Original Research Article

Component Relationship and Genetic Variability of Seed Yield and Its Contributing Traits in Greengram (*Vigna radiata* L. Wilczek)

ABSTRACT

After pigeonpea and chickpea, greengram is the third most significant pulse crop in Asia. Pulses are the primary source of protein needed to satisfy both the daily need and the daily consumption for a balanced diet. Pulses are essential to achieving the diet's protein requirements for humans. Because they are the least expensive type of protein, they are referred to as poor people's meat. It is the primary source of vital amino acids for India's vegetarian population. There are twenty genotypes of Greengram in this experiment, plus one check. Three replications of the experiment were carried out at RBD during the month of Zaid in 2023. Thirteen characters' worth of data were collected in order to investigate genetic advancement, variability, heritability, correlation, and path analysis. The majority of the traits under study have significant genetic diversity in the available germplasm, according to analysis of variance. According to the mean performance of grain yield and its constituents, CO-7 performed better than AMULYA, SML-20-10, and IPM-2-14. A detailed examination of the variability coefficients showed that there was no environmental influence on the expression of the traits under study, as evidenced by the small difference between PCV and GCV. For biological yield, number of pods per plant, and number of seed yield per plant, high to moderate estimations of GCV & PCV were noted. For the seed index, plant height, harvesting index, and quantity of seeds per pod, high estimates of heritability were noted. Since they are less affected by environmental factors and have a greater potential for genetic determination, high heritability estimates can be used for genetic improvement. For the seed index, number of branches per plant, and number of clusters per plant, low estimations of genetic advance were noted. According to correlation, plant height, major branches per plant, clusters per plant, pods per plant, biological yield, and harvest index all positively and significantly correlated with grain yield per plant. Path analysis revealed that plant height, cluster size per plant, biological yield, and harvest index have a direct impact on yield at both the phenotypic and genotypic levels. These characteristics are therefore acknowledged as the effective and prospective

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characteristics for direct selection in order to increase Greengram productivity in the current experimental materials.

Key words:- Genetic variability, PCV, GCV, Correlation, Path analysis.

INTRODUCTION

With a diploid chromosome count of 2n=2x=22, green gram (Vigna radiata L. Wilczek), a vital pulse crop, is a member of the Fabaceae family and is widely grown. It is also known as mungbean and is tolerant to many cropping regimes. Divided into three subgroups—Vigna radiata subsp. radiata, which is domesticated, and subsp. sublobata and subsp. glabra, which are wild—mungbean is an important crop in India, especially for the country's large vegetarian population because it's a rich source of high-quality, readily digestible protein. Mungbean seeds have between 59 and 65% of carbs, 22 to 28% total protein, 21 to 25% amino acids, 1.5 to 2.63% lipids, 1.0 to 1.5% fat, 3.5 to 4.5% fiber, and 4-5% ash in their nutritional makeup. A serving of mungbean seeds has between 334 and 344 kcal of energy. With 54% of the world's production and 65% of the cultivated area, India is the leading producer of mungbeans. India produces 2.12 million tons, with a production rate of 489 kg per hectare, on around 4.34 million hectares of dedicated crop land. Self-pollinating and with a quick maturation period, mungbean improves the lives of small-scale farmers and accounts for 22–24% of the total protein supply. Grain that is mature has 62.6g of carbohydrates, 16.3g of fiber, 1.2g of fat, 23.9g of protein, and 347 calories per 100 grams. The degree and direction of the relationship between yield and the contributing characters are clarified by correlation analysis, although the specific effects of each character may not be adequately captured. To determine how characteristics affect seed production directly and indirectly, path analysis is crucial.

2. MATERIALS AND METHODS

The study was conducted in Prayagraj, Uttar Pradesh, during the Zaid season of 2023 at the Department of Genetics and Plant Breeding's field experimental center, which is housed at the Naini Agricultural Institute of the Sam Higginbottom University of Agriculture, Technology, and Sciences. The experimental site is located at 25.570 degrees North latitude and 81.560 degrees East longitude, or 98 meters above sea level. The climate of this region is subtropical, with exceptionally hot and cold seasons. Particularly during the rabi season, temperatures can

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drop as low as 1-2 degrees Celsius in December and January, while during Zaid, they can reach to 46–48 degrees Celsius.

2.1 EXPERIMENTAL MATERIAL

During the Zaid season of 2023, the Department of Genetics and Plant Breeding at SHUATS, Prayagraj (Allahabad) provided the experimental material for this study. Twenty distinct genotypes of greengram were grown using three replications of a randomized block design (RBD), as indicated in Table 1. A net area of roughly 60 square meters and a gross area of roughly 121 square meters were produced by planting each genotype with a spacing of 30 by 10 cm. After ten days of seeding, the seeds were thinned out so that each hill had one healthy seedling. Thirteen different characteristics were recorded, including plant height (cm), days to 50% flowering, days to 50% pod setting, number of primary branches per plant, days to maturity, number of clusters per plant, number of pods per plant, length of pod, number of seeds per pod, biological yield, seed index, harvest index, and number of seeds per plant. For every replication, five randomly chosen individual plants belonging to each genotype were used for the observations. To determine the outcomes for the aforementioned qualities, biometrical and statistical analyses were performed on the recorded data.

2.2 STATISTICAL ANALYSIS

The correlation coefficient was estimated using the formula provided by Searle [2], and the significance test was performed using the procedure outlined by Snedecor and Cochran [3]. With the aid of path coefficient analysis, the correlation coefficient was further divided into direct and indirect effects as proposed by Wright [4] and further developed by Dewey and Lu [7]. Since it was believed to be a factor that was influenced by the other characteristics, sometimes referred to as independent variables, as causes, seed yield was classified as a dependent variable. The aforementioned analysis was carried out using the programs "RLanguage" and INDOSTAT.

