

## Original Research Article

### **Direct and Indirect Effects of Yield Contributing Characters on Seed Yield in Greengram (*Vigna radiata* (L.) Wilczek)**

#### **ABSTRACT**

A study using a randomised block design was carried out during the kharif of 2021 to examine the genetic variability, correlation and path analysis of 40 genotypes of Greengram. The morphological data were recorded, and statistical studies of genetic variability, correlation, and path analysis were carried out. The analysis of variance, which revealed changes across genotypes for all variables, confirmed the presence of sizable genetic variability in the experimental material. Based on average performance, the genotypes LGG 574 (8.80) and PDM 139 (8.34), Pant Mung 6 (7.78), and IPM 99-125 had the highest seed yields (7.40). For the number of primary branches, high PCV, GCV, heritability, and genetic progress as a percentage of mean were reported. According to association studies, the characteristics plant height, primary branch count per plant, cluster count per plant, pod count per plant, seed count per pod, harvest index, and biological yield had high and significant positive genotypic and phenotypic correlation coefficients. Path analysis showed that Days to 50% pod setting, plant height, number of pods per plant, number of seeds per pod, and biological yield per plant all contributed significantly to high positive direct effects. It suggests that there is a real relationship between these qualities, and that yield improvement will benefit from direct selection for these features.

**Keywords:** Greengram, GCV, PCV, Correlation, Path analysis.

#### **INTRODUCTION**

Greengram is the third-largest pulse crop in India and is grown on around 8% of the country's total pulse land. It is referred to as "poor man's meat" since it offers a less expensive source of protein and has a protein level of 24.7%. Lysine, an amino acid that is lacking in cereal grains, is rather abundant in the protein. Ascorbic acid, thiamine, riboflavin, niacin, pantothenic acid, and vitamin A are among the vitamins and minerals found in abundance in greengram seeds (Tang *et al.*, 2014). Greengram is a self-pollinated species that has substantial variation both within and among closely related species (Bisht *et al.*, 2005). "The

level of genetic variety present in the base population is primarily responsible for the base population serving as a valuable source of base population for delivering a wide range of genetic improvement. The lack of genetic variation with high yield potential has been identified as one of the obstacles to progress in greengram production (Ramanujam, 1978). Green gramme [*Vigna radiata* (L.) Wilczek] is an old and well-known pulse crop in Asian nations. In addition to India, it is grown in Burma, Sri Lanka, Pakistan, and a few other East Asian nations. The area of this crop in India is 5.20 million hectares, and its productivity is 2.97 million tonnes and 572 kg per ha. (Anonymous 2020–2021).

There is a rising need for greengram to be made accessible to the ordinary public at fair prices as India's population continues to grow and the malnourished sector suffers. This necessitates the development of high yielding cultivars that may offer high productivity as well as high production. The pulse improvement programmes highlighted the necessity to find genotypes for new niches and generate variability for high yield potential. The objective of the current study is to evaluate genetic parameters of Greengram genotypes for yield and yield contributing characters and to assess the magnitude of character association in seed yield and its attributing traits and to estimate direct and indirect effects of yield contributing characters on seed yield. Because the gene action that affects yield and its auxiliary traits increase yield per unit area, understanding the genetic makeup of varieties is essential.

When beginning breeding efforts to increase production and the contributing traits, the degree of their genetic diversity, heritability, and predicted genetic advance are of the utmost importance. The genetic advance along with the genotypic and phenotypic coefficients of variation and heritability are crucial factors in enhancing characteristics (Denton and Nwangburuka, 2011). Prior to being introduced to a specific local environment, varieties must first be chosen and evaluated for their quantitative and yield abilities in any breeding effort, according to (Johnson *et al.* 1955). How successfully selection works in a population of plants depends on how genetically diverse that population is. As a result, the degree of diversity found in a character's germplasm determines whether genetic improvement of that character will be successful. The assessment helps determine the relative value of different genotypes in terms of particular traits.

An important technique in choosing the right genotype is correlation analysis, which shows the degree of interdependence of key plant characteristics. The majority of plant breeding programmes focus on increasing yield, which is a complex characteristic depending on

numerous other component qualities that are further related among themselves. Consequently, the correlation study is ineffective. The choice of suitable plant types for successful plant breeding programmes depends on the determination of the correlation and path coefficient between yield and yield criteria. In order to quantify the direct and indirect effects of the causative components on the effective component, route analysis was carried out. Given these considerations, the current study was created to screen the greengram germplasm accessions, study the genetic variability, heritability, genetic progress, correlation, and path analysis for yield and yield-related traits that will help in isolating promising lines for the hybridization programme, as well as to explore high yield potential and quality traits.

