Assessment of Correlation and Path Analysis for seed yield and yield contributing traits in Mungbean (*Vigna radiata* (L) R. Wilczek)

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Abstract: - The current research study on Assessment of Correlation and Path Analysis for seed yield and yield contributing traits in mungbean (*Vigna radiata* (L.) R Wilczek) was granted to evaluate correlation coefficient analysis and path coefficient analysis in eight genotypes of mungbean were sown in randomized block design (RBD) with three replications during kharif season (2024) at School of Agricultural Sciences G H Raisoni University, Saikheda. The observation was recorded for nine characters and the nine characters are days to maturity, days to 50% flowering, plant height (cm), number of pods per plant, number of primary branches per plant, pod length (cm), number of seeds per pod, 100 seed weight (gm) and seed yield per plant (gm). According to the analysis, Genotypic correlation coefficients were generally higher than phenotypic ones, suggesting that most associations with yield were genetically controlled. Seed yield per plant showed highly significant and positive correlation with number of primary branches, number of pods per plant, number of seeds per pod, and 100-seed weight at both levels, making these key traits for yield improvement. Number of Pod length also had a strong positive association with number seeds per plant. Path analysis indicated that number of pods per plant, 100-seed weight, and number of seeds per pod exerted major direct positive effects on yield, while plant height had a negative effect at the phenotypic level. The residual effects were 0.361 (genotypic) and 0.457 (phenotypic), showing that most yield variation was explained by the studied traits. Overall, the findings suggest that the number of pods per plant, number of seeds per pod and 100-seed weight are the most reliable selection criteria for genetic improvement of seed yield in mungbean.

Index Terms: - Mungbean, correlation coefficient analysis, path coefficient analysis, green gram

I. INTRODUCTION

In South and Southeast Asia mungbean is one of the crucial legume crops. It constitutes third-most prominent pulse crop in India. The main regions where it is grown in several Indian states. It was extensively cultivated in the prehistoric period. According to Ayurvedic principles, mung beans are highly recommended for individuals struggling with obesity and excess body fat. Their richness in fiber and protein, combined with low fat content, makes them a healthy dietary choice. Throughout harvest, the crop's cultivation increases the soil's fertility by adding 30 to 40 kg N/ha. The subsequent crop, which often includes a cereal, needs approximately 25% less nitrogen as a result. The "Outlook report from ANGRAU" suggests that 31.5 lakh tonnes of green grams have been produced in 2021–2022, with production rate of 783 kg/ha. Estimation 40.38 million hectares of land, this represents 11% of the total production of pulses. Based on the first predictions for kharif 2022-2023, 17.5 lakh tonnes of green gram were produced on 33.37 lakh hectares. The states of Madhya Pradesh (1.57 lakh ha), Orissa (1.48 lakh ha), Maharashtra (3.94 lakh ha), Karnataka (4.40 lakh ha), and Rajasthan (20.89 lakh ha). Additionally, 2.60 million tons of green gram produced overall in 2020–21. (Anon 2020–21).

Correlation can be divided into direct and indirect effects of independent traits on dependent traits through path analysis, which is based on standardized partial regression (Wright, 1921). In breeding programs, it is important to assess traits that influence seed yield either directly or indirectly. Simple correlation alone does not fully explain the relative contribution of each trait to seed yield. Path analysis is therefore considered an essential tool for plant breeders. It separates correlation coefficients analysis into direct and indirect components, giving clarity on their influence on yield. This study applied path analysis to green gram germplasm to evaluate yield potential and quality traits. The analysis also considered genetic variability, heritability, and genetic advance. Such knowledge is highly useful for selecting suitable breeding strategies. Correlation coefficients are important in identifying the most effective traits for yield improvement. However, correlation does not clearly distinguish the individual effects of each trait. Path analysis addresses this gap by highlighting traits that have true direct effects on yield. It also quantifies the indirect effects mediated through other traits. Identifying specific yield-influencing traits among many attributes remains a challenge in crop improvement. This is why path analysis provides more accurate information than conventional correlation studies. It helps breeders understand the true relationship between yield and its contributing traits. The degree of genetic variability among genotypes forms the basis for exploiting yield potential (Muthusamy et al., 2019). Using correlation, models for direct and indirect contributions to yield can be built. Studies have shown that associations among key plant traits can be effectively explained using this approach (Perera et al., 2017). By partitioning correlation into components, path analysis gives a more complete picture of how traits interact. Ultimately, it allows for better understanding of the causal relationship between variables and seed yield.