2.1.1 GENETIC VARIABILITY

Genetic advancement was determined using the technique outlined by Johnson et al. [12], heritability in the broad sense (h2) as recommended by Burton and De [11], and genotypic and

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phenotypic coefficients of variation (GCV and PCV) were calculated using the formula established by Burton [10].

2.1.2 CORRELATION COEFFICIENT ANALYSIS

The degree of a character's relationship to yield and among the yield-contributing factors was used to calculate the correlation coefficients. The correlations between genotype and phenotype were calculated using the technique developed by Miller et al.

2.1.3 PATH COEFFICIENT ANALYSIS

To determine the direct and indirect effects of the various features on yield, path coefficient analysis was performed using the method first presented by Sewall Wright and later developed by Dewey and Lu

SL. NO.	NAME OF THE GENOTYPE	SL. NO.	NAME OF THE GENOTYPE
1.	VBN-3	11	C0-7
2.	SML-1668	12	MGG-295
3.	SM-20-108	13	IPM-2-14
4.	MH-421	14	SHAKTI
5.	SM-20-103	15	LGG-450
6.	TM-96-2	16	IPM-2-3
7.	LGG-460	17	AMULIYA
8.	SHIKHA	18	PUSA BAISAKHI
9.	CO-8	19	LGG-407
10.	PUSA-105	20	VIRAT (CHECK)

Table 1. List of green gram genotypes used in present investigation

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RESULT AND DISCUSSION

4.3 Estimation of Genetic parameters:

4.3.1 Variability

One of the important considerations in any crop improvement is the detailed study of genetic variability. Variability plays an important role in crop breeding. Variability is a measure by estimation of mean genotypic and phenotypic variation, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic gain.

An insight into magnitude of variability present in crop species is of most important as it provides the basis for selection. The total variation present in a population arises due to genotypic and environmental effects. Presence of genetic variability in the breeding materials is essential for a successful plant breeding programme. The estimates of variance i.e., genotype and phenotype, coefficient of variation, heritability and genetic advance for all the thirteen characters studied have been presented in the given table 3

4.3.2 Phenotypic and Genotypic Coefficient of Variation:

In the present study it is indicated that from the table 3 that in general, estimates of phenotypic coefficient of variation was found higher than their corresponding genotypic coefficient of variation, indicating that the influence of environment on the expression of these characters. A close examining of GCV and PCV reveals that the difference between genotypic and phenotypic variability was very less for all the characters studied, which indicates the low effect of environment on the expression of these characters.

In the present investigation the phenotypic coefficient of variation was estimated to be high for pod per plant (31.32) followed by seed yield (20.43), biological yield (17.20), seeds per pods (16.07) and moderate estimates of PCV were recorded for cluster per plant (15.87), plant height (14.76), pod length (14.07), seed index (13.37), primary branches (12.44), whereas low estimates of PCV was recorded for harvest index (10.07), days to 50% pod setting (9.02), days to 50% flowering (9.74), days to maturity (6.46)

Genotypic coefficient of variation also showed a similar trend in all traits studied and was observed to be high for pod per plant (27.38) followed by seed yield (17.04), seeds per pods (14.11) biological yield (14.02), and moderate estimates of PCV were recorded for seed index(13.24), plant height (13.10), pod length (12.30) cluster per plant (12.70), primary

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branches (10.50), whereas low estimates of PCV was recorded for days to maturity (4.96), days to 50% flowering (8.02), days to 50% pod setting (8.84), harvest index (8.90).

Pods per plant, seed yield, biological yield, seeds per pod, plant height, and pod length all showed high to moderate phenotypic and genotypic coefficients of variation on average. This suggests that there is enough variability in these traits to allow for genetic improvement through trait selection.

4.3.3 Heritability:

The overall amount of genotypic variability present in the material is reflected in the estimations of genotypic coefficient of variation (GCV). Heritability, on the other hand, measures the percentage of this genotypic diversity that is passed down from parents to their offspring. The concept of wide sense heredity was introduced by Lush (1947). It establishes how effectively we can use genotypic variability in a breeding program. Gene frequencies have an impact on genotypic variation and its constituent parts. Because gene frequencies range throughout populations, estimates of heritability for a given attribute also differ among populations. Table 4 displays the heritability estimates derived from the current study.3. A high heritability score in general means that the personality is least impacted by environmental effects.

In the present investigation, the heritability estimates were found to be high for seed index (98.204), 50% pod setting (95.967), plant height (78.786), harvest index (78.134), seeds per pod (77.139), pod length (76.458), pods per plant (76.406) moderate estimates of heritability are branches per plant (71.223), seed yield (69.582), 50% flowering (67.868), biological yield (66.429), clusters per plant (64.004) & days to maturity (59.04).

4.3.4 Genetic advance:

Furthermore, heritability does not indicate the degree of genetic improvement that might arise via genotype selection. Thus, understanding genetic advancement in conjunction with heritability is really beneficial. The improvement in the mean selected families over the base population is known as genetic progress (Lush 1949, Johnson et al., 1955).

Table 3. showed that in the present investigation high estimates of genetic advance were observed for pods per plant (14.68), moderate estimates are observed in days to 50% pod

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setting (9.11), harvest index (6.90), plant height (6.64), biological yield (6.24), days to maturity (5.54), days to 50% flowering (4.99) and low estimates of genetic advance observed in seed index (0.99), primary branches per plant (1.08), clusters per plant (1.23), pod length (1.67), seeds per pod (2.70), seed yield (3.31).