## **MATERIALS AND METHODS**

The Department of Genetics and Plant Breeding at Sam Higginbottom University of Agriculture, Technology, and Sciences, Prayagraj, undertook a field experiment in Kharif 2021. Three replications of the experiment were run using the Randomized Block Design (RBD) method. On July 2021, the 40 genotypes of greengram were planted in raised beds. The spacing between plants and rows was maintained at 30 cm<sup>2</sup> per cm<sup>2</sup>. To prevent damage from insect pests and diseases, all suggested procedures were followed, and plant protection measures were promptly put into place. Days to 50% flowering, Days to 50% pod setting, Plant Height (cm), Number of Primary Branches Per Plant, Days to Maturity, Number of Clusters Per Plant, Number of Pods Per Plant, Pod Length, Number of Seeds Per Pod, Biological Yield Seed Index, Harvest Index, and Seed Yield Per Plant from Competitive Plants That Were Randomly Selected and Tagged, Excluding. On five randomly chosen plants per plot, all of the traits were noted with the exception of the days to flowering and days to maturity. Days to flowering and days to maturity were observed across the entire plot. All weights were measured using a physical balance and recorded in grammes. The descriptions served as the foundation for the observations. The application of fertilizer, weeding, irrigation, and pesticides, among other agricultural procedures, was done at the appropriate periods. According to Panse and Sukhatme, "The analysis of variance of RBD and their importance for all the characters were worked out as proposed" (1967). The equations provided by Johnson *et al.*, "were adopted for the calculation of the various genetic factors, viz., ECV, GCV, PCV, and heritability" (1955). According to Al-Jibouriet *al.*,

"correlation co-efficient was estimated by utilising the equations" (1958). The Dewey and Lu approach was used to do the path co-efficient analysis (1959).

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## RESULTS AND DISCUSSION

The current study's analysis of variance revealed that each attribute had a sizable genetic variance. The existing gene pool may have had enough room to incorporate promising lines for yield and component qualities, according to this indication. The perception of great variability may be caused by the utilisation of multiple data sources and environmental factors that have an impact on phenotypes. The genotype LGG 574 (8.80) had the highest biological yield, followed by PDM 139 (8.34), Pant Mung 6 (7.78), and IPM 99-125 (7.40). LGG 574 has the most primary branches and clusters. Indicating the importance of environmental factors on these traits, the estimated genotypic variance and phenotypic variance revealed that, for all yield-related and yield-attributing characters, phenotypic variation was higher than genotypic variance. There is a chance that the environment may have an impact on how the trait under research expresses because it was found that the phenotypic coefficient of variance was higher than the genotypic coefficient of variation. Similar findings were reported by Ramakrishnan *et al* (2018). The most obvious variations between GCV and PCV could be seen in the number of seeds produced, the quantity of clusters per plant, and the quantity of pods per plant. Both Tabasumet *al.* (2010) and Sheetalet *al.* reported results that were similar (2014). Days to maturity (83.254), plant height (80.163), primary branch count (88.552), number of pods per plant (67.602), number of seeds per plant (77.891), seed index (98.782), harvest index (77.847), biological yield per plant (66.808), and seed yield per plant (76.097) were the categories with the highest heritability. Similar outcomes were also reported by Muthuswamyet *al* (2019). The plant height (26.224), number of primary branches (68.006), number of pods per plant (28.558), number of seeds per plant (21.061), number of seeds per pod (21.808), number of seeds per plant (seed index (32.93), biological yield per plant (23.633), and number of seeds per plant were found to have the highest estimates of genetic advance as a percentage of mean (34.474). The results concurred with earlier studies by Patel *et al.*, (2013), Pinchhyoet *al.*, (2016), and Kumar *et al.*, (2014).

The phenotypic correlation coefficient for number of primary branches per plant (0.387\*\*), harvest index (0.621\*\*), pods per plant (0.629\*\*), clusters per plant (0.669\*\*), number of seeds per pod (0.222\*), plant height (0.326\*\*), and biological yield (0.862\*\*) all showed positive significant associations with grain yield per plant in the current study, indicating a strong relationship between these traits and the yield. The association between the

correlation and the pod length (0.1709), days to 50% flowering (0.0233), days to maturity (0.1245), and days to 50% pod setting (0.0578) indicated a positive but non-significant relationship. A poor, nonsignificant correlation with the seed index (-0.1184).

In the present investigation genotypic correlation coefficients for grain yield per plant showed positive significant association with days to 50% flowering (-0.0177), Days to fifty percent pod initiation (0.0067), number of primary branches per plant (0.366\*\*), harvest index (0.680\*\*), number of pods per plant (0.561\*\*), number of clusters per plant (0.786\*\*), number of seeds per pod (0.279\*) and pod length (0.197\*), which indicated the strong association of these traits with the yield. The correlation showed positive non-significant association with seed index (-0.1463) and days to maturity (0.0721). Negative significant association with plant height (0.438\*\*). Negative non-significant association with biological yield (0.870\*\*).