II. MATERIAL AND METHODS

The field trial was undertaken during kharif season in the year 2024-2025. The experiment was performed at School of Agricultural Sciences G H Raisoni University, Saikheda. The research study consists of eight mungbean genotypes, including AKM-9911, BM-2002-1, PDM-139, AKM-9904, BM-2003-2, Vaibhav, IPM 205-7, IPM 410-3. Eight genotypes of mungbean sown in randomized block 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% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, pod length, 100 seed weight, seed yield per plant. 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 statistical analysis. Statistical analysis included estimation of phenotypic and genotypic correlation and path coefficient analysis. R studio software and Excel used for analysis of data.

III. RESULTS AND DISCUSSION

1. Correlation coefficient analysis: -

The main goal of plant breeding is to enhance crop production and seed yield, which requires understanding the relationships between different yield components. These traits are complex, influenced by both genetic architecture and environmental conditions, and correlations can be studied at phenotypic and genotypic levels. While phenotypic correlations include environmental effects, genotypic correlations reveal the true genetic relationships. Trait associations may arise from linkage, pleiotropy, or physiological factors, with linkage being more common in crosses between diverse strains. As noted by Falconer et al. (1981), some genes may improve multiple traits simultaneously (positive correlation), while others may enhance one trait but reduce another (negative correlation). Thus, analyzing these interrelationships is essential to combine desirable yield-contributing traits in a single genotype. For each of nine-character combinations under investigation, correlation coefficient was calculated at genotypic and phenotypic level.

1.1 Genotypic correlation coefficient: -

At the genotypic level Days to 50% flowering had highly positive and significant correlation with days to maturity (0.73) and positive and significant correlation with 100-seed weight (0.21), but showed highly negative and significant correlation with number of pods per plant (-0.77) and seed yield (-0.30). Days to maturity was positive and significant association with 100-seed weight (0.48), plant height (0.32) and number of seeds per pod (0.24), while negative and significant interrelation with number of pods per plant (-0.64) and seed yield per plant (-0.37). Plant height had positive and significant correlation with pod length (0.29) and number of seeds per pod (0.20). Number of primary branches per plant were positive and significant interrelation with seed yield per plant (0.30) and number of pods per plant (0.26). Number of pods per plant showed a strong positive and significant correlation with seed yield per plant (0.54) but a negative and significant interrelation with 100-seed weight (-0.30). Number of seeds per pod had positive and significant interrelation with seed yield per plant (0.45) and pod length (0.32). Pod length had a positive and significant association with seed yield per plant (0.23). 100 seed weight had positive and significant interrelation with seed yield per plant (0.34). Importantly, the traits most strongly and significantly associated with seed yield per plant were number of pods per plant, number of seeds per pod, 100-seed weight, and number of primary branches per plant (Table 1).

1.2 Phenotypic correlation coefficient: -

At phenotypic level, Days to 50% flowering had positive and significant interrelation with days to maturity (0.55) but showed significant negative correlations with number of pods per plant (-0.35) and seed yield per plant (-0.32). Days to maturity expressed positive and significant interrelation with 100-seed weight (0.35) and plant height (0.27), but negative and significant interrelated to number of pods per plant (-0.58). Plant height had positive and significant interrelation with pod length (0.27) and number of seeds per pod (0.25). Number of primary branches per plant showed strong positive and significant interrelation with seed yield per plant (0.32) and number of pods per plant (0.28). Number of pods per plant had highly positive and significant interrelation with seed yield per plant (0.43) and number of pods per plant had negative and significant interrelation with 100-seed weight (-0.25). Number of seeds per pod had highly positive and significant interrelation with seed yield per plant (0.48) and pod length (0.21), while Pod length had a positive and significant association with seed yield per plant (0.24), while 100-seed weight showed positive and significant interrelation with seed yield per plant (0.38). Overall, the most important traits positively associated with seed yield per plant were number of seeds per pod, number of pods per plant, 100-seed weight, and number of primary branches per plant (Table 2), making them key contributors for yield improvement.

