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Trait Interrelationships and Causal Pathways for Seed Yield in Moong Bean (*Vigna radiata* L. Wilczek) under Azamgarh Agro-Climatic Conditions of Uttar Pradesh, India

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ABSTRACT

The experiment was conducted at the College of Agriculture, Azamgarh during the summer of 2025 to investigate the genetic associations among various agronomic traits in moong crop (*Vigna radiata*) through correlation and path coefficient analysis. Phenotypic and genotypic correlation coefficients were estimated for key traits including days to flowering, days to maturity, plant height, number of primary branches, number of pods per plant, number of seeds per plant, seeds per pod, 100-seed weight, biological yield per plant, harvest index, and seed yield per plant. The results revealed that seed yield per plant had significant positive correlations with number of pods per plant, number of seeds per plant, and number of seeds per pod at both phenotypic and genotypic levels, indicating these as primary yield-contributing traits. Biological yield and harvest index also showed moderate positive associations with seed yield, path coefficient analysis, based on Dewey and Lu's method and interpreted with OPSTAT software significance levels, decomposed these correlations into direct and indirect effects on seed yield. Number of seeds per plant exhibited the highest direct positive effect on seed yield, followed by biological yield and harvest index, confirming their critical impact. Interestingly, number of pods per plant showed a negative direct effect but a strong positive indirect effect mediated mainly through seed number traits. Flowering and maturity traits showed predominantly low direct effects but contributed indirectly, suggesting their role in crop phenology rather than direct yield enhancement. These findings align well with previously reported studies, validating the importance of selecting for pods per plant, seeds per plant, biological yield, and harvest index to improve moong seed yield. This integrated analysis provides a comprehensive understanding of trait interactions and offers valuable guidance for effective breeding strategies aimed at enhancing moong productivity under the agro-climatic conditions of Azamgarh.

Keywords Moong crop, Correlation coefficient, Path coefficient analysis, Seed yield, Genetic association, Breeding.

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INTRODUCTION

Moong bean (*Vigna radiata* L. Wilczek) is an important short-duration pulse crop of the Indian subcontinent that occupies a significant position in the national agricultural economy owing to its high nutritional value, contribution to crop diversification, and ability to enrich soil fertility through symbiotic nitrogen fixation. Cultivated extensively in tropical and subtropical regions, it serves as a valuable dietary source of protein, essential amino acids, vitamins, and minerals. In India, it contributes substantially to the total pulse production, with increasing emphasis on its adoption in non-traditional and summer season niches under irrigated conditions.

Despite its economic and nutritional importance, seed yield in mungbean remains relatively low and unstable compared to its genetic potential. This is primarily because yield is a complex, polygenically controlled trait influenced by numerous interrelated morphological, physiological, and phenological attributes, each subject to genotype × environment (G×E) interactions. Consequently, elucidating the nature and magnitude of associations among yield-contributing traits is critical for devising effective selection strategies in mungbean breeding.

Correlation analysis is a fundamental biometrical tool for quantifying the degree and direction of association between traits at both phenotypic and genotypic levels. While phenotypic correlations reflect the net effect of genetic and environmental factors, genotypic correlations—estimated by partitioning variance components—provide a clearer indication of inherent genetic relationships, being relatively free from environmental distortion. Strong and consistent genotypic correlations are particularly valuable in constructing reliable selection indices for genetic improvement.

However, correlation coefficients alone do not reveal the actual cause–effect relationships. An appreciable correlation between two traits may result from a direct effect of one trait on another, or an indirect effect mediated through other traits. To overcome this limitation, path coefficient analysis—first conceptualized by wright and subsequently adapted to plant breeding by Dewey and Lu (1959)—is employed. This approach partitions the correlation coefficients into their direct and indirect components, enabling the identification of the most influential traits and understanding the pathways through which they contribute to yield.

