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ASSESSMENT OF GENETIC VARIABILITY, CORRELATION AND PATH CO-EFFICIENT STUDIES ON YIELD AND ITS COMPONENT IN MUNGBEAN (*VIGNA RADIATA* L. WILCZEK)

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ABSTRACT

The present study evaluated twenty-five diverse greengram (*Vigna radiata* L. Wilczek) genotypes during kharif 2024 season for analysis and estimation of genetic variability, correlation and path coefficient for sixteen quantitative traits and their relationship with yield. A random block experimental design using three field repetitions took place at the Department of Genetics and Plant Breeding, SHUATS, Prayagraj, India. Tests between different genotypes showed marked variations for each measured trait which demonstrated wide genetic diversity. Genetic variation expressed through high phenotypic and genotypic coefficients of variation in primary branches and seed yield per plant and harvest index was observed simultaneously with high heritability and genetic advance levels for maturity days, seed yield and pod length because of the dominant additive gene expression. Seed yield demonstrated powerful positive correlations with harvest index and flowering traits according to correlation analysis. The path coefficient analysis demonstrated harvest index as the dominant trait which directly boosts seed yield and both days to 50% flowering and pod setting rank second. Selection targets based on these traits possess the potential to enhance genetic improvements which can improve yield potential in greengram breeding programs.

***Keywords* :** Correlation; genetic variability; greengram; heritability; path coefficient.

Introduction

Legume or pulses are the most essential source of protein for a major vegetarian country like India. The most frequently cultivated and consumed pulses include mungbean, chickpea, blackgram along with lentil and pigeonpea. They are known to contain protein along with carbohydrates which have dietary fiber content and provide b-complex vitamins and multiple health-promoting phytochemicals and mineral components (Nasir and Sidhu, 2012). They have the unique capacity to capture atmospheric nitrogen for their growth thus making them beneficial for soil maintenance strategies focused on lowering greenhouse gas emission rates (Lemke *et al*., 2007).

Greengram commonly known as Mungbean or golden gram (*Vigna radiata*) that belongs to Fabaceae (chromosome no. 2n=22), provides critical nutritional value while enhancing soil quality along with its high importance as crop production. The nutritional complex of protein along with dietary fiber and vitamins and minerals makes greengram essential to healthy diet patterns in vegetarian and vegan cultures (Yi-Shen *et al*., 2018). Greengram demonstrates an outstanding dual function because it maintains nutritional value and shows a remarkable capacity to convert atmospheric nitrogen into soil nutrient content (Senaratne *et al*., 1995). It enters a partnership with rhizobia bacteria to change atmospheric nitrogen into usable forms which strengthen soil nutrient levels. Soil receives improved fertility from natural nitrogen fixation solutions that help green gram crops improve the following crops in rotational patterns (Senaratne *et al*., 1995). When used in farming green gram requires minimal fertilizer input because this nutrient-efficient crop helps decrease nutrient losses through runoff thus protecting ecosystems and conserving resources (Rank *et al.*, 2025). India maintains its position as the top mungbean producer worldwide through cultivating 2.17 million tons of mungbean on 4.32 million hectares of land (Mishra *et al.*, 2020). The adaptable qualities and beneficial characteristics of mungbean deserve greater sustained breeding programs because of its potential to enhance food security and malnutrition relief in vulnerable populations. To meet rising pulse demand because of population growth and dietary changes we need a strategic focus on both increasing mungbean production levels and productivity and understanding genetic relationships between yield-determining traits and their direct and indirect effect on yield (Mishra *et al.*, 2020). Knowledge of genetic variations in mungbean germplasm serves as the foundation for breeding strategies targeted at yield improvement along with improving other important characteristics (Somta *et al.*, 2022).

