



Trait Relationship and their Contribution to Seed Yield in Mungbean: A Correlation and Path Analysis Approach

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ABSTRACT

A field experiment with 27 genotypes of mungbean was conducted during late *kharif* (Sep, 2025–Dec, 2025) at College Farm, College of Agriculture, Navsari Agricultural University, Bharuch to study the correlation and path coefficient analysis for seed yield and its components traits. The results revealed a highly significant and positive association of seed yield plant⁻¹ with branches plant⁻¹, clusters plant⁻¹, pods cluster⁻¹, pods plant⁻¹, seeds pod⁻¹ and 100-seed weight at genotypic and phenotypic levels. While, pod length showed significant and positive association at genotypic level only, indicating that these attributes were mainly influencing the seed yield in mungbean. Path coefficient analysis indicated that seeds pod⁻¹ exerted the highest positive direct effect on seed yield plant⁻¹, followed by pods cluster⁻¹, clusters plant⁻¹, 100-seed weight, plant height, pods plant⁻¹ and branches plant⁻¹. In contrast, days to 50% flowering, days to maturity, pod length and crude protein content negative direct effects on seed yield plant⁻¹ suggesting indirect contributions through other traits. The traits namely seeds pod⁻¹, pods cluster⁻¹, clusters plant⁻¹, 100-seed weight, plant height, pods plant⁻¹ and branches plant⁻¹ not only showed high positive direct effects but also maintained significant positive correlations with seed yield plant⁻¹. The significant association of these traits with yield was mainly attributed to their substantial direct contribution rather than indirect influences through other characters. Hence, direct selection for these attributes could be effectively utilized in breeding programs for improving seed yield in mungbean.

KEYWORDS: Correlation coefficient, path coefficient, mungbean

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, author have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Mungbean (*Vigna radiata* (L.) Wilczek) is the third most important pulse crop in India. This self-pollinating legume belongs to family Fabaceae. It belongs to the subgenus *ceratotropis* in the genus *Vigna* and is a diploid grain legume ($2n=22$) crop with a genome size of 579 Mb (Arumuganathan and Earle, 1991). Mungbean is short day, warm season crop, grown mainly in arid and semi-arid regions. It is drought tolerant and has ability to grow under climate and medium to low rainfall situation. It is tolerant to moisture stress and heat as well (Abbas et al, 2018). It has ability to grow under low input conditions. It is grown on a variety of soils including black, red lateritic, gravelly and sandy soils. Well drained fertile sandy loam soil with a pH between 6.2–7.2 is best for mungbean cultivation (Anita et al, 2025). In India, green gram productivity is 453 kg ha⁻¹ which occupy 35.43 lakh ha area and total production of 16.07 lakh t. In Gujarat, Green gram is cultivated over an area of 66.48 ha, yielding a total production of 35.18 lakh t with productivity of 529.09 kg ha⁻¹ (Anonymous, 2024–25). According to Vavilov (1939) green gram is native to India and Central Asia. Mung bean is a self-pollinating cleistogamous crop. It has a monocarpellary gynoeceum, a diadelphous androeceum (9+1), 3 large and 2 small fused sepals, five petals (1 standard, 2 wings and 2 keels). The stigma is curved and hairy. The pods of the mung bean plant are long and narrow, with a length of 5–15 cm and a width of 3–4 mm (Mohammed et al, 2020). The pods have a characteristic curvature. Seeds are small, ovoid and green when immature. When mature, they normally turn yellow or brown. Each pod typically contains around 10–15 seeds (Dhunde et al., 2021 and Kamani et al., 2024). They are warm season annuals, highly branched and having trifoliate leaves like the other legumes. Both, upright and vine types of growth habit occur in mungbean, with plants varying from one to five feet in length. The yellow flowers are borne in clusters of 12–15 near the top of the plant. Mature pods are variable in color yellowish brown to black, about five inches long and contain 10 to 15 seeds. Mature seed color can be yellow, brown, mottled black or green, depending upon variety. Mungbean is warm season crop requiring 90–120 days of frost-free conditions from planting to maturity. Adequate rainfall is required from flowering to late pod fill in order to ensure good yield. Pod maturity in mungbean is not uniform because the plants flower over an extended period (Parsaniya et al., 2022 and Thonta, 2023). Generally, harvest should begin when one half to two-thirds of the pods is matured. Seeds might be between (13–15%) moisture at this time (Datta, 2012).