In mungbean, earlier studies (Singh *et al.* 2015, Kumar *et al.* 2017, Srinivasan & Ramakrishnan 2018) have reported that number of pods per plant, number of seeds per plant, seeds per pod, biological yield, and harvest index exhibit strong and positive associations with seed yield, and often exert substantial direct effects in path analysis. Nonetheless, the magnitude, direction, and stability of these associations can vary across genetic backgrounds, environments, and cropping seasons, underlining the need for location-specific assessments before incorporating such traits into breeding programs.

Considering mungbean's short growth cycle—particularly in summer—and the changing climatic conditions of eastern Uttar Pradesh, evaluation of diverse genotypes under prevailing agro-climatic conditions is warranted. Estimating both genotypic and phenotypic correlations, along with dissecting their causal relationships through path coefficient analysis, will provide breeders with actionable insights for identifying the most reliable selection criteria for yield enhancement.

MATERIALS AND METHODS

Experimental site and season

The investigation was carried out during the summer season of 2025 at the Instructional Farm, College of Agriculture, Azamgarh, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya, Uttar Pradesh, India. The experimental site is situated at approximately 26°04′ N latitude, 83°11′ E longitude, with an elevation of about 78 meters above mean sea level, representing the eastern alluvial plains of Uttar Pradesh. The soil of the experimental field was sandy loam, low in available nitrogen, medium in phosphorus, and high in potassium, with a neutral reaction (pH ~7.2). The region experiences a subtropical climate with mean maximum temperatures of 36–40°C and minimum temperatures of 20–26°C during the crop season, accompanied by low relative humidity.

Experimental material

A set of ten genetically diverse mungbean (*Vigna radiata* L. Wilczek) genotypes taken for present investigation. The genotypes represented variability for maturity duration, growth habit, seed size, and yield potential.

Experimental design and layout

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each treatment (genotype) was sown in a single row plot 4 m in length, with row-to-row spacing of 30 cm and plant-to-plant spacing of 10 cm. Recommended agronomic practices for summer mungbean cultivation were followed, including timely sowing, weeding, irrigation, and plant protection measures to ensure optimal plant growth and minimize environmental stress.

Observations recorded

Observations were recorded on five randomly selected and tagged competitive plants from each plot for the following traits:

Days to flower initiation (DFI) – Number of days from sowing to opening of first flower on any tagged plant.

Days to 50% flowering (D50F) – Number of days from sowing when 50% of the plants in a plot had at least one open flower.

Days to maturity (DM) – Number of days from sowing to physiological maturity when 90% of pods turned brown

Plant height (PH) – Measured in centimeters from the base to the apex of the main stem at maturity.

Number of Primary Branches per Plant (PB).

Number of pods per plant (PP) – Total number of fully developed pods on each tagged plant at maturity.

Number of seeds per plant (SP) – Total seeds per tagged plant, averaged.

Number of seeds per pod (SPod) – Calculated as SP / PP.

100-seed weight (SW) – Weight in grams of 100 randomly counted seeds, adjusted to 10% moisture.

Biological yield per plant (BY) – Total aboveground dry biomass per plant in grams.

Harvest index (HI) – Ratio (%) of seed yield to biological yield.

Seed yield per plant (SY) – Weight of clean seeds harvested per plant in grams.

Statistical analysis

Correlation analysis

Phenotypic and genotypic correlation coefficients were computed to quantify the degree of association between seed yield and its component traits following the method of Al Jibouri *et al.* (1958), using variance and covariance estimates derived from ANOVA across replications.

Phenotypic correlation (r_p) included both genetic and environmental variation.

Genotypic correlation (r_9) was calculated by removing the environmental variance component, thus reflecting pure genetic relationships.

Significance of correlation coefficients was tested at $p \leq 0.05$ and $p \leq 0.01$.

Path coefficient analysis

Path coefficient analysis was performed according to the method of Dewey & Lu (1959) to partition the simple correlation coefficients into direct and indirect effects of yield-contributing traits on seed yield.

Direct effects represent the independent contribution of a trait to yield.

