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STUDY OF GENETIC ASSOCIATION AND PATH COEFFICIENT ANALYSIS IN GREEN GRAM [*VIGNA RADIATA* (L.) WILCZEK] GENOTYPE

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ABSTRACT

In a study, twenty genotypes of green gram were assessed during the *kharif* season of 2023. The research was conducted at the Experimental Research Centre of the Department of Genetics and Plant Breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Naini, Prayagraj, U.P., India. The experiment followed a Randomized Block Design with three replications. From the present investigation it is concluded that analysis of variance showed significant variation among different genotypes for all characters studied. Harvest index exhibited high estimates of GCV and PCV. Genetic parameters also revealed that high heritability (broad sense) was observed for days to maturity, plant height, and number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, seed index, biological yield and harvest index. Correlation coefficient analysis revealed that seed yield per plant exhibited significant and positive association with plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, seed index and harvest index at genotypic level. Path coefficient analysis revealed that characters like days to maturity, number of primary branches per plant, number of seeds per pod, number of clusters per plant and harvest index exhibited direct positive effect at genotypic level. This indicated that seed yield was mainly a product of direct and indirect effects of above attributing characters and priority should be given to these characters during selection for improvement in green gram.

Key words : *Vigna radiata*, GCV, PCV, Heritability, Genetic advance, Genotype.

Introduction

Green gram also called mungbean is botanically referred to as *Vigna radiata* (L.) Wilczek is a member of the Papilionaceae sub-family of the Leguminosae family. With chromosome number $2n=2x=22$, it is a diploid self-pollinating species (Karpechenko, 1925). According to Vavilov (1935), the Indo-Burma region of central Hindustan is most likely where mungbean originated. It is mostly grown in south-east Asia, including China, India, Burma and other regions. *Vigna radiata sublobata* is the mungbean's wild ancestor. In India, 40.38 lakh hectares are used for green gram production and 3.15 million tonnes were produced in 2021–2022 (Source: DES, Government of India, Ministry of Agriculture & Farmers Welfare, 2022-23). In terms of green gram production and area, Rajasthan leads Maharashtra and

Karnataka in 2019–20. In Uttar Pradesh, green gram is grown on 0.58 lakh hectares of land, with a projected production of 0.36 million tonnes in 2021–2022. Because of its high protein content (25–28%) and exceptional digestibility, green gram is regarded as a high-quality pulse. Green gram is an excellent source of high-quality, readily digestible protein for the majority of vegetarians in India. It contains 334–344 kcal of energy per serving, with a dry weight of 59–65% carbohydrates, 22–28% total protein, 21–25% amino acids, 1.5–2.63% lipids, 1.0–1.5% fat, 3.5–4.5% fibre and 4-5% ash. It meets the protein needs of the nation's vegetarian population. Compared to most other legumes, green gram seeds have higher levels of iron and folate and are a good source of dietary protein (Keatinge *et al.*, 2011). Many essential amino acids are present in it, such as lysine, leucine, isoleucine,

and phenylalanine (Lambrides and Godwin, 2007). Genetic variability accounts for both quantitative and qualitative traits. Plant breeders may find it helpful to have a thorough understanding of the qualitative and quantitative trait classification of mungbean germplasm when making selections and improving the crop. A prerequisite for any crop improvement programme is genetic variability and the quantification of that variability for both qualitative and quantitative characteristics of economic importance. The breeder selects better parents to start a successful breeding programme based on their understanding of genetic advancement and heritability. Therefore, superior parents with greater heritability and genetic advancement for a variety of traits are crucial for any yield improvement programme (Khan *et al.*, 2005). For crop improvement, variation in various traits within the source population is essential, as breeding and selection efforts would be ineffective without a significant amount of heritable variability. Furthermore, the most accurate representation of the degree of improvement anticipated from selection and the dependability of selection based on phenotype would come from estimates of genetic advance and heritability (Falconer, 1989). Despite being the world's largest producer of green gram, India's productivity rate is remarkably low when compared to its likely production. As a result, there is a remarkable scope for its advancement through the development of high-yielding, disease- and pest-resistant cultivars with better nutritional values for human health. One of the main obstacles to raising the efficiency of green gram production has been identified as the lack of adequate variability. The presence of a broad spectrum of genetic variability in key economic population characteristics is essential for the successful breeding of plants. The amount that a selected population's characteristics have improved over the base population under a specific selection pressure is known as the genetic advance. An evaluation of the selection processes is also beneficial. There will be significant progress over the mean population if the value of genetic advancement increases in the subsequent population. It is more accurate to estimate heritability in conjunction with genetic advancement than heritability on its own. According to Johnson *et al.* (1955), studying estimated heritability in conjunction with genetic advancement would yield more accurate results than studying heritability on its own. With the aforementioned goals in mind, the current experiment aimed to assess genetic variability and identify the appropriate attributes for a genetic improvement programme by means of genotype manipulation.