Correlation coefficient analysis is a statistical technique which measures the degree and association between two or more variables. Estimates of correlation coefficient are

useful in identifying the component traits which can be used for yield improvement of mungbean. Path coefficient analysis provides a thorough understanding of contribution of various characters by partitioning the correlation coefficient into components of direct and indirect effects (Wright, 1921), which helps the breeder in determining the yield components. To accumulate optimum contribution of yield contributing characters, it is essential to know the association of various characters along with path coefficients. Therefore, present study was conducted to assess correlation and path analysis to identify component traits for developing high yielding varieties of mungbean.

2. MATERIALS AND METHODS

The genotypes were evaluated for different quantitative traits in RBD (randomized block design) during late *kharif* (Sep, 2025–Dec, 2025) 2025 with spacing 45×15 cm² respectively, in 3 replications at College Farm, College of Agriculture, Navsari Agricultural University, Bharuch. The experimental material for the current study included 27 mungbean genotypes viz., AM-15-3-2, AM-15-7-2, AM-15-8-1, AM-15-26-1, AM-15-48-4, AM-15-48-11, AM-15-52-1, AM-K18-6, AM-K18-11, AM-K18-14, AM-K18-16, AM-K18-19, AM-K18-22, AM-K18-23, AM-S19-1, ANDGG 1804, ANDGG 1805, ANDGG 1807, ANDGG 1808, ANDGG 1810, ANDGG 2011, ANDGG 2020, ANDGG 2029, AM-S22-9, AM-S22-10, GAM 5 and GAM 6. All the recommended cultural practices were followed up to harvest. At maturity data were recorded for Days to 50% flowering, days to maturity, plant height (cm), branches plant⁻¹, clusters plant⁻¹, pods cluster⁻¹, pods plant⁻¹, seeds pod⁻¹, pod length (cm), 100-seed weight (g), crude protein content (%) and seed yield plant⁻¹ (g) on five randomly selected plants from each replication of individual genotypes.

Standard statistical procedure was used for the genotypic and phenotypic correlation coefficients were calculated as under by adopting the procedure expounded by Miller et al. (1958) and genotypic and phenotypic path coefficient procedure was adopted from Wright (1921), Dewey and Lu (1959). Analysis was performed in variability package in R Studio software.

3. RESULTS AND DISCUSSION

When selection was applied for improvement of any single trait, changes were likely to occur, not only for the trait under selection but on the other trait also. This was because of inter-relationship between two or more traits due to genetic or environmental factors. Though true association could only be depicted by genotypic correlation coefficient. Hence, understanding the extent of genetic association between yield and its contributing characters were useful

in isolating the most desirable genotypes. The genotypic and phenotypic correlation coefficients of twelve characters were presented in Table 1.

In the present investigation, correlation analysis revealed a similar pattern at both genotypic and phenotypic levels. In most cases, the genotypic correlation coefficients were higher than the corresponding phenotypic correlations, indicating a strong inherent genetic association between the characters studied. However, in a few instances, phenotypic correlations were slightly higher than genotypic correlations, suggesting that environmental factors and other non-genetic influences might have contributed to the observed associations. These results were in agreement with earlier findings reported by Anita et al. (2025). In the present investigation, highly significant association of

seed yield plant⁻¹ in desirable direction at both genotypic and phenotypic levels was observed for various traits viz., branches plant⁻¹, clusters plant⁻¹, pods cluster⁻¹, pods plant⁻¹, seeds pod⁻¹ and 100-seed weight. Seed yield plant⁻¹ showed positive significant correlation at genotypic level with pod length. Comparable findings were documented by Dhunde et al. (2021) for branches plant⁻¹, pods cluster⁻¹ and Thonta (2023) for clusters plant⁻¹. Alom et al. (2014) for pods plant⁻¹; Mohammed et al. (2020) for seeds pod⁻¹; Reddy et al. (2011) for 100-seed weight.