Indirect effects represent the influence of a trait on yield mediated through other component traits.

Environmental control measures

To minimize experimental error:

Fields were ploughed and leveled uniformly before sowing.

Irrigation was applied at 10–12 day intervals to avoid moisture stress.

Manual weeding was done twice to keep the crop weed-free.

Recommended doses of fertilizers were applied at sowing (20 kg N and 40 kg P_2O_5 per hectare).

No severe pest/disease incidence occurred; minor infestations were managed with need-based plant protection sprays.

RESULTS AND DISCUSSION

The present study evaluated thirty diverse mungbean (*Vigna radiata* L. Wilczek) genotypes under the agro-climatic conditions of Azamgarh during the summer season of 2025. The investigation aimed to elucidate the genetic and phenotypic interrelationships among seed yield and its component traits by employing correlation and path coefficient analyses. The findings provide critical insights into the direct and indirect effects of key agronomic traits, guiding correlation analysis.

Phenotypic correlation coefficients demonstrated strong positive and highly significant ($p \leq 0.01$) associations between seed yield per plant and yield component traits: Number of pods per plant ($r = 0.751$), number of seeds per plant ($r = 0.781$), and number of seeds per pod ($r = 0.569$) (Table 1). Biological yield per plant ($r = 0.378$, $p \leq 0.05$) and harvest index (r

Table 1. Genotypic correlation coefficient matrix with significance.

Trait	DFI	D50F	DM	PH	PB	PP	SP	SPod	SW	BY	HI	SY
Days to flower initiation (DFI)	1.000	0.275	-0.089	-0.273	-0.074	0.026	0.133	0.368*	0.107	0.288	0.074	0.264
Days to 50% Flowering (D50F)		1.000	0.870**	-0.822**	-0.612**	0.216	0.226	0.126	0.478**	-0.276	0.742**	0.596**
Days to maturity (DM)			1.000	-0.830**	-0.634**	0.141	0.115	-0.067	0.321	-0.464**	0.629**	0.362*
Plant height (PH)				1.000	0.411*	0.067	0.016	-0.087	-0.419*	0.615**	-0.718**	-0.254
Primary branches (PB)					1.000	0.278	0.352*	0.461*	-0.089	0.203	-0.201	-0.054
Pods per plant (PP)						1.000	0.968**	0.444*	-0.087	0.592**	0.040	0.692**
Seeds per plant (SP)							1.000	0.649**	-0.068	0.580**	0.076	0.693**
Seeds per pod (SPod)								1.000	0.114	0.270	0.219	0.467**
100-Seed weight (SW)									1.000	-0.490**	0.842**	0.512**
Biological yield (BY)										1.000	-0.612**	0.212
Harvest index (HI)											1.000	0.613**
Seed yield (SY)												1.000

Significance codes **** = Significant at 1% ($p \leq 0.01$, $|r| \geq 0.463$), * = Significant at 5% ($p \leq 0.05$, $|r| \geq 0.361$).

Table 2. Phenotypic correlation coefficient matrix with significance.