This suggests that enhancing these traits can significantly boost seed yield, as supported by previous studies (Sarkar et al., 2014; Baisakh et al., 2016). Pod length also showed a positive correlation with seed yield. Additionally, a strong association was observed between days to 50% flowering and days to maturity, consistent with findings by Prasanna et al. (2013) and Mohammed et al. (2020). Days to maturity was also positively linked to 100-seed weight. Plant height showed significant positive correlations with pod length and seeds per pod at the genotypic level, as reported by several researchers (Himabindu & Lavanya, 2017; Mohammed et al., 2020; Garg et al., 2017). These associations indicate that improving one trait may positively influence others, ultimately enhancing overall seed yield in mung bean.

2. Path Coefficient Analysis: -

Path analysis can be studied at phenotypic and genotypic levels. It was conducted using seed yield per plant as the dependent variable and traits such as days to maturity, day to 50% flowering, plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod, and 100-seed weight as independent variables. There are two path actions for each components direct effect on seed production and an indirect effect through other components that correlation cannot reveal.

2.1 Genotypic Path Coefficient Analysis: -

Genotypic path coefficient analysis demonstrated that number of pods per plant (0.718), 100 seed weight (0.525) and number of seed per pod (0.303) had highly positive and direct effect on seed yield. Whereas, days to maturity (0.058), pod length (0.037), number of primary branches per plant (0.003) expressed moderate to lower positive direct effect on seed yield. Days to 50% flowering (-0.23) and plant height (-0.032) expressed negative and direct effect on seed yield per plant. Residual effect at genotypic path coefficient analysis was found to be 0.361 (Table 3).

2.2 Phenotypic Path Coefficient Analysis: -

Phenotypic path analysis demonstrated that number of pods per plant (0.702), 100 seed weight (0.499), number of seeds per pod (0.302) had positively highly direct effect on seed yield. Whereas, pod length (0.022), number of primary branches per plant (0.011), day to 50% flowering (0.002), days to maturity (0.001) expressed moderate to lower positive direct effect on seed production. Although plant height (-0.007) expressed negatively direct effect on seed yield.

Residual effect at phenotypic path coefficient analysis was found to be 0.457 (Table 3).

In the study, genotypic path analysis in this study revealed that number of pods per plant, seeds per pod, and 100-seed weight had a positive direct effect on seed yield, confirming the findings of Goyal et al. (2021), Azam et al. (2018), and Kumar et al. (2018). Conversely, plant height and days to 50% flowering showed a negative direct impact on yield, as also noted by Prasanna et al. (2013), Garg et al. (2017), Abbas et al. (2018), and Azam et al. (2018), indicating their limited value in yield improvement. Phenotypic path analysis revealed that pods per plant, seeds per pod, and 100-seed weight had a strong positive direct effect on seed yield, aligning with findings by Parihar et al. (2018), Prasanna et al. (2013), and Khanpara et al. (2012). Plant height showed a negative direct effect, as reported by Abbas et al. (2018) and Goyal et al. (2021). Residual effects were 0.361 (genotypic) and 0.457 (phenotypic), indicating most key traits were included. These results support combining path and correlation analysis for effective yield improvement in mungbean, as noted by Manivelanb et al. (2019) and Kumar et al. (2018).