A breeding program focused on improving the seed yield offers great potential for advancing greengram production. This requires high variability within its underlying population to achieve success. Measuring genetic variation among experimental populations constitutes the fundamental aspect of any improvement program. A successful crop improvement program requires absolute application of genetic variability assessment through both phenotypic and genotypic coefficient of variation as well as heritability and genetic advance measurements. The results from association analysis demonstrate the precise nature and degree of quantitative relation between yield and its determining traits for subsequent genotype enhancement. The main objective of present research investigation was to estimate the genetic variability, correlation, heritability, and genetic advance for different important quantitative characters in a set of diverse genotypes of mungebean.

Materials and Methods

The experimental material for the current study includes 25 greengram genotypes *viz.,* GM-6, IC-39294, IC-121221, RMG-344, IC-119048, MH-1142, GM-7, GAM-5, IC-332327, IPM-2-14, IC-119027, IC-76378, GM-4, IC-11468, IC-249567, IC-305241, SML-832, VGG-17-00-2, IC-39280, PM-6, MH-421, KHAKI, TJM-3, IPM-205-07 and S-8 (MOHINI). These genotypes were evaluated for different quantitative traits in RBD design (Randomized Block Design) during kharif 2024 with spacing 30 x 10 cm respectively in 3 replications at the experimental farm of the Department of Genetics and Plant Breeding, SHAUTS, Prayagraj. All the recommended cultural practices were followed up to harvest. At maturity data were recorded for plant height, Days to 1st flowering, Days to 50% flowering, Number of primary branches, Number of secondary branches, Days to 50% pod setting, Days to maturity, Number of pod per cluster, number of seeds per pod, Pod length, Total number of nodule per plant, Active nodule per plant, biological yield, harvest index, 100 seed weight and total yield on five randomly selected plants from each replication of individual genotype.

Standard statistical procedure was used for the analysis of variance, genotypic and phenotypic coefficients of variation (Burton, 1952), heritability (Hanson *et al.*, 1956). The genotypic and phenotypic correlation coefficients were computed using genotypic and phenotypic variances and covariances. The path co-efficient analysis was done according to the method by Dewey and Lu (1959).

Results and Discussion

In the current study, analysis of variance revealed significant treatment for plant height, days to 1st flowering, days to 50% flowering, days to maturity, number of primary branches, number of secondary branches, number of pods per cluster, days to 50% pod setting, number of seeds per pod, pod length, total number of nodules per plant, active number of nodules per plant, biological yield, harvest index and yield. Harvest index showed the maximum treatment sum of square while number of pods per cluster showed the minimum treatment sum of square as indicated in Table 1.

Table 1: Analysis of variance in 25 greengram genotypes

S. No.	**Source of variation**	**Mean Sum of Squares**		
		Repli-cation	**Treat-ment**	**Error**
	Degree of freedom	**2**	**24**	**48**
1	Plant Height	6.114	56.069**	2.37
2	Days to 1st flowering	9.627	10.389**	0.994
3	Days to 50% Flowering	20.907	23.969**	1.717
4	Number of primary branches	0.828	1.297**	0.069
5	Number of secondary branches	0.053	1.914**	0.102
6	Days to 50% pod setting	7.387	19.403**	1.652
7	Days to Maturity	0.4	90.998**	0.319
8	Number of pods per cluster	0.239	0.716**	0.081
9	Number of seeds per pod	0.222	1.769**	0.119
10	Pod length	0.056	2.593**	0.031
11	Total number of nodules per plant	0.671	0.984**	0.074
12	Active number of nodules per plant	0.292	2.197**	0.054
13	Biological yield	0.339	6.058**	0.641
14	Harvest index	9.086	144.105**	3.764
15	100 Seed weight	0.891	2.902**	0.116
16	Total yield	0.050	3.826**	0.072