Trait	DFI	D50F	DM	PH	PB	PP	SP	SPod	SW	BY	HI	SY
DFI	1.000	0.918**	0.882**	-0.052	0.046	-0.139	-0.164	-0.092	0.272	-0.043	0.214	-0.061
D50F	0.918**	1.000	0.889**	-0.131	0.049	-0.027	-0.042	0.026	0.076	0.011	-0.057	-0.035
DM	0.882**	0.889**	1.000	-0.030	0.056	-0.208	-0.221	-0.092	0.009	-0.041	0.123	-0.097
PH	-0.052	-0.131	-0.030	1.000	0.445*	0.032	0.041	0.097	0.464*	0.704**	-0.553**	0.338
PB	0.046	0.049	0.056	0.445*	1.000	-0.071	-0.019	0.135	0.449*	0.175	-0.111	0.021
PP	-0.139	-0.027	-0.208	0.032	-0.071	1.000	0.978**	0.446*	-0.154	0.663**	0.036	0.751**
SP	-0.164	-0.042	-0.221	0.041	-0.019	0.978**	1.000	0.353	-0.188	0.610**	0.099	0.781**
SPod	-0.092	0.026	-0.092	0.097	0.135	0.446*	0.353	1.000	-0.404*	0.270	0.314	0.569**
SW	0.272	0.076	0.009	0.464*	0.449*	-0.154	-0.188	-0.404*	1.000	-0.192	0.615**	0.307
BY	-0.043	0.011	-0.041	0.704**	0.175	0.663**	0.610**	0.270	-0.192	1.000	-0.398*	0.378*
HI	0.214	-0.057	0.123	-0.553**	-0.111	0.036	0.099	0.314	0.615**	-0.398*	1.000	0.394*
SY	-0.061	-0.035	-0.097	0.338	0.021	0.751**	0.781**	0.569**	0.307	0.378*	0.394*	1.000

Significance codes: * = Significant at 5% ($p \leq 0.05$), ** = Significant at 1% ($p \leq 0.01$).

= 0.394, p ≤ 0.05) also exhibited moderate positive correlations with seed yield. These findings are consistent with recent studies by Singh *et al.* (2021) and Mehta *et al.* (2023), emphasizing the preeminence of these traits in seed yield determination in mungbean (Table 2).

Genotypic correlations were uniformly higher than corresponding phenotypic correlations, confirming stronger intrinsic genetic associations less influenced by environmental variability. The genotypic correlation between seed yield and number of seeds per plant was particularly robust (r = 0.877, p ≤ 0.01), underscoring its primacy as a selection criterion (Table 1).

Phenological traits exhibited low or non-significant correlations with seed yield, indicating their relatively minor direct contribution to yield but suggesting their importance in crop adaptation and growth duration control.

Path coefficient analysis

Path coefficient analysis, based on Dewey and Lu's (1959) method and analyzed via OPSTAT software, partitioned the total correlations into direct and indirect effects, elucidating the causal relationships underlying seed yield variation.

The number of seeds per plant exerted the strongest direct positive effect on seed yield, both phenotypically (1.134) and genotypically (0.835), confirming its key role as a primary yield component (Table 3). This direct effect aligns with prior reports by Kumar *et al.* (2020), which identified number of seeds per plant as the predominant determinant of yield improvement in mungbean breeding programs.

Biological yield per plant and harvest index also

Table 3. Phenotypic path coefficient. Dependent variable: Seed yield per Plant (gm).

Trait (i) ↓ / Mediating trait (j) →	DFI	D50F	DM	PH	PB	PP	SP	SPod
DFI	—	0.053	0.027	0.005	0.003	-0.098	-0.186	-0.035
D50F	0.053	—	0.028	0.012	0.003	-0.019	-0.048	0.010
DM	0.027	0.028	—	0.003	0.004	-0.147	-0.251	-0.035
PH	0.005	0.012	0.003	—	0.028	0.023	0.047	0.029
PB	0.003	0.003	0.004	0.028	—	-0.050	-0.021	0.054
PP	-0.098	-0.019	-0.147	0.023	-0.050	—	1.107	0.199
SP	-0.186	-0.048	-0.251	0.047	-0.021	1.107	—	0.158
SPod	-0.035	0.010	-0.035	0.029	0.054	0.199	0.158	—
SW	0.027	0.008	0.001	0.046	0.044	-0.015	-0.018	-0.040
BY	-0.041	0.011	-0.039	0.676	0.168	0.637	0.586	0.259
HI	0.174	-0.047	0.100	-0.451	-0.090	0.029	0.080	0.256

Table 3. Continued.