Table 1. Estimation of Genotypic correlation coefficients among nine characters in Mungbean 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**	0.73**	0.13	0.012	-0.47*	-0.13	-0.056	0.21*	-0.30**
Days to maturity		1**	0.32**	0.14	-0.64**	0.24*	0.042	0.48**	-0.37*
Plant height (cm)			1**	0.18	-0.15	0.20**	0.29**	-0.14	0.20
No. of primary branches per plant				1**	0.26**	0.14	0.12	0.19	0.30**
No. of pod per plant					1**	-0.073	0.067	-0.30**	0.54**
No. of seed per pod						1**	0.32**	0.104	0.45**
Pod length (cm)							1**	-0.023	0.23*
100 seed weight (g)								1**	0.34**
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 Mungbean 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**	0.55**	0.19	0.020	-0.35**	-0.012	-0.050	0.23	-0.32*
Days to maturity		1**	0.274*	0.054	-0.58**	0.160	0.08	0.35**	-0.18
Plant Height (cm)			1**	0.17	-0.16	0.25*	0.27*	0.14	0.16
No. of primary branches per plant				1**	0.28*	0.12	0.15	0.19	0.32**
No. of pods per plant					1**	0.074	0.063	-0.25**	0.43**
No. of seeds per pod						1**	0.213*	0.024	0.48**

Pod Length (cm)							1**	-0.034	0.24*
100 seed weight (g)								1**	0.38**
Seed yield per plant (g)									1**

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

Table 3. Estimation of genotypic and phenotypic path analysis for direct and indirect effects of yield components on seed yield per plant in Mungbean.

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	-0.023	-0.026	-0.0015	0.006	0.018	0.007	0.024	-0.026
	P	0.002	0.001	0.059	0.063	-0.005	-0.003	-0.006	0.011
Days to maturity	G	0.091	0.058	0.005	0.010	-0.128	0.016	0.042	0.031
	P	0.029	0.001	0.005	0.002	-0.004	0.002	0.018	0.005
Plant height(cm)	G	-0.032	-0.007	-0.032	-0.010	0.016	-0.004	-0.051	-0.005
	P	-0.013	-0.003	-0.007	-0.088	0.003	-0.002	-0.032	-0.002
No. of primary branches per plant	G	-0.015	0.005	0.002	0.003	0.014	0.005	0.007	0.001
	P	0.031	0.006	0.071	0.011	0.031	0.022	0.004	0.003
No. of pods per plant	G	-0.408	-0.685	-0.115	0.204	0.718	-0.072	0.050	-0.357
	P	-0.342	-0.333	-0.108	0.198	0.702	-0.052	0.037	-0.241
No. of seeds per pod	G	-0.060	0.126	0.121	0.032	-0.044	0.303	0.129	0.055
	P	-0.037	0.023	0.112	0.025	-0.040	0.302	0.110	0.040
Pod length(cm)	G	-0.084	0.004	0.002	0.004	0.138	0.014	0.037	-0.001
	P	-0.031	0.003	0.074	0.083	0.004	0.011	0.022	-.0004
100 seed weight (g)	G	0.165	0.424	0.103	0.105	-0.100	0.075	-0.016	0.525
	P	0.124	0.318	0.163	0.160	-0.101	0.062	-0.006	0.499
Seed yield per plant	G	-0.30**	-0.37*	0.20	0.30**	0.54**	0.45**	0.23*	0.34**
	P	-0.32*	-0.18	0.16	0.32**	0.43**	0.48**	0.24	0.38**

Residual effect genotypic - 0.361 and phenotypic - 0.45

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

IV. CONCLUSION

Genotypic correlations were higher than phenotypic ones, showing that environmental factors reduced trait expression at the phenotypic level. Seed yield per plant showed strong positive associations with number of pods per plant, number of primary branches per plant, 100-seed weight, and number of seeds per pod at both levels. Pod length was also significantly correlated to seed yield per plant. Yield components displayed varying degrees of association among themselves, which can be exploited to improve yield. Greater focus should be given to these key traits while selecting superior mungbean genotypes. Path analysis at the genotypic level revealed that number of pods per plant, number of seeds per pod, and 100-seed weight had direct positive effects on seed yield. The same result was observed in phenotypic path analysis. These traits therefore play a vital role in determining productivity. The low residual effect indicated that most important yield traits were included in the analysis.

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