** Significant at 1% level of probability

Through the analysis of the mean data (table 2) it was revealed that the plant height ranged from 70.4 cm to 54.20 cm, with maximum in case of KHAKI and TJM-3 while minimum in case of MH-1142. Days to 1st flowering ranged from 35.66 days to 42.33 days, with S-8 (MOHINI) which exhibited earliest flowering and took minimum days to flower, while IPM-2-14 took maximum days to flower. The time taken to reach 50% flowering ranged from 41 days to 50.33 days, where S-8 (MOHINI) took minimum days to reach 50% flowering while, IPM-2-14 took the highest days to reach 50% flowering. The number of primary branches per plant varied between 2.26 to 4.93, where highest number was in GAM-5 and lowest number was discovered in KHAKI. The number of secondary branches per plant ranges from 5.26 to 8, where the highest number was found in MH-421 while the lowest number was found in GM-6. The time taken to reach 50% pod setting ranged from 55 Days to 64.66 days where S-8 (MOHINI) took 55 days to reach at 50% pod setting while SML-832 took highest days 64.66 days to reach at 50% pod setting. The number of pods per cluster ranged from 4.8 to 6.53 in which IC-76378 has the least number of pods per cluster while GAM-5 and IC-119048 has the highest number of pods per cluster. The number of seeds per pod ranged from 9.26 to 12.26 where GM-4 has the least number of seeds per pod and IC-305241 was recorded with the highest number of seeds per pod. The mean performance of pod length ranged from 5.52 cm to 10.097 cm, where it was maximum in case of IC-305241 while, it was minimum in case of IC-76378. The difference in days to maturity ranged from 75.33 to 94.33 days where S-8 (MOHINI) matured the earliest and SML-832 took the longest to mature. The Total number of nodules per plant varied between 10.33 to 12.4, highest was found in IC-119048 while GM-7 was the lowest. Active number of nodules per plant ranges between 5 to 7.66, highest in S-8 (MOHINI) while IC-305241 and IC-39280 were the lowest. Biological yield per plant varied between 16.79 g to 21.68 g in which MH-421 has the highest biological yield per plant and IC-121221 was the lowest. The harvest index variance varied from 28.93 % to 50.95 % where IPM-205-07 had the highest harvest index and RMG-344 had the lowest harvest index. 100 seed weight or test weight ranges between 3.45 g to 6.74 g, where it was lowest for GAM-5 and highest for MH-421. Total yield per plant varied between 5.64 g to 9.11 g, where IC-11468 has the lowest yield while IPM-2-14 has the highest yield.