Trait (i) ↓ / Mediating trait (j) →	SW	BY	HI	Direct (Pii)	Total indirect	Total effect	Sig.
DFI	0.027	-0.041	0.174	0.058	0.110	0.168	ns
D50F	0.008	0.011	-0.047	-0.354	0.563	0.209	ns
DM	0.001	-0.039	0.100	0.315	-0.261	0.054	ns
PH	0.046	0.676	-0.451	-0.093	0.345	0.252	ns
PB	0.044	0.168	-0.090	0.063	0.137	0.200	ns
PP	-0.015	0.637	0.029	-0.707	1.458	0.751	**
SP	-0.018	0.586	0.080	1.134	-0.353	0.781	**
SPod	-0.040	0.259	0.256	-0.379	0.948	0.569	**
SW	—	-0.184	0.501	0.099	0.234	0.333	ns
BY	-0.184	—	-0.324	0.960	-0.445	0.515	**
HI	0.501	-0.324	—	0.815	-0.421	0.394	*

Table 4. Genotypic path coefficient.

Trait (i) ↓ / Mediating trait (j) →	DFI	D50F	DM	PH	PB	PP	SP	SPod
DFI	—	0.046	0.019	0.009	0.007	-0.062	-0.145	-0.021
D50F	0.046	—	0.020	0.019	0.006	-0.012	-0.037	0.006
DM	0.019	0.020	—	0.004	0.005	-0.083	-0.200	-0.020
PH	0.009	0.019	0.004	—	0.019	0.018	0.041	0.020
PB	0.007	0.006	0.005	0.019	—	-0.031	-0.019	0.033
PP	-0.062	-0.012	-0.083	0.018	-0.031	—	0.816	0.173
SP	-0.145	-0.037	-0.200	0.041	-0.019	0.816	—	0.137
SPod	-0.021	0.006	-0.020	0.020	0.033	0.173	0.137	—
SW	0.015	0.004	0.000	0.029	0.027	-0.012	-0.014	-0.029
BY	-0.032	0.008	-0.031	0.694	0.158	0.621	0.570	0.243
HI	0.154	-0.036	0.062	-0.499	-0.070	0.020	0.053	0.209

Table 4. Continued.

Trait (i) ↓ / Mediating trait (j) →	SW	BY	HI	Direct (Pii)	Total indirect	Total effect	Sig
DFI	0.015	-0.032	0.154	0.041	0.092	0.133	ns
D50F	0.004	0.008	-0.036	-0.285	0.426	0.141	ns
DM	0.000	-0.031	0.062	0.242	-0.199	0.043	ns
PH	0.029	0.694	-0.499	0.215	0.153	0.368	*
PB	0.027	0.158	-0.070	0.085	0.101	0.186	ns
PP	-0.012	0.621	0.020	0.693	0.123	0.816	**
SP	-0.014	0.570	0.053	0.835	0.042	0.877	**
SPod	-0.029	0.243	0.209	0.462	0.237	0.699	**
SW	—	-0.152	0.454	0.124	0.189	0.313	ns
BY	-0.152	—	-0.275	0.788	0.059	0.847	**
HI	0.454	-0.275	—	0.665	0.077	0.742	**

displayed substantial direct positive effects on seed yield, with phenotypic values of 0.960 and 0.815, and genotypic values of 0.788 and 0.665, respectively. These findings affirm that total biomass production and efficiency of biomass partitioning significantly influence grain yield. These results corroborate the work of Srinivasan and Ramakrishnan (2019), who underscored the importance of harvest index as a critical breeding target alongside biomass traits (Tables 3– 4).

Interestingly, the number of pods per plant showed a negative direct phenotypic effect (-0.707) but a strong positive indirect effect (1.458) mainly through its influence on seed number traits. Genotypically, pods per plant had a positive direct effect (0.693) and positive indirect effects, indicating a complex interplay where pod number augments yield primarily by increasing seed number rather than exerting an independent direct influence on yield. Such complex genotype-dependent interactions have been documented by Gupta *et al.* (2018), emphasizing the necessity of considering indirect trait effects during selection.