4.3.5 Genetic advance as percent of mean:

High estimate of genetic advance as percent of mean was recorded for pods per plant (49.30), seed yield (29.28), seed index (27.04), seeds per pod (25.53), plant height (23.96), biological yield (23.54). Moderate estimate of genetic advance as percent of mean was recorded for pod length (22.16), clusters per plant (20.94), branch per plant (18.28), days to 50% pod setting (17.84). while low estimate of genetic advance as percent of mean was recorded for harvest index (16.21), days to 50% flowering (13.61), & days to maturity (7.86).

Characters with high heritability estimates demonstrated that heritable factors dominated trait variance, while traits with moderate heritability revealed equal contributions from both environment and genetics to trait expression. Furthermore, qualities with high heritability showed that environmental factors rather than genetics mostly controlled how these traits expressed themselves.

In general, traits with high heritability estimates can be used to improve genetics because they have a big genetic determination potential and are less affected by environmental factors.

Table 2. Analysis of variance for 13 characters of greengram genotypes

ANOVA Summary				
Sl.No.	**Source**	**Mean Sum of Squares (MSS)**		
		Replication	**Treatment**	**Error**
	Degrees of freedom	**2**	**19**	**38**
1	Days to 50% flowering	0.3170	29.996**	4.089
2	Days to 50% pod setting	1.7170	62.031**	0.857
3	Plant height (cm)	0.0350	43.101**	3.55
4	Number of branches per plant	0.010	1.314**	0.156
5	Days to maturity	8.150	45.168**	8.483
6	Number of clusters per plant	0.4720	1.968**	0.31
7	Number of pods per plant	5.2670	219.846**	20.517
8	Number of seeds per pod	0.730	7.311**	0.657
9	Pod length (cm)	0.1290	2.833**	0.264
10	Seed Index (g)	0.0090	0.711**	0.004
11	Biological yield per plant (g)	13.9130	48.436**	6.983
12	Harvest Index (%)	1.7860	47.114**	4.02

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13	Seed yield per plant (g)	3.2270	12.727**	1.619

Table 3. Estimates of genetic parameters for different quantitative characters in Greengram

Sl.No.	Genetic Parameters	GCV	PCV	h2 (Broad Sense)	GA	GAM
1	Days to 50% flowering	8.02	9.74	67.868	4.99	13.61

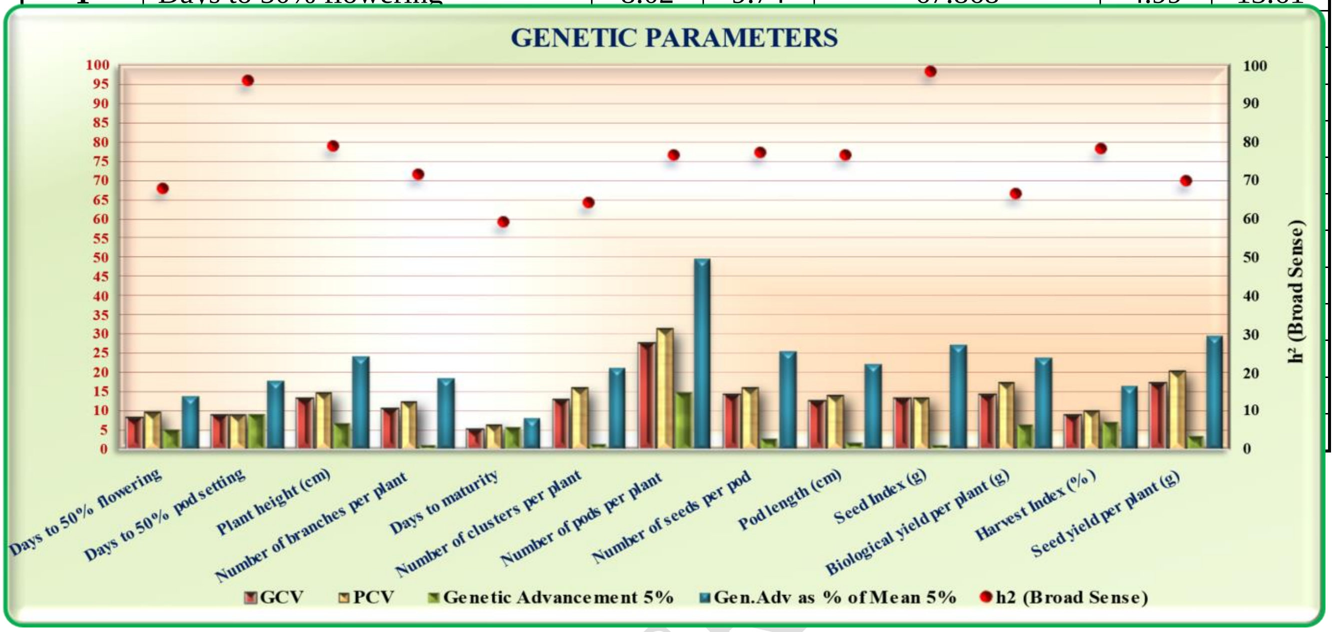

Figure 1. Histogram depicting Genotypic and Phenotypic Coefficient of Variation for different characters in Greengram

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4.4 Correlation Coefficient analysis:

A statistical tool for determining the strength and direction of a relationship between two or more crop variables is correlation coefficient analysis. One of the complex characteristics that is influenced by a number of interrelated environmental and genotypic factors is yield. Using appropriate selection indices can greatly increase the efficiency of crop breeding projects by taking advantage of the relationship that exists between yield and its contributing factors. The examination of correlation coefficients is helpful in selecting multiple qualities that simultaneously affect yield.

