and its chromosomal number is 2n=22 (Dana 1980). This is one of the most essential short-term legume crops for symbiotic nitrogen fixation, pasture reclamation, integrated agricultural systems, food, fodder, and soil conservation. Due to these circumstances and terminal drought, it continues to be produced in marginal fields, which substantially decreases its yield. Its yield is severely affected by the extreme lack of moisture it encounters, and its provenance is that it still prospers on marginal soils. Pulses reduce the possibility of plant diseases and pesticide use by stimulating the expansion of soil microbes. By merging them with cereals in crop rotation, legumes additionally assist in interrupting pest cycles, which promotes overall productivity. When integrated into crop rotations, pulses decrease the possibility of soil erosion and depletion. As cover crops, pulses add substantially more carbon to the soil than cereals or grasses, and crop rotations consisting of pulses have a higher potential for preserving carbon (C) in the soil than monocrop systems (Singh 2018). In addition to being rich in micronutrients (20–30% protein), pulses enhance soil productivity in terms of prospective crop yields. There have been reports of pulses improving harvest rates by 20–40% (Srivastava et al., 2010). The relative importance belonging to different yield-contributing qualities is shown by path-coefficient and correlation coefficient analysis, which increases efficacy of grain output component-based selection for higher yields. By assessing the relationship between multiple plant features, the correlation coefficient study gives the related attribute that selection may depend on to improve genetic architecture or yield growth. Researchers can evaluate the indirect and direct impact of various variables to the grain output by using path analysis, which separates correlation coefficient in order to measures about indirect and direct impacts. Path analysis has been utilized by plant breeders to find features that could be used as selection criteria to increase crop yields (Dewey and Lu, 1959).

II. MATERIAL AND METHODS

The field trial was undertaken during kharif season in the year 2024-2025. The experiment was performed at School of Agriculture Sciences G H Raiosni University, Saikheda. The research study consists of eight genotypes, including MG-801, TAU-1, Ajeet-3, Vaman-1, NUL-7(Vishwas), AKU-10-1(Blackgold), AKU-15, Phule vasu. Eight genotypes of blackgram sown in randomized blocked design (RBD). Every variety was kept in single row with the spacing of 30 x 15 cm^2. Data for nine traits was recorded: Days to 50 percent flowering, Days to maturity, Plant height (cm), Number of primary branches per plant, Number of pods per plant, Pod length (cm), Number of seeds per pod,100-seed weight (g), Seed yield per plant (g). Five randomly plants were chosen for each genotype in each replication (except from days to maturity and days to 50% flowering, noted on plot basis). Mean value were later applied for statiscal analysis. Genotypic and phenotypic correlation coefficients were calculated using the method of Al-Jibouri et al. (1958). Path coefficient analysis was performed to partition correlations into direct and indirect effects on seed yield, using Dewey and Lu's (1959) methodology. Data were analyzed using R studio software and Excel.

III. RESULTS AND DISCUSSION

1. Correlation coefficient analysis: -

Seed yield is a complex trait influenced by multiple components, and understanding their interrelationships is essential for crop improvement. Correlation analysis at phenotypic and genotypic levels revealed stronger associations at the genotypic level, indicating inherent genetic relationships among traits. The computed correlation coefficients for nine quantitative characters are presented in Tables 1 and 2.

1.1 Genotypic correlation coefficient: -

At the genotypic level, days to 50% flowering exhibited a highly significant positive correlation with days to maturity (0.75). Plant height showed highly significant positive associations with primary branches (0.99), pods per plant (0.95), and seed yield per plant (0.79). Primary branches per plant also exhibited strong positive correlations with pods per plant (0.94) and seed yield per plant (0.82). Similarly, pods per plant showed a highly significant positive correlation with seed yield per plant (0.77). A strong positive association was also recorded between 100-seed weight and seed yield per plant (0.81). Overall, seed yield per plant was found to be highly and positively associated with primary branches per plant (0.82), 100-seed weight (0.81), plant height (0.78), and pods per plant (0.77).