Table 2: Mean values for yield and its components in 25 greengram genotypes

Genotype	PH	D1F	D5F	NPB	NSB	D5PS	DM	NPPC	NSP	PL	TNNOP	ANNOP	BY	HI	SW	TY
GM-6	61.333	37.667	43	3	5.267	59	77.733	5.6	10.333	6.78	11.467	6.733	17.307	40.073	5.423	7.393
IC-39294	58.067	36.667	42.667	3.067	5.4	59.333	76.067	5.8	10.733	7.207	11.2	5.2	17.053	50.414	6.366	8.218
IC-121221	59.933	39.333	45.333	2.8	5.4	59.667	77.733	6	9.8	7.18	11.8	5.4	16.796	39.765	4.297	7.513
RMG-344	58.667	37.667	42	2.533	7.333	58.667	87.733	5.533	10.733	7.703	11.467	6.733	19.831	28.929	3.766	5.843
IC-119048	60.933	36.333	41.333	3.067	6.133	58	76.267	6.533	10.467	7.303	12.4	5.2	17.857	43.35	5.572	7.705
MH-1142	54.2	40.667	48	4.2	7.267	63.333	76.2	5.4	11.4	7.2	10.6	7.533	20.297	44.394	6.119	8.991
GM-7	59.2	38.667	45.667	4.133	6.933	59.667	75.867	6.267	10.4	6.727	10.333	6.133	19.9	35.026	5.276	7.288
GAM-5	64.6	39.667	47.333	4.933	7.2	62.667	80.8	6.533	10.067	7.623	10.8	5.667	19.04	30.418	3.457	6.144
IC-332327	59.467	37.667	43.667	3.4	5.667	58.667	75.8	5.467	9.867	6.62	11.4	5.333	17.773	47.755	5.601	7.268
IPM-2-14	64.467	42.333	50.333	4.267	6.6	61	81.533	5.533	10.333	7.457	10.733	5.733	18.97	50.161	6.33	9.116
IC-119027	56.4	37.667	43.667	3.467	6.467	59	75.933	5.733	10.467	6.613	10.4	5.6	18.513	32.003	4.376	6.06
IC-76378	59.6	38.667	46.667	3.533	6.467	60.667	88.6	4.8	9.4	5.527	10.8	5.4	17.438	43.635	5.26	7.908
GM-4	60.533	36.333	42	4	6.533	55.667	76.467	5.133	9.267	8.837	11	6.733	18.297	38.448	4.55	6.725
IC-11468	60.4	38	43.333	3.2	6.4	58.333	87.533	6	10.467	7.007	12	5.333	17.314	31.65	3.652	5.646
IC-249567	58	39.667	45	3.6	6.2	60.333	76.933	5.867	10.467	7.91	12	5.6	17.817	47.251	6.223	8.514
IC-305241	57.867	36.667	44	3.6	6.6	57.667	84.533	5.533	12.267	10.097	11.533	5	18.098	34.237	4.705	6.376
SML-832	66.8	40.667	49.667	4.133	7.133	64.667	94.333	6.4	10.8	8.47	10.533	6.533	19.899	48.097	6.273	8.995
VGG-17-00-2	65.867	36.667	42.667	3.8	7.6	57.667	87.333	5.467	12	8.923	11.133	6.6	20.987	34.916	5.016	7.045
IC-39280	59.2	39.667	48.333	4.4	6.6	62.667	76.2	5.2	9.867	8.193	11.2	5	18.989	30.701	4.189	5.712
PM-6	61.867	41.667	48.667	3.4	7.467	64	76.467	6.333	10.933	7.75	10.867	6.267	20.728	41.096	5.563	8.304

MH-421	62	41	48.667	2.8	8	62.667	75.6	5.8	10.6	8.15	11.267	6.533	21.68	38.588	6.748	8.418
KHAKI	70.4	39.333	48	2.267	7.8	62.667	84.4	5.2	10.533	8.41	12.333	7.467	21.363	32.281	4.351	6.619
TJM-3	70.4	38.667	42.667	3.2	7.8	58.667	80.533	5.867	10.933	7.353	11.067	7.533	19.983	38.113	5.396	7.035
IPM-205-07	68.533	41.333	46.667	3.933	7.6	62.667	86.8	5	12.067	8.073	11.8	6.667	19.598	50.955	5.948	8.84
S-8 (MOHINI)	66.933	35.667	41	4.467	7.467	55	75.333	6.4	11.533	8.02	11.133	7.667	18.012	35.795	3.53	5.867
C.D.	2.535	1.642	2.158	0.434	0.527	2.116	0.931	0.467	0.567	0.29	0.449	0.384	1.318	3.195	0.561	0.441
SE(m)	0.889	0.576	0.757	0.152	0.185	0.742	0.326	0.164	0.199	0.102	0.157	0.135	0.462	1.12	0.197	0.155
SE(d)	1.257	0.814	1.07	0.215	0.261	1.049	0.461	0.232	0.281	0.144	0.223	0.191	0.654	1.584	0.278	0.219
C.V.	2.49	2.574	2.898	7.384	4.721	2.139	0.702	4.949	3.241	2.301	2.424	3.799	4.227	4.909	6.654	3.65
max.	70.4	42.333	50.333	7.384	8	64.667	94.333	6.533	12.267	10.097	12.4	7.667	21.68	50.955	6.748	9.116
min.	54.2	35.667	41	2.267	5.267	55	75.333	4.8	9.267	5.527	0.223	0.067	0.291	0.392	0.814	0.272
mean	61.82668	38.73348	45.2134	3.568	6.77336	60.09348	80.50924	5.73596	10.62936	7.64532	10.80088	5.87728	18.26096	37.9348	4.93512	7.05688