When choosing the optimal technique to increase a crop's production, it is crucial to consider the existence of morpho-genetic variation in the crop's agronomic traits. A thorough understanding of the traits that significantly correlate with yield is essential, since these traits can serve as indicators or indirect selection criteria to improve the average performance of different cultivars within a newly established plant population. Currently, the estimates of variance and covariance for all conceivable character combinations were used to compute the genotypic and phenotypic correlation coefficients. The results are shown in tables 4 and 5, along with a brief description of each.

4.4.1 Genotypic Correlation Coefficient:

Correlation between grain yield &other component characters:

Grain yield or economic yield shows a positive significant association with days to 50% flowering (0.328*), plant height (0.480**), days to maturity (0.366*), clusters per plant (0.672**), pods per plant (0.801**), seeds per pod (0.428**), pod length (443**), biological yield (0.874**), harvest index (0.522**), while positive non-significant association showed with primary branches per plant (0.157), The negative significant association showed with seed index (-0.430**), and negative non-significant association showed with days to 50% pod setting (-0.2114). The results are shown in (table 4).

4.4.2 Phenotypic Correlation Coefficient Analysis:

Correlation between grain yield and other component characters:

Grain yield showed a significant positive association with days to plant height(0.276*), days to maturity (0.319*), clusters per plant (0.669**), pods per plant (0.731**), seeds per pod (0.312*), pod length (0.306*), biological yield (0.872**), harvest index (0.470*), while positive non-significant association was showed days to 50% flowering (0.2124), primary branches per plant (0.1543), while negative non-significant association showed with days to 50% pod setting (-0.159), and negative significant association showed with seed index (-0.350*). The results are shown in (table 5).

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Table 4. Genotypic correlation coefficient between yield and its component traits in greengram genotypes grown during Zaid 2023 at SHUATS, Prayagraj.

Genotypic Correlation Matrix													
	Days to 50% flowering	**Days to 50% pod setting**	**Plant height (cm)**	**Number of branches per plant**	**Days to maturity**	**Number of clusters per plant**	**Number of pods per plant**	**Number of seeds per pod**	**Pod length (cm)**	**Seed Index (g)**	**Biological yield per plant (g)**	**Harvest Index (%)**	**Seed yield per plant**
Days to 50% flowering	1	-0.1176	0.452**	0.456**	0.954**	0.296*	0.342*	0.2253	0.408*	-0.383*	0.577**	-0.347*	0.328*
Days to 50% pod setting		1	0.2316	-0.0827	-0.085	-0.1083	-0.1453	0.186	0.1565	0.2398	-0.1088	-0.2369	-0.2114
Plant height (cm)			1	0.1188	0.516**	0.263*	0.401*	0.567**	0.785**	0.042	0.657**	-0.1841	0.480**
Number of branches per plant				1	0.257*	0.413*	0.0598	-0.1339	0.293*	0.278*	0.1395	0.1077	0.157
Days to maturity					1	0.1884	0.508**	0.1899	0.2334	-0.349*	0.694**	-0.441**	0.366*
Number of clusters per plant						1	0.644**	0.1906	0.339*	-0.381*	0.575**	0.365*	0.672**
Number of pods per plant							1	0.407*	0.2037	-0.455**	0.815**	0.1984	0.801**
Number of seeds per pod								1	0.731**	-0.0558	0.547**	-0.0961	0.428**
Pod length (cm)									1	0.2138	0.427**	0.1292	0.443**
Seed Index (g)										1	-0.445**	-0.1076	-0.430**
Biological yield per plant (g)											1	0.0391	0.874**
Harvest Index (%)												1	0.522**
Seed yield per plant													1

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Table 5. Phenotypic correlation coefficient between yield and its component traits in greengram genotypes grown during Zaid 2023 at SHUATS, Prayagraj.

Phenotypic Correlation Matrix													
	Days to 50% flowering	**Days to 50% pod setting**	**Plant height (cm)**	**Number of branches per plant**	**Days to maturity**	**Number of clusters per plant**	**Number of pods per plant**	**Number of seeds per pod**	**Pod length (cm)**	**Seed Index (g)**	**Biological yield per plant (g)**	**Harvest Index (%)**	**Seed yield per plant**
Days to 50% flowering	1	-0.0743	0.320*	0.287*	0.549**	0.2214	0.2504	0.1246	0.266*	-0.301*	0.365*	-0.2357	0.2124
Days to 50% pod setting		1	0.2247	-0.0785	-0.0382	-0.1023	-0.1282	0.1688	0.1255	0.2349	-0.0936	-0.1707	-0.159
Plant height (cm)			1	0.0617	0.332*	0.06	0.244	0.479**	0.627**	0.0299	0.387*	-0.1466	0.276*
Number of branches per plant				1	0.2012	0.313*	0.0818	-0.0716	0.2394	0.2258	0.1613	0.0425	0.1543
Days to maturity					1	0.2005	0.426**	0.2465	0.1053	-0.268*	0.451**	-0.1926	0.319*
Number of clusters per plant						1	0.693**	0.1586	0.1941	-0.306*	0.593**	0.306*	0.669**
Number of pods per plant							1	0.322*	0.1203	-0.394*	0.734**	0.1787	0.731**
Number of seeds per pod								1	0.543**	-0.0407	0.369*	-0.0461	0.312*
Pod length (cm)									1	0.1805	0.287*	0.0918	0.306*
Seed Index (g)										1	-0.355*	-0.0901	-0.350*
Biological yield per plant (g)											1	-0.0158	0.872**
Harvest Index (%)												1	0.470**
Seed yield per plant													1

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Table 6. Genotypical path matrix for Seed yield per plant showing direct (in bold) and indirect effects of various characters.