The genotypic correlation coefficients were typically higher than their phenotypic correlation coefficients in the correlation analysis between the yield and its contributing characters, indicating that genetics played a major role in the association. At both the genotypic and phenotypic levels, significant positive correlations were found for plant height, primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds/pods, and harvest. These findings concur with those of Hemavathy *et al.* (2015), Sultana (2015), Sheeta *et al.* (2014), Anand *et al.* (2016), Baisakh *et al.* (2016), and Dhoot *et al.* (2017).

A thorough analysis of phenotypic path diagonal values revealed a positive direct relationship between seed yield per plant and days of maturity (0.0162), the number of pods per plant (0.0259), the number of seeds per plant (0.0046), the days to fifty percent pod setting (0.0152), the height of the plant (0.0224), biological yield per plant (0.862), and harvest index (0.5113). Negative direct effects between seed production per plant and the number of primary branches per plant (-0.0002), clusters per plant (-0.0097), pod length (-0.0011), seed index (-0.0010), and days of 50% flowering (-0.0062). A thorough analysis of genotypic path diagonal values revealed a positive direct relationship between seed yield per plant and the number of Days to 50% pod initiation (0.0625), primary branches per plant (0.0181), pods per plant (0.0050), seeds per pod (0.0375), clusters per plant (0.0111), biological yield (0.7233), plant height (0.0202), seed index (0.0216), and harvest index (0.5088). Days to 50% flowering (-0.0032), pod length (-0.0556), and days to maturity (-0.0231) with seed yield per plant all showed negative direct effects.

Path analysis showed that, as compared to other parameters like plant height, the number of pods per plant, the number of seeds per pod, and the biological yield per plant, both phenotypic and genotypic levels had favourable direct effects on grain yield per plant. was previously reported by Jyothsna and Anuradha (2013), Gadakhet *et al.* (2013), Choudhary *et al.* (2016), Kapadia *et al.* (2015), and Bhutia *et al.* (2016).

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**Table1: Analysis of Variance for 13 quantitative characters in green gram in kharif, 2021**

S. No	Source	Replication	Treatment	Error
	Degrees of freedom	2	39	78
1	Days to 50% flowering	4.5750	22.454**	4.139
2	Days to fifty percent pod setting	14.80	58.132**	12.612
3	Days to maturity	2.80	39.528**	2.484
4	Plant height (cm)	3.9450	49.225**	3.751
5	Number of Primary Branches	0.0090	0.729**	0.03
6	Number of clusters per plant	0.1120	2.164**	0.527
7	Number of pods per plant	4.5840	42.066**	5.794
8	Pod length(cm)	0.1690	2.4**	0.147
9	No. of seeds/pod	0.0210	4.99**	0.431
10	Seed Index (g)	0.0060	1.024**	0.004
11	Harvest index (%)	6.5060	36.414**	3.155
12	Biological yield per plant (g)	5.8520	22.203**	3.155
13	Seed yield per plant (g)	0.5780	4.227**	0.401

**Table 2: Genetic parameters for 13 quantitative traits of 40 Greengram genotypes**

<b>S. No</b>	<b>Parameters</b>	<b>GCV</b>	<b>PCV</b>	<b>h<sup>2</sup> (Broad Sense)</b>	<b>Genetic Advance 5%</b>	<b>Gen. Adv as % of Mean 5%</b>
<b>1</b>	Days to 50% flowering	6.687	8.662	59.595	3.929	10.634
<b>2</b>	Days to fifty percent pod setting	7.752	10.49	54.609	5.93	11.801
<b>3</b>	Days to maturity	4.951	5.426	83.254	6.605	9.306
<b>4</b>	Plant height (cm)	14.218	15.88	80.163	7.181	26.224
<b>5</b>	Number of Primary Branches	35.082	37.281	88.552	0.936	68.006
<b>6</b>	Number of clusters per plant	12.756	17.889	50.843	1.085	18.737
<b>7</b>	Number of pods per plant	16.861	20.507	67.602	5.889	28.558
<b>8</b>	Pod length(cm)	11.575	12.657	83.642	1.633	21.808
<b>9</b>	No. of seeds/pod	11.584	13.126	77.891	2.241	21.061
<b>10</b>	Seed Index (g)	16.083	16.182	98.782	1.194	32.93
<b>11</b>	Harvest index (%)	10.181	11.539	77.847	6.052	18.505
<b>12</b>	Biological yield per plant (g)	14.036	17.172	66.808	4.243	23.633
<b>13</b>	Seed yield per plant (g)	19.184	21.991	76.097	2.03	34.474

Fig. 1: Graph depicting GCV, PCV, Genetic advance and Heritability for 13 quantitative characters of Greengram genotypes