Materials and Methods

To better understand the genetic variability, heritability, correlation and path analysis of green gram genotypes, the current study was conducted. The investigation, which took place at Sam Higginbottom University of Agriculture, Technology and Sciences (SHUATS), Prayagraj, during the *Kharif* season of 2023, at Experimental Research Centre, Department of Genetics and Plant breeding. Approximately 5 kilometres from Prayagraj City, the University is located on the left side of the Prayagraj–Rewa National Highway. Prayagraj is located in the central plain sub-zone of Agro-climatic zone V. Naini is located between latitudes 20° 33' 40" to 21° 50' N and longitudes 73° 27' 58" to 73° 56' 36" E. This region has a tropical climate with warm, humid monsoons, reasonably hot summers and mildly cold winters. This area typically experiences heavy rainfall from June to September. The majority of the precipitation falls during the south-west advancing monsoon, which is most noticeable in July and August. The experimental site consists of levelled land with a uniformly fertile sandy loam soil that has a high percentage of sand and little clay. Randomly selected soil samples were taken between 0 to 30 cm in depth. The soil was then analysed for pH (7.1); organic carbon (0.52%); available nitrogen (142.33 kg/ha); available phosphorus (4.56 kg/ha) and available potassium (206.11 kg/ha). Plant spacing was set at 10 cm between plants and 30 cm between rows. Data were collected from five randomly selected plants for each genotype in each replication, focusing on thirteen different traits including days to 50% flowering, days to 50% 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), number of seeds per pod, seed index (g), biological yield (g), harvest index, and seed yield per plant (g). The experiment was set up using a Randomized Block Design (RBD). The Fisher and Yates (1936) method was used to statistically analyse the data. Johanson *et al.* (1955) formulae was used to calculate GCV and PCV (1955). Heritability (in the broad sense) was eliminated by the formula Burton and Devane deduced (1953). Correlation was calculated using methods suggested by Al-Jibouri *et al.* (1958), while path coefficient analysis was worked out by method suggested by Dewey and Lu (1959).

The detail procedure adopted for recording the observations were as under:

- **Days to 50 per cent flowering** : The numbers of days taken from the date of sowing to the date at which 50 per cent plants start flowering in whole plot were recorded as days to 50 per cent flowering.

- **Days to 50 per cent pod setting :** Days to 50 per cent pod setting was taken from sowing date to the stage when pod is settled in 50% of the plants in a row.
- **Days to Maturity :** The days taken from the date of sowing to the date of physiological maturity of the plants in whole plot were recorded as days to maturity.
- **Plant height (cm) :** Plant height was measured (using measuring tape) from ground level to the top of the plant of five randomly selected plants at the time of maturity.
- **Number of Primary Branches per plant :** The numbers of branches per plant of five randomly selected plants arising from main shoot were counted and were averaged to represent numbers of branches per plant. Number of branches on per plant basis was counted at the time of harvesting.
- **Number of Clusters per plant :** The number of clusters per plant was counted from the randomly taken five plants per plot and averaged to represent numbers of clusters per plant.
- **Number of Pods per plant :** The total number of pods from five randomly taken plants were counted manually from each plot at the time of harvest.
- **Number of Seeds per pod :** Seeds per pod were taken from pods from five randomly selected plants and were counted at the time of harvest and averaged.
- **Pod length (cm) :** The length of five randomly taken pods from five randomly selected plants were measured in centimetres using scale and averaged at the time of harvest.
- **Seed Index (g) :** Weight of one hundred random seeds from total seed yield of tagged plants were recorded in grams after threshing and sun drying, and mean was worked out.
- **Biological Yield (g) :** Five randomly selected and tagged plants including all plant parts above ground were harvested, dried in sun light, weighed and averaged.
- **Harvest Index (%) :** Harvest index was computed by using following formula as suggested by Singh and Stoskoff (1971). The harvest index was worked out by using following formula:

$$\text{Harvest index (\%)} = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

- **Seed Yield per plant (g) :** The pods of five randomly selected and tagged plants were threshed together,

weighed and averaged to obtain seed yield per plant.