(PH: plant height; D1F: days to 1st flowering; D5F: days to 50% flowering; NPB: no. of primary branches; NSB: no. of secondary branches; D5PS: days to 50% flowering; DM: days to maturity; NPPC: no. of pod per cluster; NSP: no. of seeds per pod; PL: pod length; TNNOP: total no. of nodules per plant; ANNOP: active nodules per plant; BY: biological yield; HI: harvest index; SW: seed weight; TY: total yield)

The magnitude of genotypic variance was highest for harvest index followed by days to maturity, plant height and days to 50% flowering. The harvest index recorded highest phenotypic variance followed by days to maturity, plant height, days to 50% flowering. These results correspond with the findings of Rathor *et al.* (2015) and Rao *et al.* (2006). In the present study, Genotypic coefficient of variation (GCV) (table 3) was highest for number of primary branches per plant followed by harvest index and seed yield and the lowest GCV value was for days to 50% flowering followed by Plant height and days to 50% flowering, similar results were found by Jagdhane *et al.* (2017). The highest phenotypic coefficient of variation (PCV) was recorded for number of primary branches per plant followed by harvest index, and seed yield while the lowest PCV value was for days to 50% pod setting followed by total number of nodules and these findings are in accordance with Dar *et al.* (2024). The heritability for all characters ranged between 0.74 to 0.99. Maximum heritability was observed for days to maturity followed by pod length, seed yield, active number of nodules per plant and harvest index, plant height, number of primary branches and number of secondary branches, number of seeds per pod which were similar to the findings of Jagdhane *et al.* (2017). The estimates of genetic advance ranged from 0.81 to 13.55 with the highest estimate in case of harvest index followed by days to maturity and the lowest value for genetic advance was recorded for the character number of pods per cluster. These findings were in accordance with Pandit *et al.* (2022) and Jain *et al.* (2024).

Table 3: Genetic component for yield and its component in 25 greengram genotypes

TRAITS	PH	D1F	D5F	NPB	NSB	D5PS	DM	NPPC	NSP	PL	TNNOP	ANNOP	BY	HI	SW	TY
GCV	6.84	4.57	6.02	17.93	11.47	4.05	6.83	8.02	6.98	12.53	5.10	14.38	7.36	18.03	19.53	15.85
PCV	7.28	5.24	6.68	19.38	12.41	4.58	6.86	9.43	7.69	12.75	5.69	14.91	8.57	18.74	20.71	16.30
H^2	0.88	0.76	0.81	0.86	0.86	0.78	0.99	0.72	0.82	0.96	0.80	0.93	0.74	0.93	0.89	0.95
GA	8.19	3.18	5.06	1.22	1.48	4.43	11.27	0.81	1.39	1.87	1.02	1.68	2.38	13.55	1.87	2.24
GAM	13.25	8.20	11.18	34.17	21.86	7.37	13.99	14.05	13.03	25.35	9.42	28.56	13.02	35.73	37.93	31.75

(GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; H^2: heritability; GA: genetic advance; GAM: genetic advance in percentage of mean; PH: plant height; D1F: days to 1st flowering; D5F: days to 50% flowering; NPB: no. of primary branches; NSB: no. of secondary branches; D5PS: days to 50% flowering; DM: days to maturity; NPPC: no. of pod per cluster; NSP: no. of seeds per pod; PL: pod length; TNNOP: total no. of nodules per plant; ANNOP: active nodules per plant; BY: biological yield; HI: harvest index; SW: seed weight; TY: total yield)