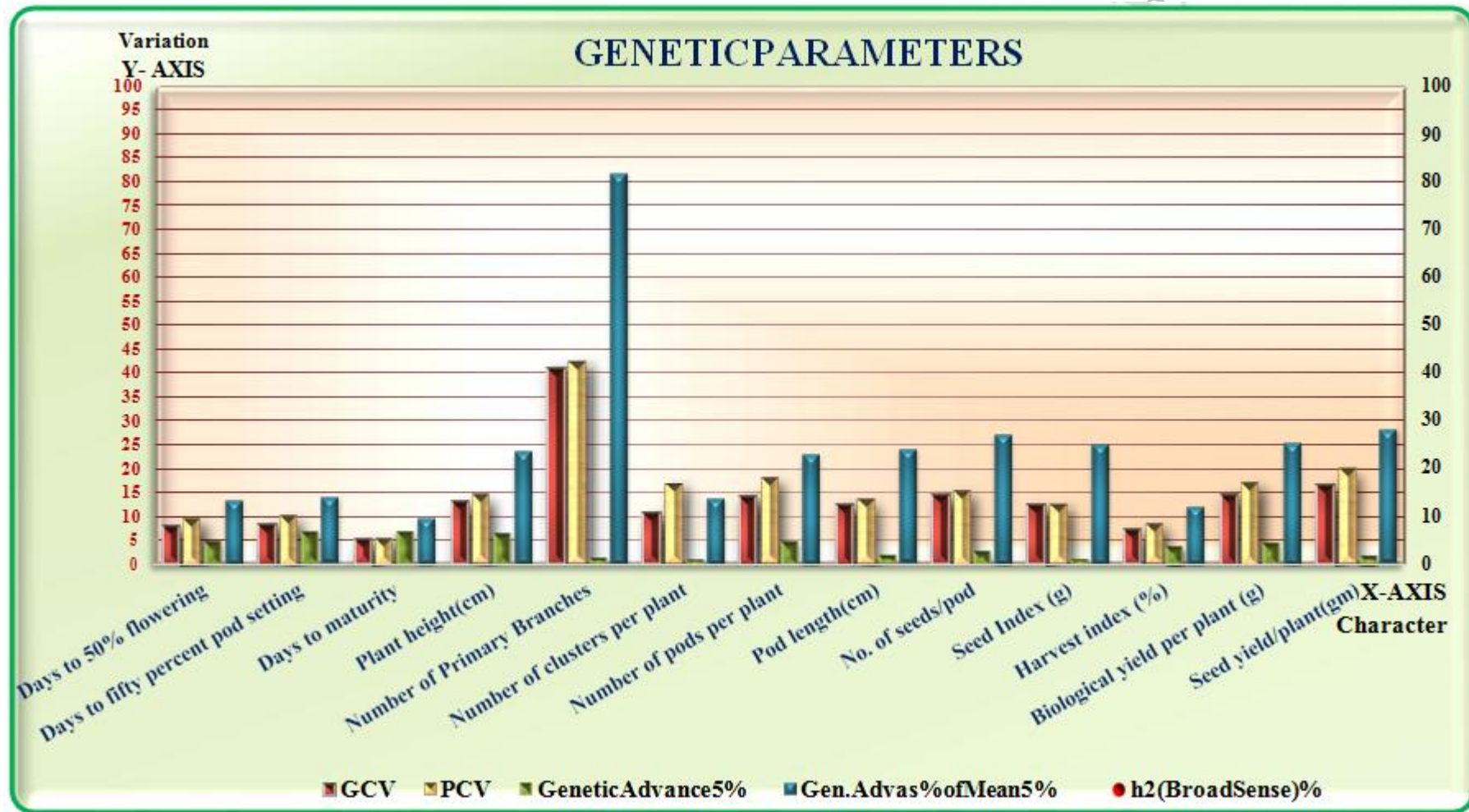


Table 3: Estimation of Phenotypic correlation coefficient between yield and yield attributing traits in 13 quantitative traits of 40

Greengram genotypes

	Days to 50% flowering	Days to fifty percent pod setting	Days to maturity	Plant height (cm)	Number of Primary Branches	Number of clusters per plant	Number of pods per plant	Pod length(cm)	No. of seeds/pod	Seed Index (g)	Harvest index (%)	Biological yield per plant (g)	Seed yield per plant (g)
Days to 50% flowering	1.0000	0.873**	0.535**	0.216*	-0.0427	0.0824	0.0459	0.197*	0.1731	-0.238*	-0.211*	0.1434	0.0233
Days to fifty percent pod setting		1.0000	0.514**	0.183*	-0.0553	0.0194	-0.0031	0.1735	0.201*	-0.1528	-0.1621	0.1546	0.0578
Days to maturity			1.0000	0.245*	0.0984	0.0613	0.1758	0.0415	0.1373	-0.0953	-0.289*	0.317**	0.1245
Plant height (cm)				1.0000	0.1095	0.1607	0.264*	0.183*	0.221*	-0.1749	-0.0577	0.422**	0.326**
Number of Primary Branches					1.0000	0.302**	0.239*	0.1309	0.0455	0.0231	0.249*	0.333**	0.387**
Number of clusters per plant						1.0000	0.695**	0.0349	0.0777	-0.0634	0.422**	0.577**	0.669**
Number of pods per plant							1.0000	-0.0838	-0.0041	-0.1521	0.379**	0.535**	0.629**
Pod length(cm)								1.0000	0.561**	0.214*	0.0508	0.184*	0.1709
No. of seeds/pod									1.0000	-0.1275	0.0491	0.242*	0.222*
Seed Index (g)										1.0000	0.0018	-0.1415	-0.1184
Harvest index (%)											1.0000	0.1450	0.621**
Biological yield per plant (g)												1.0000	0.862**
Seed yield per plant (g)													1.0000