Genotypic Path Matrix													
	Days to 50% flowering	Days to 50% pod setting	Plant height (cm)	Number of branches per plant	Days to maturity	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	Pod length (cm)	Seed Index (g)	Biological yield per plant (g)	Harvest Index (%)	Seed yield per plant
Days to 50% flowering	**-0.1215**	0.0143	-0.0549	-0.0554	-0.116	-0.036	-0.0415	-0.0274	-0.0496	0.0466	-0.0701	0.0422	0.328*
Days to 50% pod setting	0.0026	**-0.0218**	-0.0051	0.0018	0.0019	0.0024	0.0032	-0.0041	-0.0034	-0.0052	0.0024	0.0052	-0.2114
Plant height (cm)	0.0158	0.0081	**0.0349**	0.0041	0.018	0.0092	0.014	0.0198	0.0274	0.0015	0.0229	-0.0064	0.480**
Number of branches per plant	-0.0068	0.0012	-0.0018	**-0.0148**	-0.0038	-0.0061	-0.0009	0.002	-0.0043	-0.0041	-0.0021	-0.0016	0.157
Days to maturity	0.1901	-0.0169	0.1028	0.0512	**0.1992**	0.0375	0.1012	0.0378	0.0465	-0.0696	0.1381	-0.0878	0.366*
Number of clusters per plant	0.0231	-0.0085	0.0206	0.0323	0.0147	**0.0781**	0.0503	0.0149	0.0265	-0.0298	0.0449	0.0285	0.672**
Number of pods per plant	-0.0153	0.0065	-0.018	-0.0027	-0.0228	-0.0289	**-0.0449**	-0.0183	-0.0091	0.0204	-0.0366	-0.0089	0.801**
Number of seeds per pod	0.017	0.0141	0.0429	-0.0101	0.0144	0.0144	0.0307	**0.0756**	0.0552	-0.0042	0.0413	-0.0073	0.428**
Pod length (cm)	-0.0085	-0.0033	-0.0164	-0.0061	-0.0049	-0.0071	-0.0043	-0.0153	**-0.0209**	-0.0045	-0.0089	-0.0027	0.443**
Seed Index (g)	0.0012	-0.0008	-0.0001	-0.0009	0.0011	0.0012	0.0015	0.0002	-0.0007	**-0.0032**	0.0014	0.0003	-0.430**
Biological yield per plant (g)	0.4151	-0.0783	0.4729	0.1004	0.4991	0.4135	0.5864	0.3936	0.307	-0.3201	**0.7197**	0.0282	0.874**
Harvest Index (%)	-0.1847	-0.126	-0.098	0.0573	-0.2346	0.1939	0.1056	-0.0511	0.0687	-0.0573	0.0208	**0.5321**	0.522**
Seed yield per plant	0.328*	-0.2114	0.480**	0.157	0.366*	0.672**	0.801**	0.428**	0.443**	-0.430**	0.874**	0.522**	

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Table 7. Phenotypic path matrix for Seed yield per plant showing direct (in bold) and indirect effects of various characters.

Phenotypic Path Matrix													
	Days to 50% flowering	**Days to 50% pod setting**	**Plant height (cm)**	**Number of branches per plant**	**Days to maturity**	**Number of clusters per plant**	**Number of pods per plant**	**Number of seeds per pod**	**Pod length (cm)**	**Seed Index (g)**	**Biological yield per plant (g)**	**Harvest Index (%)**	**Seed yield per plant**
Days to 50% flowering	**0.0022**	-0.0002	0.0007	0.0006	0.0012	0.0005	0.0006	0.0003	0.0006	-0.0007	0.0008	-0.0005	0.2124
Days to 50% pod setting	-0.0001	**0.0014**	0.0003	-0.0001	-0.0001	-0.0001	-0.0002	0.0002	0.0002	0.0003	-0.0001	-0.0002	-0.159
Plant height (cm)	-0.0015	-0.0011	**-0.0047**	-0.0003	-0.0016	-0.0003	-0.0011	-0.0023	-0.0029	-0.0001	-0.0018	0.0007	0.276*
Number of branches per plant	-0.0065	0.0018	-0.0014	**-0.0228**	-0.0046	-0.0071	-0.0019	0.0016	-0.0055	-0.0051	-0.0037	-0.001	0.1543
Days to maturity	0.0156	-0.0011	0.0095	0.0057	**0.0285**	0.0057	0.0121	0.007	0.003	-0.0076	0.0129	-0.0055	0.319*
Number of clusters per plant	0.0033	-0.0015	0.0009	0.0047	0.003	**0.015**	0.0104	0.0024	0.0029	-0.0046	0.0089	0.0046	0.669**
Number of pods per plant	-0.0037	0.0019	-0.0036	-0.0012	-0.0063	-0.0103	**-0.0148**	-0.0048	-0.0018	0.0058	-0.0109	-0.0026	0.731**
Number of seeds per pod	0.0003	0.0003	0.001	-0.0001	0.0005	0.0003	0.0007	**0.002**	0.0011	-0.0001	0.0008	-0.0001	0.312*
Pod length (cm)	0.0027	0.0013	0.0063	0.0024	0.0011	0.002	0.0012	0.0055	**0.0101**	0.0018	0.0029	0.0009	0.306*
Seed Index (g)	-0.0046	0.0036	0.0005	0.0034	-0.004	-0.0046	-0.006	-0.0006	0.0027	**0.0151**	-0.0054	-0.0014	-0.350*
Biological yield per plant (g)	0.3199	-0.082	0.3385	0.1412	0.3951	0.5187	0.6428	0.3228	0.2509	-0.3105	**0.8755**	-0.0138	0.872**
Harvest Index (%)	-0.1152	-0.0834	-0.0716	0.0208	-0.0941	0.1495	0.0873	-0.0225	0.0448	-0.044	-0.0077	**0.4886**	0.470**
Seed yield per plant	0.2124	-0.159	0.276*	0.1543	0.319*	0.669**	0.731**	0.312*	0.306*	-0.350*	0.872**	0.470**	