1.2 Phenotypic correlation coefficient: -

At the phenotypic level, days to 50% flowering exhibited a highly significant positive correlation only with days to maturity (0.71). Plant height showed significant positive associations with primary branches (0.97), pods per plant (rp = 0.94), seed yield per plant (0.77), 100-seed weight (0.48), and seeds per pod (0.42). Primary branches per plant exhibited highly significant positive correlations with pods per plant (0.93), seed yield per plant (0.81), 100-seed weight (0.51), and seeds per pod (0.44). Pods per plant showed highly significant positive associations with seed yield per plant (0.77) and 100-seed weight (0.40). Number of seeds per pod was highly and positively correlated with seed yield per plant (0.56) and pod length (0.52). A strong positive association was also observed between 100-seed weight and seed yield per plant (0.80). Overall, seed yield per plant was found to be highly and positively associated with primary branches per plant (0.81), 100-seed weight (0.80), plant height (0.77), pods per plant (0.77), and seeds per pod (0.56).

Seed yield per plant exhibited significant positive correlations with primary branches, plant height, pods per plant, and 100-seed weight, while a positive but non-significant correlation was observed with pod length. These results are consistent with the findings of Vadivel et al. (2019), Tank et al. (2019), Priya et al. (2016) and Partap et al. (2019), who also reported strong positive associations of seed yield with plant height, primary branches, and pods per plant at both genotypic and phenotypic levels. The consistently higher genotypic correlations compared to phenotypic ones suggest that these associations are mainly governed by genetic factors such as linkage or pleiotropy, with minimal environmental influence.

2. Path Coefficient Analysis: -

Path coefficient analysis, first suggested by Dewey and Lu (1959), was employed in blackgram to partition genotypic and phenotypic correlations into direct and indirect effects, using seed yield per plant as the dependent variable. Compared to phenotypic effects, genotypic direct and indirect effects were generally larger in magnitude, indicating that simple correlation may give misleading results. Hence, correlation in combination with path analysis provides more precise information on the extent and direction of associations among yield and yield-attributing traits, thereby offering better guidance for selection in crop breeding programs.

2.1 Genotypic Path Coefficient Analysis: -

Path coefficient analysis was employed to partition the genotypic correlation coefficients of various trait pairs into direct and indirect effects. The genotypic path coefficient analysis revealed that pods per plant (8.206) as well as seed per pod (4.744) expressed positive and higher direct effect on seed yield per plant. However, negatively direct effect on seed yield per plant were contributed through height of plant (-5.680), length of pod (-3.994), primary branches per plant (-3.251), hundred seed weight (-1.405), day to maturity (-0.893) as well as day to fifty percent flowering (-0.088) at genotypic level. Characters which exhibit noted significant genotypic correlation with seed yield per plant were considered for results. The residual effect was found to be 0.0953 at genotypic path coefficient analysis.

2.2 Phenotypic Path Coefficient Analysis: -

The phenotypic path analysis (Table 3) revealed that pods per plant (0.709), 100-seed weight (0.682), pod length (0.208), and days to 50% flowering (0.191) exerted positive and relatively high direct effects on seed yield per plant. Primary branches per plant (0.072) and seeds per pod (0.041) also showed positive but low direct effects. In contrast, plant height (-0.298) and days to maturity (-0.240) contributed negative direct effects on seed yield at the phenotypic level. Only those characters exhibiting significant phenotypic correlations with seed yield per plant were considered for interpretation in the results and discussion. The residual effect was found to be 0.0225 at phenotypic path coefficient analysis.

Analysis revealed that seed yield was directly and positively influenced by pods per plant and seeds per pod, while negative direct effects were observed for days to maturity and plant height. At the phenotypic level, days to 50% flowering, primary branches, pod length, and 100-seed weight contributed positively, whereas at the genotypic level, days to 50% flowering, pod length, and 100-seed weight showed negative direct effects. These findings are in agreement with Tank et al. (2018), Sathees et al. (2019), Priyanka et al. (2016), who reported positive direct contributions of traits like pods per plant, seeds per pod, pod length, and days to 50% flowering, while adverse direct effects of primary branches and 100-seed weight were also noted by Arya et al. (2017)

Table 1. Estimation of Genotypic correlation coefficients among nine characters in Blackgram genotypes.

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of pod per plant	No. of seed per pod	Pod length (cm)	100 seed weight (g)	Seed yield per plant (g)
Days to 50% flowering	1**	0.75*	0.04	0.03	-0.032	-0.14	-0.44	-0.11	-0.17

Days to maturity		1**	0.0043	-0.087	-0.014	-0.24	-0.43	-0.025	-0.022
Plant height (cm)			1**	1.0003**	0.95**	0.43	-0.12	0.48	0.78*
No. of primary branches per plant				1**	0.94**	0.46	-0.1	0.51	0.82*
No. of pod per plant					1**	0.29	-0.06	0.4	0.77*
No. of seed per pod						1**	0.56	0.42	0.57
Pod length (cm)							1**	-0.31	0.033
100 seed weight (g)								1**	0.81*
Seed yield per plant (g)									1**

*, **: Significant at 5 % probability and 1 % probability level, respectively

Table 2. Estimation of phenotypic correlation coefficients among nine characters in Blackgram genotypes.