Association studies provided only the relation between two variables, whereas, path coefficient analysis allowed separation of the direct and their indirect effects through other traits by partitioning the correlation. Thus, correlation combined with path analysis gave better understanding of the relationship between different traits. The direct and

Table 1: Genotypic and phenotypic correlations of seed yield plant⁻¹ (g) with other characters in 27 genotypes of mungbean

Charac- ters		Days to 50% flower- ing	Days to matu- rity	Plant height	Branch- es plant ⁻¹	Clus- ters plant ⁻¹	Pods clus- ter ⁻¹	Pods plant ⁻¹	Seeds pod ⁻¹	Pod length	100- seed weight	Crude protein content	Seed yield plant ⁻¹
Days to 50% flowering	rg	1.00	0.01	0.13	-0.17	-0.53**	-0.22	-0.24	-0.01	-0.08	-0.09	0.06	-0.45*
	rp	1.00	0.01	0.13	-0.16	-0.34**	-0.09	-0.17	0.13	-0.01	-0.15	-0.02	-0.23*
Days to maturity	rg		1.00	-0.16	-0.21	0.11	0.01	-0.07	-0.44*	0.23	0.09	-0.57**	-0.04
	rp		1.00	-0.03	-0.10	0.05	-0.02	-0.07	-0.07	0.08	0.08	-0.13	0.01
Plant height	rg			1.00	-0.15	0.07	0.24	0.23	0.14	0.27	0.01	0.32	-0.06
	rp			1.00	-0.16	0.02	0.12	0.11	0.06	0.06	0.05	0.09	-0.13
Branches plant ⁻¹	rg				1.00	0.32	0.20	0.60**	0.82**	-0.01	0.38*	0.36	0.38*
	rp				1.00	0.26*	0.18	0.48**	0.44**	-0.02	0.27*	0.19	0.30**
Clusters plant ⁻¹	rg					1.00	-0.05	0.71**	0.05	0.07	0.37	0.04	0.45*
	rp					1.00	-0.07	0.61**	0.08	0.12	0.25*	0.11	0.32**
Pods cluster ⁻¹	rg						1.00	0.20	0.24	0.36	0.31	-0.04	0.44*
	rp						1.00	0.18	0.13	0.22*	0.30**	-0.06	0.29**
Pods plant ⁻¹	rg							1.00	0.48*	0.13	0.18	0.09	0.51**
	rp							1.00	0.23*	0.05	0.14	0.09	0.38**
Seeds pod ⁻¹	rg								1.00	0.02	0.01	0.17	0.46*
	rp								1.00	-0.06	-0.01	0.10	0.22*
Pod length	rg									1.00	0.49**	-0.50**	0.38*
	rp									1.00	0.33**	-0.16	0.14
100-seed weight	rg										1.00	-0.07	0.43*
	rp										1.00	-0.03	0.26*
Crude protein content	rg											1.00	-0.39*
	rp											1.00	-0.19

Note: * $p < 0.05$, ** $p < 0.01$

indirect effects of various quantitative traits on yield were presented in Table 2 and Figure 1.

In the present investigation, high positive direct effect on seed yield plant⁻¹ was recorded for seeds pod⁻¹ followed by pods cluster⁻¹, cluster plant⁻¹, 100-seed weight, plant height, pods plant⁻¹ and branches plant⁻¹. Our findings were consistent with those reported by Alom et al. (2014) for days to plant height (cm), Abbas et al. (2018) and Thonta (2023) for cluster plant⁻¹, Kumar et al. (2013) for pods cluster⁻¹, Rao et al. (2006), Parsaniya et al. (2022) and Kamani et al. (2024) for pods plant⁻¹ and Kumar et al. (2013), Anita et al. (2025) for seeds pod⁻¹. while Reddy et al. (2011) for 100-seed weight. Negative direct effect on seed yield plant⁻¹ were unveiled by days to 50% flowering, days to maturity, pod length and crude protein content. Comparable outcomes were revealed by Dhunde et al. (2021)) for days to maturity; Parsaniya et al. (2022) for crude protein content; Thonta (2023) for pod length; Alom et al. (2014) for days to 50% flowering.