Table 4: Estimation of Genotypic correlation coefficient between yield and yield attributing traits in 13 quantitative traits of 40

Greengram genotypes

	Days to 50% flowering	Days to fifty percent pod setting	Days to maturity	Plant height (cm)	Number of Primary Branches	Number of clusters per plant	Number of pods per plant	Pod length(cm)	No. of seeds/pod	Seed Index (g)	Harvest index (%)	Biological yield per plant (g)	Seed yield per plant (g)
Days to 50% flowering	1.0000	0.934**	0.761**	0.373**	-0.1149	-0.0215	0.0693	0.312**	0.232*	-0.318**	-0.360**	0.191*	-0.0177
Days to fifty percent pod setting		1.0000	0.743**	0.316**	-0.181*	-0.1023	-0.0363	0.302**	0.247*	-0.211*	-0.282*	0.1635	0.0067
Days to maturity			1.0000	0.300**	0.0909	0.0031	0.1540	0.0758	0.1052	-0.1068	-0.401**	0.345**	0.0721
Plant height (cm)				1.0000	0.1197	0.414**	0.397**	0.197*	0.248*	-0.198*	-0.1250	0.645**	0.438**
Number of Primary Branches					1.0000	0.355**	0.210*	0.1595	0.0711	0.0182	0.256*	0.317**	0.366**
Number of clusters per plant						1.0000	0.855**	0.0799	0.0833	-0.0985	0.619**	0.624**	0.786**
Number of pods per plant							1.0000	-0.1411	-0.0081	-0.182*	0.388**	0.470**	0.561**
Pod length(cm)								1.0000	0.722**	0.230*	0.0921	0.208*	0.197*
No. of seeds/pod									1.0000	-0.1443	0.0538	0.329**	0.279*
Seed Index (g)										1.0000	-0.0018	-0.185*	-0.1463
Harvest index (%)											1.0000	0.236*	0.680**
Biological yield per plant (g)												1.0000	0.870**
Seed yield per plant (g)													1.0000