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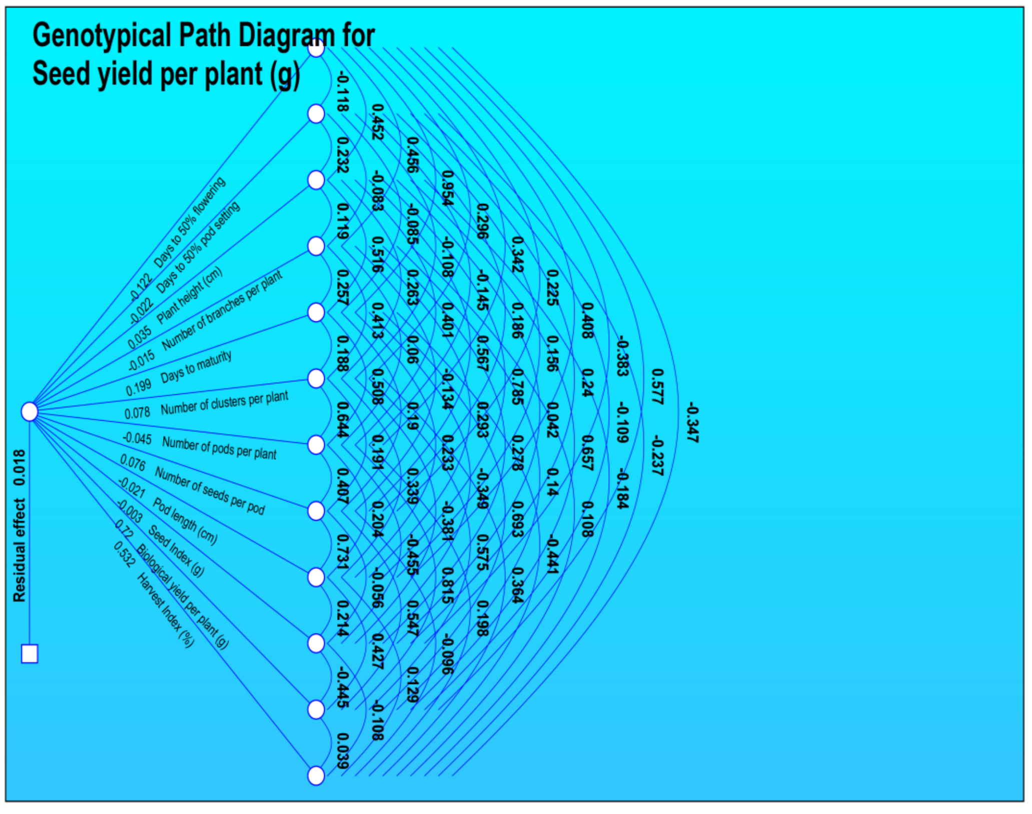