The present study (table 4) reveals that the genotypic correlation is much higher than the phenotypic correlation, the genotypic correlation coefficient analysis showed positive relationships between seed yield per plant and several other traits. Among these, days to first flowering, days to 50% flowering, days to 50% pod setting, harvest index, and test weight which exhibits strong and significant positive correlations, indicating these traits are closely associated with higher seed yield at the genotypic level and are important for yield improvement and similar findings were reported by researcher Kumar *et al.* (2021). Seed yield per plant demonstrated positively correlated yet insignificant relationships with number of primary branches, active number of nodes per plant, biological yield, plant height, days to maturity, and number of seeds per pod. Similar reports have been reported by Anita *et al.* (2025) and Dutt *et al.* (2020). These traits demonstrate a supportive relationship to yield potential even though the statistical significance is uncertain. The combinations of test weight together with harvest index and flowering and pod setting schedules represent fundamental genetic features which strongly influence yield capabilities for breeding purposes.

In table 5 it is observed that different traits demonstrate positive connections with seed yield when assessed at the phenotypic level. Notably, days to first flowering, days to 50% flowering, days to 50% pod setting, harvest index, and test weight all showed a strong and significant positive phenotypic correlation with seed yield, indicating their crucial role in determining yield potential and findings agree with Parihar *et al.* (2018). The yield associations with plant height were combined with number of primary branches and active number of nodules per plant along with biological yield show positive correlations despite insignificance and findings correlate with Dutt *et al.* (2020). The selection of early flowering along with optimized pod setting and improved harvest index and seed weight produces enhanced overall seed yields, but different traits show secondary impacts under specific environmental settings.

Table 4: Genotypic correlation for seed yield and its associates in 25 greengram genotypes

	PH	D1F	D5F	NPB	NSB	D5PS	DM	NPPC	NSP	PL	TNNOP	ANNOP	BY	HI	SW	TY
PH	1															
D1F	0.189	1														
D5F	0.135	0.926**	1													
NPB	0.011	0.16	0.270*	1												
NSB	0.560**	0.354**	0.322**	0.147	1											
D5PS	0.133	0.958**	0.977**	0.101	0.319**	1										
DM	0.396**	0.138	0.184^{NS}	-0.05	0.293**	0.206	1									
NPPC	0.09	-0.042	-0.112	0.138	0.009	-0.024	-0.218	1								
NSP	0.266*	-0.033	-0.078	0.068	0.473**	-0.011	0.260*	0.1	1							
PL	0.286*	-0.073	0.029	0.128	0.411**	-0.052	0.197	-0.026	0.55**	1						
TNNOP	0.172^{NS}	-0.214	-0.33**	-0.62**	-0.185	-0.202	0.059	-0.117	0.087	0.201	1					
ANNOP	0.534**	0.09	-0.013	-0.031	0.666**	0.017	0.069	-0.056	0.339**	0.168	-0.131	1				
BY	0.436**	0.506**	0.522**	0.007	0.927**	0.542**	0.176	0.003	0.381**	0.382**	-0.219	0.615**	1			
HI	0.012	0.347**	0.239*	0.07	-0.30**	0.249*	-0.021	-0.107	0.032	-0.191	-0.014	-0.082	-0.208	1		
SW	-0.052	0.467**	0.384**	-0.086	-0.04	0.411**	-0.092	-0.098	0.146	-0.076	-0.133	0.015	0.208	0.840**	1	
TY	0.027	0.637**	0.526**	0.034	-0.017	0.534**	0.024	-0.039	0.105	-0.115	-0.148	0.086	0.185	0.890**	0.935**	1

* Significant at 5% Level of Significance ** significant at 1% Level of Significance

(PH: plant height; D1F: days to 1st flowering; D5F: days to 50% flowering; NPB: no. of primary branches; NSB: no. of secondary branches; D5PS: days to 50% flowering; DM: days to maturity; NPPC: no. of pod per cluster; NSP: no. of seeds per pod; PL: pod length; TNNOP: total no. of nodules per plant; ANNOP: active nodules per plant; BY: biological yield; HI: harvest index; SW: seed weight; TY: total yield)

Table 5: Phenotypic correlation for seed yield and its associates in 25 greengram genotypes