Results and Discussion

Analysis of Variance

For the purposes of the experimental design, analysis of variance was performed on the mean sum squares data for 13 characters. Table 1 displays the variance analysis for the various characters that was calculated. For all the studied characters, the analysis of variance revealed highly significant differences ($= 0.01$ & 0.05) among 20 genotypes, indicating that there is a sizable amount of genetic variation among the Indian green gram germplasm. Additionally, it demonstrated the range of green gram genetic improvement through selection. The data on the values of different characters and the analysis of variance showed significant differences among genotypes for all 13 characters indicating that the material has adequate genetic variability to support the breeding programme for improving the pod yield of green gram. The findings are consistent with research by Das and Barua (2015), Pulagampalli and Lavanya (2017).

Genetic parameters

From Table 2, wide range of differences for GCV were observed ranging from 4.08% (days to 50% pod setting) to 25.89% (harvest index), suggesting a significant degree of genotype variability. PCV ranged from days to maturity (5.56%) to harvest index (26.36%). A comparison of the coefficients of variance revealed that for every character, the phenotypic coefficient of variance (PCV) was greater than the genotypic coefficient of variance (GCV), indicating that the environment had an impact on the expression of the character. Ahmad *et al.* (2014), Raturi *et al.* (2015) and Ghimire *et al.* (2018) have previously reached similar conclusions.

Harvest index showed the highest GCV and PCV in green gram germplasm. While number of primary branches, number of clusters per plant, seed index, biological yield showed the moderate GCV and PCV in green gram germplasm. When compared to other characters, these ones showed a high level of genetic variability, which suggests there is room for improvement in crops through hybridization and selection-induced variability. For number of pods per plant, number of seeds per pod, pod length, plant height, days to maturity, days to 50% pod setting and days to 50% flowering, the low GCV and PCV values of variances were noted.

High PCV and GCV were recorded for harvest index in green gram was earlier reported by Vinay *et al.* (2010), Tiwari *et al.* (2014) and Pulagampalli and Lavanya (2017). Moderate PCV and GCV were recorded for

Table 1 : Analysis of Variance (ANOVA) for 13 characters in green gram.

Mean Sum of Squares				
S. no.	Source of variation	Replication (df=2)	Genotypes (df=19)	Error (df=38)
1	Days to 50% flowering	18.52	16.52*	6.96
2	Days to 50% pod setting	2.06	15.89*	10.53
3	Days to Maturity	2.90	37.44**	3.58
4	Plant height (cm)	133.25	1,140.63**	4.49
5	Number of primary branches	1.27	4.98**	0.43
6	Number of clusters per plant	0.11	1.95**	0.16
7	Number of pods per plant	0.38	3.92**	0.41
8	Number of seeds per pod	0.10	2.39**	0.30
9	Pod length (cm)	0.32	1.38**	0.20
10	Biological yield (g)	3.73	45.95**	2.51
11	Seed Index	0.17	1.12**	0.11
12	Harvest Index	1.29	201.43**	2.46
13	Seed yield per plant	0.42	2.11**	0.52

*,** at 5% and 1% level of significance, respectively.

Table 2 : Genetic Parameters for 13 characters of 20 Green gram genotype.