Fig. 2. Genotypic Path Diagram for Seed Yield per plant

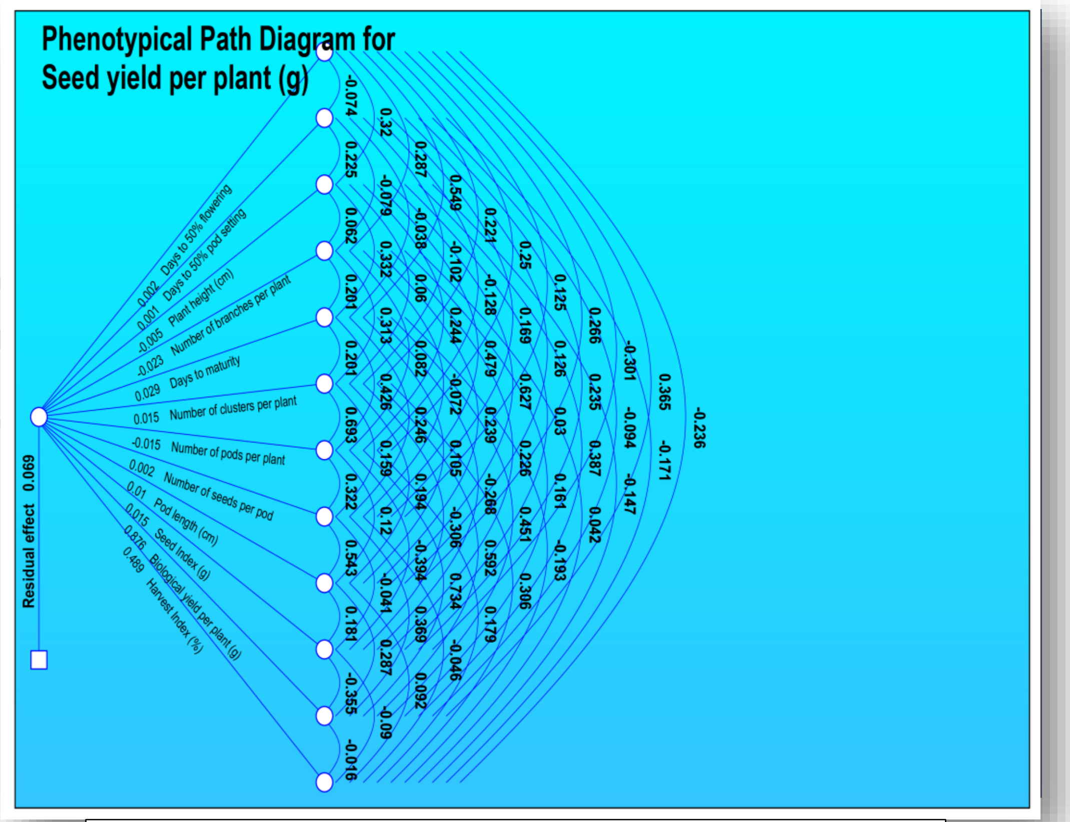

Fig. 3. Phenotypic Path Diagram for Seed Yield per plant

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4.5 Path coefficient Analysis:

The amount of independence of variables increases as the number of independent variables influencing a particular dependent variable increase, making indirect association more complex and important. In such a case, correlation is insufficient to explain the true association for effective character manipulation. It does not additionally indicate the cause-and-effect relationship. It is possible that no one knows which of the independent variables has the most direct effect on yield. Consequently, path coefficient analysis that assesses indirect character association in an array of probes has been suggested. **(Ariyo *et al.,* 1987)**. Path coefficient analysis divides correlation coefficients into direct and indirect effects. It is essentially a standardised partial regression analysis that deals with a closed system of linearly connected variables. Such data provides a reasonable basis for allocating appropriate weight ages to specific yield components. The results obtained have been presented in the tables 6 and 7

4.5.1 Genotypic path coefficient analysis:

Table 6 and Figure 2. provide the genotypic path coefficient analysis matrix for each character. Of the characters studied, biological yield had the greatest impact on seed yield per plant, followed by harvest index, days to maturity, clusters per plant, seed per pod and plant height. On the other hand, seed index showed the greatest negative effect followed by primary branches per plant, pod length, days to 50% pod setting, pods per plant and days to 50% flowering.

4.5.2 Phenotypic Path Co-efficient Analysis:

The phenotypic level path coefficient analysis (Table 7 and figure 3.) showed that the biological yield per plant had the greatest positive direct effect on seed yield per plant followed by harvest index, days to maturity, seed index, pod length, days to 50% flowering, number of clusters per plant, days to 50% pod setting, and number of seeds per pod, are listed in order of importance. while plant height, number of pods per plant, and number of primary branches, all had significant negative direct effects on the amount of seeds produced per plant.

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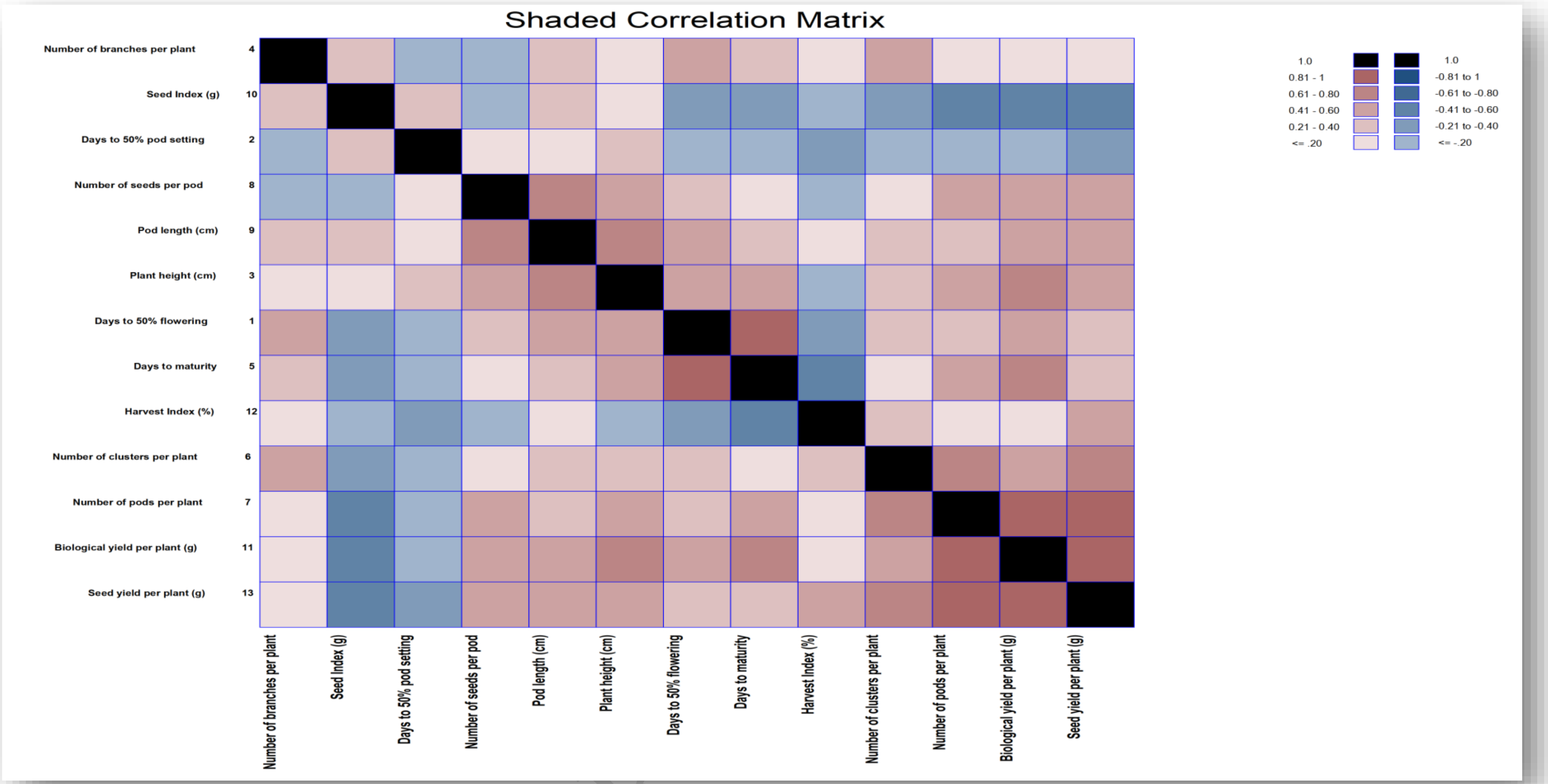