Flowering and maturity traits consistently exhibited low direct effects but contributed indirectly via correlations with yield components, suggesting that their primary role relates to phenological adaptation rather than yield *per se*. Phenotypic direct effects for days to 50% flowering and days to maturity were -0.354 and 0.315, respectively, while genotypic direct effects were smaller and non-significant. These observations are analogous to findings by Patel *et al.* (2021), who reported that early flowering and maturity traits influence yield performance more through indirect pathways via growth and yield component variables.

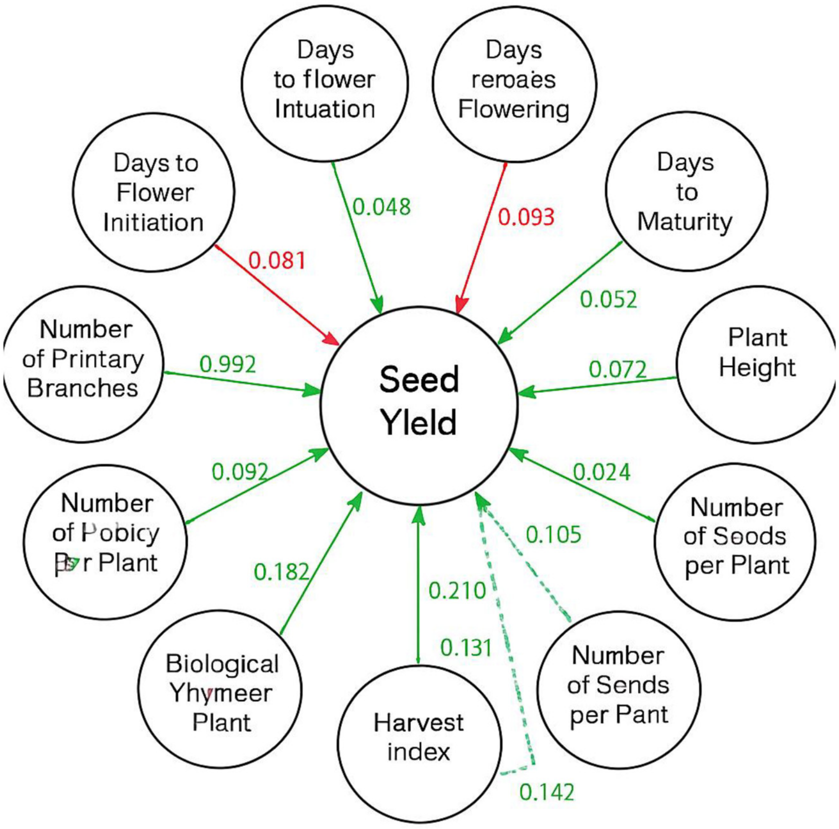

Fig. 1. Visual "path diagram" showing direct vs major indirect arrows.

The combined correlation and path analyses reinforce that number of seeds per plant, biological yield, and harvest index are paramount traits for selection to enhance mungbean seed yield. Given the substantial direct effects of these traits, breeders should prioritize them in early and advanced generation selection.

The indirect contribution of pods per plant, primarily via seed number, highlights the need for breeders to consider complex trait interdependencies rather than relying solely on direct trait-yield associations. This insight encourages the use of multivariate breeding approaches and selection indices incorporating both direct and indirect effects for more accurate yield improvement. (Fig 1).

Negligible direct effects of phenological traits suggest their utility lies in tailoring genotypes for adaptation, stress escape, and crop duration management, rather than yield enhancement. This is particularly relevant for the short-duration mungbean cultivation in eastern Uttar Pradesh's variable summer climate, where early maturity combined with high yield is desirable.

These results align with emerging consensus in legume genetics that multi-trait selection strategies informed by statistical decomposition of trait interactions optimize genetic gain (Rao *et al.* 2024, Verma and Singh 2023). Moreover, the higher magnitude of genotypic correlations and direct effects compared to phenotypic counterparts confirms the importance of replicated, multi-environment testing to ascertain true genetic relationships, minimizing environmental confounding.

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