	PH	D1F	D5F	NPB	NSB	D5PS	DM	NPPC	NSP	PL	TNNOP	ANNOP	BY	HI	SW	TY
PH	1															
D1F	0.143	1														
D5F	0.112	0.869**	1													
NPB	0.043	0.147	0.218	1												
NSB	0.514**	0.286*	0.275*	0.145	1											
D5PS	0.076	0.723**	0.759**	0.09	0.283*	1										
DM	0.364**	0.11	0.161	-0.044	0.266*	0.187	1									
NPPC	0.071	-0.062	-0.06	0.15	0	0.011	-0.175	1								
NSP	0.208	-0.007	-0.106	0.088	0.435**	-0.008	0.229*	0.031	1							
PL	0.253*	-0.053	0.039	0.119	0.357**	-0.029	0.194	-0.013	0.469**	1						
TNNOP	0.139	-0.182	-0.241*	-0.502**	-0.168	-0.144	0.069	-0.009	0.04	0.187	1					
ANNOP	0.476**	0.071	-0.027	-0.026	0.582**	0.045	0.062	-0.047	0.314**	0.169	-0.122	1				
BY	0.355**	0.387**	0.372**	-0.037	0.768**	0.425**	0.155	-0.099	0.327**	0.322**	-0.217	0.504**	1			
HI	0.029	0.296**	0.197	0.079	-0.274*	0.199	-0.023	-0.072	0.035	-0.186	0	-0.076	-0.18	1		
SW	-0.037	0.401**	0.333**	-0.042	-0.052	0.361**	-0.082	-0.069	0.097	-0.075	-0.105	0.008	0.176	0.766**	1	
TY	0.028	0.536**	0.459**	0.043	-0.003	0.472**	0.03	-0.035	0.111	-0.111	-0.112	0.067	0.147	0.829**	0.853**	1

* Significant at 5% Level of Significance ** significant at 1% Level of Significance

(PH: plant height; D1F: days to 1st flowering; D5F: days to 50% flowering; NPB: no. of primary branches; NSB: no. of secondary branches; D5PS: days to 50% flowering; DM: days to maturity; NPPC: no. of pod per cluster; NSP: no. of seeds per pod; PL: pod length; TNNOP: total no. of nodules per plant; ANNOP: active nodules per plant; BY: biological yield; HI: harvest index; SW: seed weight; TY: total yield)

Analysis of direct and indirect effects (table 6) demonstrates that harvest index demonstrates the strongest positive influence on seed yield per plant thus establishing itself as an essential yield determining factor and similar findings were found in Nalajala *et al.* (2022). The evaluation shows that days to 50% flowering and days to 50% pod setting together demonstrate significant contributions to yield output and these findings agree with Parihar *et al.* (2018). The positive effects of traits, including days to 50% flowering and plant height extend through intermediate pathways to yield components like pod length and secondary branches. The number of secondary branches demonstrates a significant interdependent influence over yield. The analysis reveals that compound effects of traits across multiple intermediary features can either magnify or obscure their actual influence on yield levels thus influencing breeding program selections.

Table 6: Direct and indirect effects on yield and its component in 25 greengram genotypes