Fig. 4. Genotypic Correlation

UND

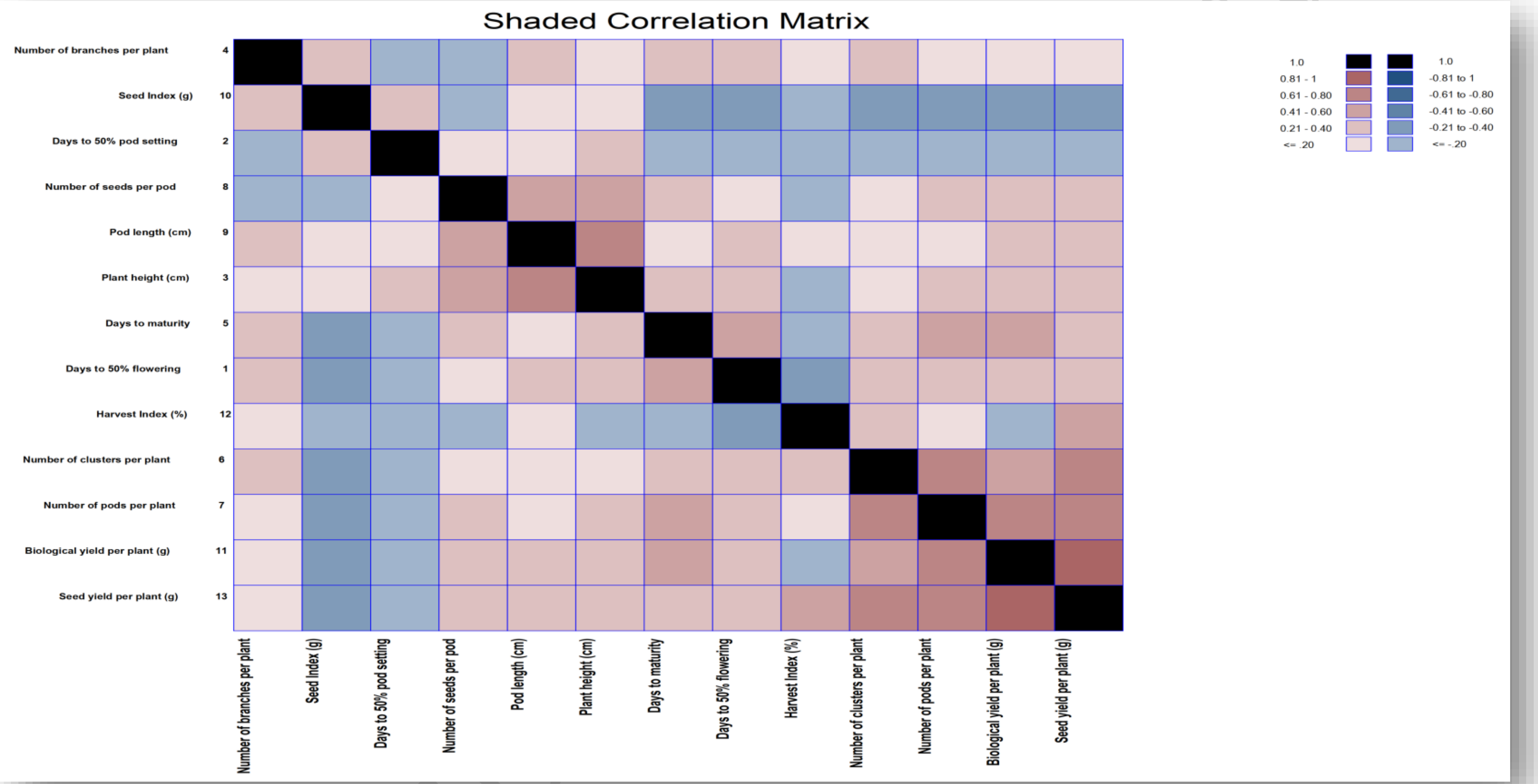

Fig. 5. Phenotypic Correlation

4. CONCLUSION

The current study found that traits such as number of pods per plant, number of seeds per pod, number of clusters per plant, and biological yield displayed high genotypic coefficients variation (GCV), while traits such as number of pods per plant, number of seeds per pod, number of biological yield, and number of seeds per pod displayed high phenotypic coefficients variation (PCV) and high heritability as indicated by seed index. Genetic gain expressed as a percentage of mean revealed number of pods per plant. The number of pods, clusters, and harvest index per plant, as well as biological yield per plant, all significantly and favorably correlate with seed yield per plant. After harvest index, number of clusters per plant, and number of seeds per pod, the route analysis showed that biological yield per plant had the most direct impact on seed yield per plant. Consequently, these characteristics could be regarded as the most significant yield-contributing characteristics.

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