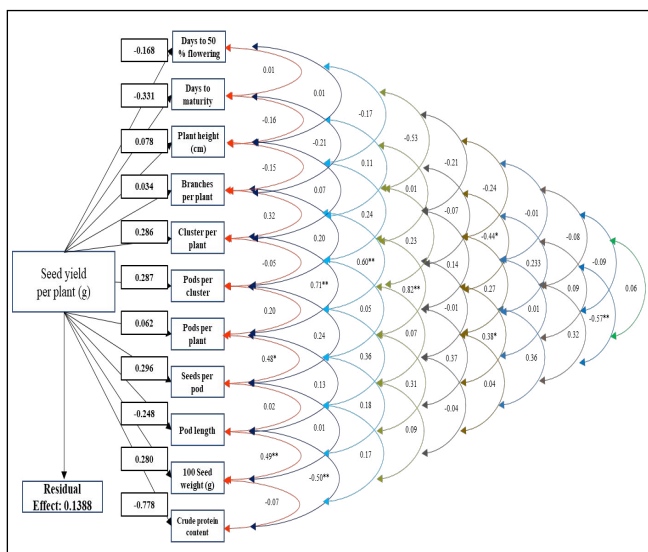


Figure 1: Path diagram showing genotypic correlation and direct effects of various traits on seed yield in mungbean

Table 2: Direct and Indirect effects of 12 causal variables on seed yield plant⁻¹ (g) in 27 genotypes of mungbean

Charac- ters	Days to 50% flowering	Days to maturity	Plant height	Branch- es plant ⁻¹	Clus- ters plant ⁻¹	Pods clus- ter ⁻¹	Pods plant ⁻¹	Seeds pod ⁻¹	Pod length	100- seed weight	Crude protein content	Seed yield plant ⁻¹
Days to 50% flowering	-0.168	-0.004	0.010	-0.006	-0.153	-0.063	-0.015	-0.003	0.021	-0.027	-0.047	-0.457*
Days to maturity	-0.002	-0.331	-0.013	-0.007	0.032	0.005	-0.004	-0.132	-0.057	0.026	0.445	-0.040
Plant height	-0.023	0.055	0.078	-0.005	0.020	0.069	0.014	0.043	-0.068	0.003	-0.252	-0.062
Branches plant ⁻¹	0.030	0.071	-0.012	0.034	0.093	0.057	0.037	0.243	0.004	0.106	-0.287	0.382*
Clusters plant ⁻¹	0.090	-0.037	0.005	0.011	0.286	-0.014	0.044	0.016	-0.018	0.105	-0.034	0.456*
Pods cluster ⁻¹	0.037	-0.005	0.018	0.006	-0.014	0.287	0.012	0.071	-0.091	0.087	0.032	0.442*
Pods plant ⁻¹	0.040	0.023	0.018	0.020	0.204	0.057	0.062	0.143	-0.032	0.051	-0.072	0.516**
Seeds pod ⁻¹	0.002	0.147	0.011	0.028	0.015	0.069	0.030	0.296	-0.006	0.005	-0.137	0.463*
Pod length	0.014	-0.077	0.021	-0.001	0.020	0.105	0.008	0.007	-0.248	0.138	0.392	0.382*
100 - seed weight	0.016	-0.031	0.001	0.013	0.107	0.089	0.011	0.005	-0.122	0.280	0.058	0.431*
Crude protein content	-0.010	0.189	0.025	0.012	0.012	-0.011	0.005	0.052	0.125	-0.021	-0.778	-0.396*

Note: * $p < 0.05$, ** $p < 0.01$

In the present study, the residual effect at the genotypic level was estimated to be 0.1388, indicating that additional component traits, other than those considered in this study, might also contribute to variation in seed yield plant⁻¹.

Improvement in seed yield required proper attention to all yield-contributing traits that influenced yield either directly or indirectly. The findings of the present study revealed that seeds pod⁻¹ exhibited the highest positive direct effect on seed yield plant⁻¹, followed by pods cluster⁻¹, clusters plant⁻¹, 100-seed weight, plant height, pods plant⁻¹ and branches plant⁻¹. These traits also showed strong positive correlations with seed yield, indicating their important role in yield determination. It was further observed that the highly significant correlations of seeds pod⁻¹, pods cluster⁻¹, clusters plant⁻¹, 100-seed weight, pods plant⁻¹ and branches plant⁻¹ with seed yield were mainly due to their substantial positive direct effects. Therefore, selection based directly on these characters would be effective and beneficial for enhancing seed yield in mungbean breeding programmes.

4. CONCLUSION

The traits seeds pods⁻¹, pods cluster⁻¹, cluster plant⁻¹, 100-seed weight, plant height, pods plant⁻¹ and branches plant⁻¹ had the high positive direct effect along with significant correlation with seed yield plant⁻¹. Hence, direct selection for these traits may be useful for further improvement of seed yield in mungbean.

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