	D5F	PH	NPB	NSB	D5PS	DM	NPPC	NSP	PL	TNNOP	ANNOP	BY	HI	TY
D5F	**0.20852**	-0.01737	-0.02173	0.01567	0.06384	0.00295	-0.00489	-0.00517	-0.00036	0.00708	-0.00245	0.049	0.16415	0.459^{**}
PH	0.02328	**-0.15563**	-0.00432	0.02933	0.00638	0.00669	0.00576	0.01018	-0.00237	-0.00408	0.04263	0.04672	0.02377	0.028
NPB	0.04553	-0.00675	**-0.0995**	0.00829	0.00754	-0.00082	0.01216	0.00429	-0.00111	0.01476	-0.00232	-0.00493	0.06583	0.043
NSB	0.05732	-0.08006	-0.01447	**0.05701**	0.02377	0.0049	0.00002	0.02124	-0.00334	0.00493	0.05212	0.10125	-0.22818	-0.003
D5PS	0.15828	-0.0118	-0.00892	0.01611	**0.08411**	0.00345	0.00091	-0.00037	0.00027	0.00424	0.00402	0.05598	0.16587	0.472^{**}
DM	0.03351	-0.05664	0.00442	0.01518	0.01577	**0.01838**	-0.01419	0.01118	-0.00182	-0.00202	0.00551	0.02037	-0.01929	0.03
NPPC	-0.01257	-0.01105	-0.01492	0.00001	0.00095	-0.00322	**0.0811**	0.00149	0.00012	0.00026	-0.00423	-0.01299	-0.05961	-0.035
NSP	-0.02207	-0.03244	-0.00873	0.02479	-0.00064	0.00421	0.00248	**0.04885**	-0.00439	-0.00119	0.02811	0.04306	0.02877	0.111
PL	0.00807	-0.03933	-0.0118	0.02035	-0.00241	0.00357	-0.00106	0.02291	**-0.00936**	-0.0055	0.01511	0.0425	-0.15451	-0.111
TNNOP	-0.0502	-0.02161	0.04997	-0.00957	-0.01212	0.00126	-0.00072	0.00197	-0.00175	**-0.0294**	-0.0109	-0.02859	-0.00038	-0.112
ANNOP	-0.00571	-0.07406	0.00258	0.03317	0.00378	0.00113	-0.00383	0.01532	-0.00158	0.00358	**0.0896**	0.06641	-0.06319	0.067
BY	0.07754	-0.05517	0.00372	0.04381	0.03573	0.00284	-0.00799	0.01596	-0.00302	0.00638	0.04515	**0.13178**	-0.1499	0.147
HI	0.04114	-0.00445	-0.00787	-0.01564	0.01677	-0.00043	-0.00581	0.00169	0.00174	0.00001	-0.0068	-0.02374	**0.83202**	0.829^{**}

Residual effect = 0.15112

Diagonal values indicated direct effect

(PH: plant height; D1F: days to 1st flowering; D5F: days to 50% flowering; NPB: no. of primary branches; NSB: no. of secondary branches; D5PS: days to 50% flowering; DM: days to maturity; NPPC: no. of pod per cluster; NSP: no. of seeds per pod; PL: pod length; TNNOP: total no. of nodules per plant; ANNOP: active nodules per plant; BY: biological yield; HI: harvest index; TY: total yield)

Seed yield is directly affected mostly by harvest index above all other traits followed by biological yield, days to 50% flowering and days to 50% pod setting. Seed yield is directly influenced by days to 50% flowering in conjunction with pod length and total number of nodes per plant. indirect effects included Positive indirect effects of days to 50 % flowering and days to 50 % pod setting on the yield which manifested through harvest index and biological yield, respectively. These reports agree to Rao *et al.* (2006), Singh *et al.* (2009), Hemavathy *et al.* (2015) and Reddy *et al.* (2011).

The residual effect (0.151) indicates that the component characters under study were responsible for about 85% of variability in seed yield per plant. Seed yield presents the most substantial correlation with harvest index which reaffirms its dominance as a yield determining factor. According to the analysis traits demonstrating minor direct effects still generate important indirect influences on seed yield which shows how essential comprehensive direct and indirect pathways should be incorporated into seed yield improvement breeding programs.

Conclusion

The research analysis of 25 greengram genotypes exhibited substantial genetic diversity for multiple quantitative traits which demonstrates potential breeding prospects. Data obtained through correlation and path coefficient analysis confirmed that harvest index along with flowering characteristics directly influence seed yield performance and should be taken into consideration for greengram breeding and improvement program. The study reveals that linking direct selection with indirect effects in breeding strategies has a potential for major greengram productivity improvements when programs focus on traits with high heritability along with strong yield relationships.

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Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

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