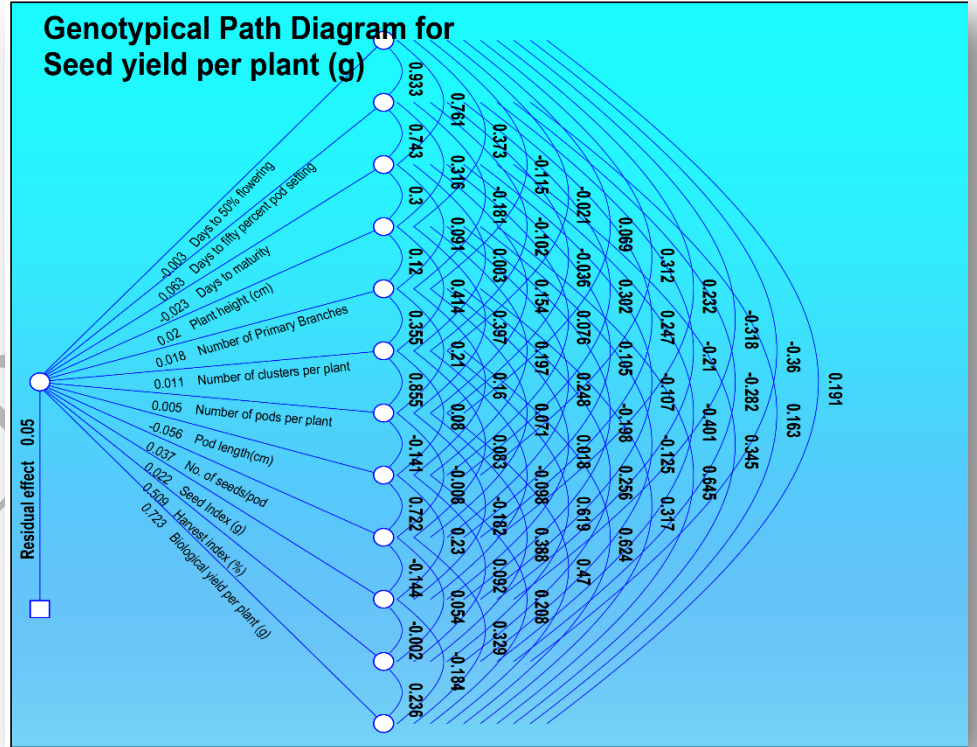
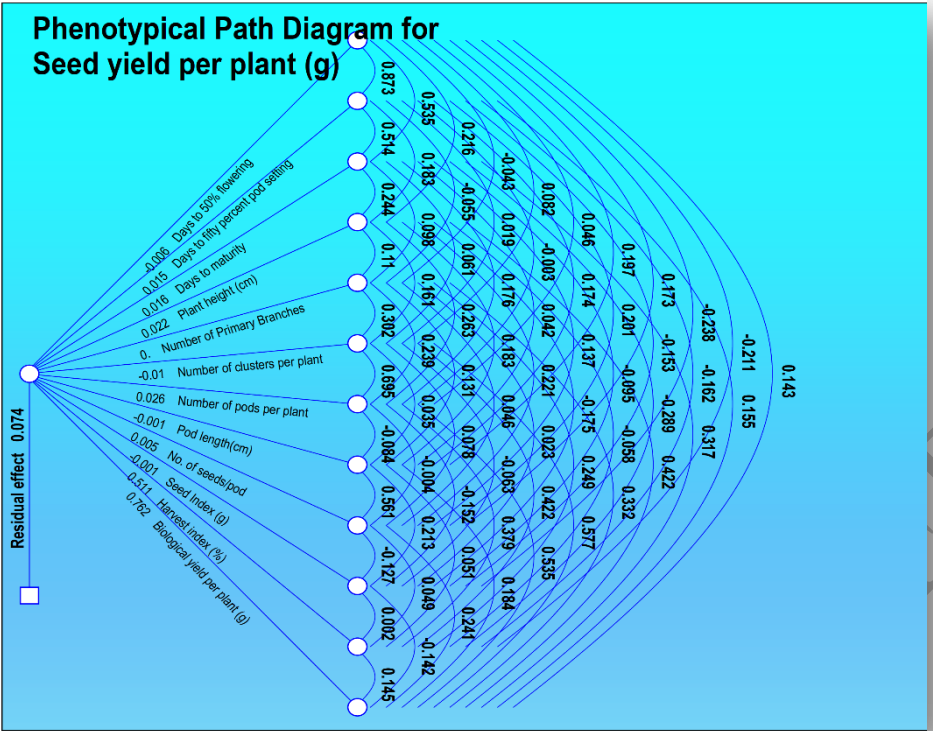
Table 5: Estimation of phenotypic path between yield and yield attributing traits in 13 quantitative traits of 40 Greengram genotypes

	Days to 50% flowering	Days to fifty percent pod setting	Days to maturity	Plant height (cm)	Number of Primary Branches	Number of clusters per plant	Number of pods per plant	Pod length(cm)	No. of seeds/pod	Seed Index (g)	Harvest index (%)	Biological yield per plant (g)	Seed yield per plant (g)
<b>Days to 50% flowering</b>	-0.0062	-0.0054	-0.0033	-0.0013	0.0003	-0.0005	-0.0003	-0.0012	-0.0011	0.0015	0.0013	-0.0009	0.0233
<b>Days to fifty percent pod setting</b>	0.0133	0.0152	0.0078	0.0028	-0.0008	0.0003	0.0000	0.0026	0.0031	-0.0023	-0.0025	0.0024	0.0578
<b>Days to maturity</b>	0.0087	0.0083	0.0162	0.0040	0.0016	0.0010	0.0028	0.0007	0.0022	-0.0015	-0.0047	0.0051	0.1245
<b>Plant height (cm)</b>	0.0048	0.0041	0.0055	0.0224	0.0025	0.0036	0.0059	0.0041	0.0050	-0.0039	-0.0013	0.0094	0.326**
<b>Number of Primary Branches</b>	0.0000	0.0000	0.0000	0.0000	-0.0002	-0.0001	-0.0001	0.0000	0.0000	0.0000	-0.0001	-0.0001	0.387**
<b>Number of clusters per plant</b>	-0.0008	-0.0002	-0.0006	-0.0016	-0.0029	-0.0097	-0.0067	-0.0003	-0.0008	0.0006	-0.0041	-0.0056	0.669**
<b>Number of pods per plant</b>	0.0012	-0.0001	0.0046	0.0068	0.0062	0.0180	0.0259	-0.0022	-0.0001	-0.0039	0.0098	0.0138	0.629**
<b>Pod length(cm)</b>	-0.0002	-0.0002	0.0000	-0.0002	-0.0001	0.0000	0.0001	-0.0011	-0.0006	-0.0002	-0.0001	-0.0002	0.1709
<b>No. of seeds/pod</b>	0.0008	0.0009	0.0006	0.0010	0.0002	0.0004	0.0000	0.0026	0.0046	-0.0006	0.0002	0.0011	0.222*
<b>Seed Index (g)</b>	0.0002	0.0001	0.0001	0.0002	0.0000	0.0001	0.0001	-0.0002	0.0001	-0.0010	0.0000	0.0001	-0.1184
<b>Harvest index (%)</b>	-0.1078	-0.0829	-0.1477	-0.0295	0.1275	0.2159	0.1936	0.0260	0.0251	0.0009	0.5113	0.0741	0.621**
<b>Biological yield per plant (g)</b>	0.1093	0.1179	0.2414	0.3215	0.2534	0.4398	0.4074	0.1400	0.1840	-0.1078	0.1105	0.7621	0.862**
<b>Seed yield per plant (g)</b>	0.0233	0.0578	0.1245	0.326**	0.387**	0.669**	0.629**	0.1709	0.222*	-0.1184	0.621**	0.862**	1.0000