Characters	Days to 50% flowering	Days to maturity	Plant Height (cm)	No. of primary branches per plant	No. of pod per plant	No. of seed per pod	Pod Length (cm)	100 seed weight (g)	Seed yield per plant (g)
Days to 50% flowering	1**	0.71**	0.04	0.0083	-0.02	-0.13	-0.33	-0.11	-0.16
Days to maturity		1**	-0.01	-0.08	-0.14	-0.23	-0.31	-0.04	-0.21
Plant Height (cm)			1**	0.97**	0.94**	0.42*	-0.13	0.48*	0.77**
No. of primary branches per plant				1**	0.93**	0.44*	-0.11	0.51*	0.81**
No. of pods per plant					1**	0.28	-0.05	0.40*	0.77**
No. of seeds per pod						1**	0.52**	0.40*	0.56**
Pod Length (cm)							1**	-0.29	0.03
100 seed weight (g)								1**	0.80**
Seed yield per plant (g)									1**

*, **: Significant at 5 % probability and 1 % probability level, respectively

Table 3. Estimates of genotypic and phenotypic path analysis for direct (bold) & indirect effects of yield components on seed yield per plant in Blackgram.

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 seed weight (g)
Days to 50% flowering	G	**0.191**	-0.172	-0.011	0.000	-0.020	-0.005	-0.068	-0.079
	P	**-0.088**	-0.674	-0.282	-0.100	-0.269	-0.706	1.793	0.154
Days to maturity	G	0.137	**-0.240**	0.003	-0.006	-0.010	-0.009	-0.065	-0.027
	P	-0.066	**-0.893**	-0.024	0.283	-0.121	-1.185	10746	0.0361
Plant height(cm)	G	0.007	0.002	**-0.298**	0.071	0.667	0.017	-0.027	0.330
	P	-0.004	-0.003	**-5.680**	-3.251	7.860	2.043	0.502	-0.685
No. of primary branches per plant	G	0.001	0.020	-0.292	**0.072**	0.665	0.018	-0.023	0.352
	P	-0.002	0.077	-5.681	**-3.251**	7.780	2.207	0.417	-0.726
No. of pods per plant	G	-0.005	0.003	-0.281	0.068	**0.709**	0.0115	-0.011	0.276
	P	0.002	0.013	-5.440	-3.082	**8.206**	1.376	0.272	-0.575
No. of seeds per pod	G	-0.025	0.055	-0.127	0.032	0.199	**0.041**	0.110	0.277
	P	0.013	0.223	-2.446	-1.512	2.381	**4.744**	-2.237	-0.593
Pod length(cm)	G	-0.063	0.075	0.038	-0.008	-0.039	0.021	**0.208**	-0203
	P	0.039	0.390	0.713	0.339	-0.559	2.657	**-3.994**	0.447
100 seed weight (g)	G	-0.022	0.009	-0.144	0.037	0.287	0.016	-0.061	**0.682**
	P	0.009	0.022	-2.769	-1.681	3.359	2.003	1.271	**-1.405**
Seed yield per plant	G	-0.17	-0.022	0.78**	0.82**	0.77**	0.57	0.033	**0.81****
	P	-0.16	-0.21	0.77**	0.81**	0.77**	0.56**	0.03	**0.80****

Genotypic residual effect = 0.0953 and Phenotypic residual effect = 0.0225

* Significant level at 5% and ** 1% level respectively. Bold values are show direct and normal values shows indirect effects.

IV. CONCLUSION

Genotypic correlations were generally higher than phenotypic correlations, indicating environmental influence in masking genetic relationships. Seed yield per plant showed significant positive association with primary branches per plant, pods per plant, 100-seed weight, and plant height, highlighting these as key traits for selection. Path analysis further revealed that plant height, primary branches per plant, pods per plant, seeds per pod, and 100-seed weight exerted strong positive direct effects on seed yield, with low residual effects confirming the importance of these traits. Thus, these yield components can be considered reliable selection criteria for genetic improvement in blackgram.

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