**Table 6: Estimation of genotypic path between yield and yield attributing traits in 13 quantitative traits of 40 Greengram genotypes.**

	Days to 50% flowering	Days to fifty percent pod setting	Days to maturity	Plant height (cm)	Number of Primary Branches	Number of clusters per plant	Number of pods per plant	Pod length(cm)	No. of seeds/pod	Seed Index (g)	Harvest index (%)	Biological yield per plant (g)	Seed yield per plant (g)
<b>Days to 50% flowering</b>	-0.0032	-0.0030	-0.0024	-0.0012	0.0004	0.0001	-0.0002	-0.0010	-0.0007	0.0010	0.0011	-0.0006	-0.0177
<b>Days to fifty percent pod sett</b>	0.0584	0.0625	0.0465	0.0198	-0.0113	-0.0064	-0.0023	0.0189	0.0155	-0.0132	-0.0177	0.0102	0.0067
<b>Days to maturity</b>	-0.0176	-0.0172	-0.0231	-0.0069	-0.0021	-0.0001	-0.0036	-0.0018	-0.0024	0.0025	0.0093	-0.0080	0.0721
<b>Plant height (cm)</b>	0.0075	0.0064	0.0061	0.0202	0.0024	0.0084	0.0080	0.0040	0.0050	-0.0040	-0.0025	0.0131	0.438**
<b>Number of Primary Branches</b>	-0.0021	-0.0033	0.0016	0.0022	0.0181	0.0064	0.0038	0.0029	0.0013	0.0003	0.0046	0.0057	0.366**
<b>Number of clusters per plant</b>	-0.0002	-0.0011	0.0000	0.0046	0.0040	0.0111	0.0095	0.0009	0.0009	-0.0011	0.0069	0.0070	0.786**
<b>Number of pods per plant</b>	0.0003	-0.0002	0.0008	0.0020	0.0010	0.0042	0.0050	-0.0007	0.0000	-0.0009	0.0019	0.0023	0.561**
<b>Pod length(cm)</b>	-0.0173	-0.0168	-0.0042	-0.0109	-0.0089	-0.0044	0.0079	-0.0556	-0.0402	-0.0128	-0.0051	-0.0116	0.197*
<b>No. of seeds/pod</b>	0.0087	0.0093	0.0039	0.0093	0.0027	0.0031	-0.0003	0.0271	0.0375	-0.0054	0.0020	0.0123	0.279*
<b>Seed Index (g)</b>	-0.0069	-0.0046	-0.0023	-0.0043	0.0004	-0.0021	-0.0039	0.0050	-0.0031	0.0216	0.0000	-0.0040	-0.1463
<b>Harvest index (%)</b>	-0.1833	-0.1437	-0.2040	-0.0636	0.1301	0.3148	0.1972	0.0469	0.0274	-0.0009	0.5088	0.1201	0.680**
<b>Biological yield per plant (g)</b>	0.1379	0.1183	0.2493	0.4666	0.2291	0.4512	0.3398	0.1503	0.2382	-0.1334	0.1707	0.7233	0.870**
<b>Seed yield per plant (g)</b>	-0.0177	0.0067	0.0721	0.438**	0.366**	0.786**	0.561**	0.197*	0.279*	-0.1463	0.680**	0.870**	1.0000

**Fig. 2: Phenotypic and Genotypic path diagrams for seed yield per plant**



## CONCLUSION

The current experiment's results show that Analysis of Variance indicated considerable variances across the 40 genotypes, demonstrating the ability to select promising lines from the available germplasm. Based on average performance, LGG 574 (8.80) had the greatest reported seed yield, followed by PDM 139 (8.34), Pant Mung 6 (7.78), and IPM 99-125. (7.40). Number of primary branches had high PCV, GCV, heritability, and genetic advancement as a percentage of mean. Plant height, primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds/pod, harvest index, and biological yield were all found to have a high and significant positive genotypic and phenotypic correlation coefficient. Days had a high positive direct effect on fifty percent pod setting, plant height, number of pods per plant, number of seeds per pod, and biological yield per plant, according to path analysis. As a result, when developing a selection strategy for increasing yield in greengram, the aforementioned characteristics should take precedence.

## REFERENCE

- Al-jibouri, H. A., Miller, P. A. And Robinson, H. F. (1958). Genotypic and environmental variance in upland cotton of interspecific origin. *Journal of Agronomy*, 50: 633-635.
- Anand, G., Anandhi, K. and Paulpandi, V.K. (2016). Genetic variability, correlation and path analysis for yield and yield components in F6 families of Greengram (*Vigna radiata* (L.) Wilczek) under rainfed condition. *Electron. J. Plant Breed.*, 7:434-437.
- Baisakh, B., Swain, S.C., Panigrahi, K.K., Das, T.R. and Mohanty, A. 2016. Estimation of genetic variability and character association in micro mutant lines of greengram (*Vignaradiata* (L.) Wilczek) for yield attributes and cold tolerance. *Legume Genomics and Genetics*.7(2): 1-9
- Bhutia P, Lal GM, Thomas N. Studies on genetic variability, correlation and path analysis in greengram [*Vigna radiata* (L.) Wilczek] germplasm. *Int J Agric Sci*. 2016;8(51):2267-72.
- Choudhary P, Payasi SK, Urmaliya K. Genetic association and path analysis for yield contributing traits in greengram [*Vigna radiata* (L.) Wilczek]. *Int J Agric Sci*. 2016;8(52):2465-8.
- Denton, O. A., and Nwangburuka, C. C. (2011). Heritability, genetic advance and character association in six related characters of *Solanum anguivi*. *Asian J. Agric. Sci.*, 5:201-207.
- Dewey DR, Lu KH. A correlation and path coefficient analysis of components of wheat grass seed production. *Agronomy Journal*.

1959; 51:515-518.

DhootRupal, K.G., Modha, D. Kumar and Dhoot.M. 2017. Correlations and Path Analysis Studies on yield and its components in mungbean (*Vignaradiata* (L.) Wilczek)

Int.J.Curr.Microbiol.App.Sci. 6(5):370-378.

Din, N., Rabani, G., Tariq, M., Naeem,M. K. and Iqbal.M. S. 2015. Character association and path analysis of yield and yield components in mungbean (*Vignaradiata* (L.) Wilczek). J. Agric. Res. 53(2): 165-293.

Muthuswamy,A.;Jamunarani,M.andRamakrishnan,P.(2019).Geneticvariability, character association and path analysis studies in green gram(*Vignaradiata* (L.)Wilczek).Int.J.Curr.Microbial.App.Sci.8(4) :1136-1146

Hemavathy, A.T., Shunmugavalli,N. and Anand.G. 2015. Genetic variability, correlation and path coefficient studies on yield and its components in mungbean (*Vignaradiata*(L.)Wilezek).Legume Research.,38 (4) : 442-446.

Johnson HW, Robinson HF, Comstock RF. Estimation of genetic environmental variability in soyabean. Agronomy Journal. 1955; 47:314-318.

Jyothsna M, Anuradha CH. Genetic variability, correlation and path coefficient analysis for yield and yield components in greengram [*Vigna radiata* (L.) Wilczek]. J Res. 2013;41(3):3.

Kapadia VN, Raiyani AM, Parmar MB. Genetic studies of variability, correlation and path coefficient analysis for greengram [*Vigna radiata* (L.) Wilczek] yield and its yield components. Trends. 2015;8(5): 1270-3.

Kumar, K., Prasad, Y., Mishra, S.B., Pandey, S.S. and Kumar, R. 2013. Study ongenetic variability, correlation and path analysis with grain yield and yield attributing traits in greengram [*Vigna radiata* (L.) Wilczek]. The Bioscan, 8(4): 1551-1555.

Panse V.G. and Sukhatme,P. V. 1967 Statistical methods for agricultural workers I.C.A.R. Publication New Delhi: 259.

Ramanujam, S. 1978. Biometrical basis for yield improvement in mungbean.Proceeding of 1<sup>st</sup>International mungbean symposium.32: 210-213.

Ramakrishnan,C.K.Divya.;Savithramma,D.L.andVijayabharathi,A.(2018)Studies onGeneticVariability,Correlation andPathAnalysisforYieldandYieldRelatedTraitsinGreengram[*Vignaradiata*(L.)Wilczek].Int. J.Curr.Microbiol.App.Sci.7(3):2753-2761.

Tang, D., Dong, Y., Guo, N., Li, L. and Ren, H. 2014. Metabolomics analysis of the polyphenols in germinating mung beans (*Vigna radiata*) seeds and sprouts. J. Sci. Food Agric., 94(8): 1639–1647.