S. no.	Characters	Range	GCV (%)	PCV (%)	h ² (Broad sense) (%)	Genetic advance	Genetic advancement as percent of Mean
1	Days to 50% flowering	31.43-39.88	4.94	8.82	31.41	2.06	5.71
2	Days to 50% pod setting	41.00-50.27	4.08	8.19	24.88	1.90	4.20
3	Days to Maturity	62.00-76.59	4.85	5.56	75.92	6.03	8.70
4	Plant height (cm)	59.78-81.83	8.65	9.17	89.05	11.75	16.82
5	Number of primary branches	5.34-11.33	15.01	17.01	77.91	2.24	27.29
6	Number of clusters per plant	5.87-8.40	10.76	12.13	78.74	1.41	19.67
7	Number of pods per plant	10.13-14.60	8.67	10.08	74.02	1.92	15.37
8	Number of seeds per pod	6.77-9.67	9.87	11.83	69.62	1.43	16.97
9	Pod length (cm)	5.76-8.53	8.90	10.92	66.50	1.06	14.96
10	Biological yield (g)	20.13-33.73	13.74	14.89	85.20	7.24	26.12
11	Seed Index	2.76-4.56	15.82	18.11	76.29	1.05	28.46
12	Harvest Index	16.77-43.76	25.89	26.36	96.43	16.47	52.36
13	Seed yield per plant	7.40-10.40	7.89	11.09	50.61	1.07	11.56

number of pods per plant, number of seeds per pod was earlier concluded by Tabasum *et al.* (2010), Jeberson *et al.* (2015). Moderate PCV recorded for number of clusters per plant was earlier reported by Ahmad *et al.* (2010), Reddy *et al.* (2014) and Ghimire *et al.* (2018). While low PCV and GCV were recorded for days to 50% flowering, days to 50% pod setting, days to maturity. Similar results were reported earlier by Garg *et al.* (2017) and Ghimire *et al.* (2018). The results obtained for PCV and GCV showed that there is considerable possibility of further improvement through hybridization followed by appropriate selection for these characters.

Genetic variability

Given that environmental factors can modify a genotype's phenotypic expression at different stages of development, the heritability estimate of a quantitative character is crucial. The degree to which genotypes can be effectively selected based on phenotypic variation is indicated by their heritability. However, because the environment can mask the genotypic effect, selection might not be effective for a character with low heritability. The amount of heritable variation determines how selection responds. Therefore, it is desirable to partition the observed variability into heritable and non-heritable components. Burton (1952) suggested that GCV along

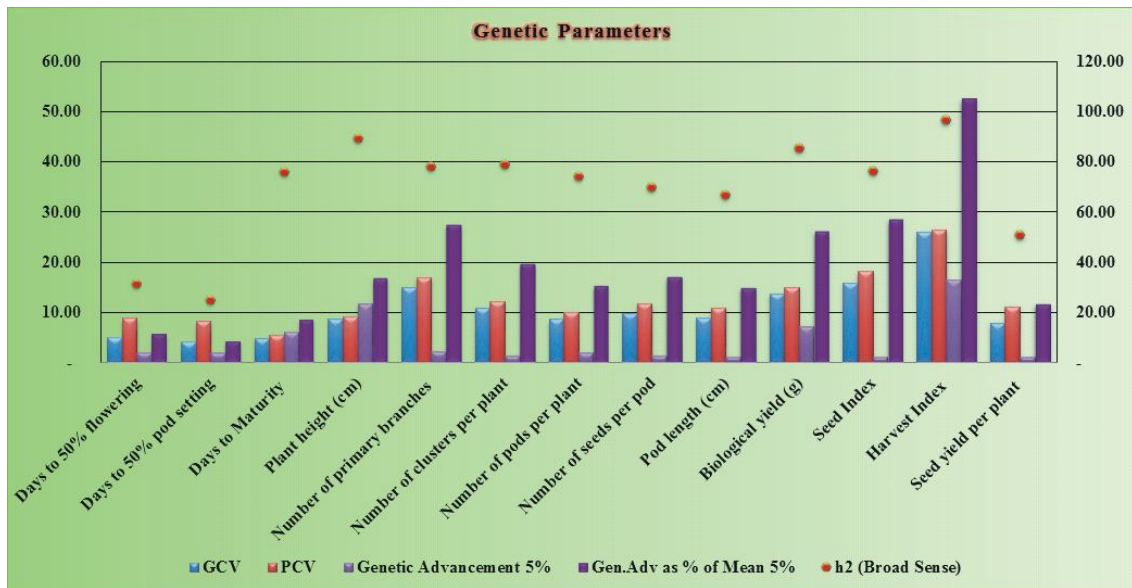


Fig. 1 : Genetic variability parameters for 13 characters of 20 Indian green gram genotype.

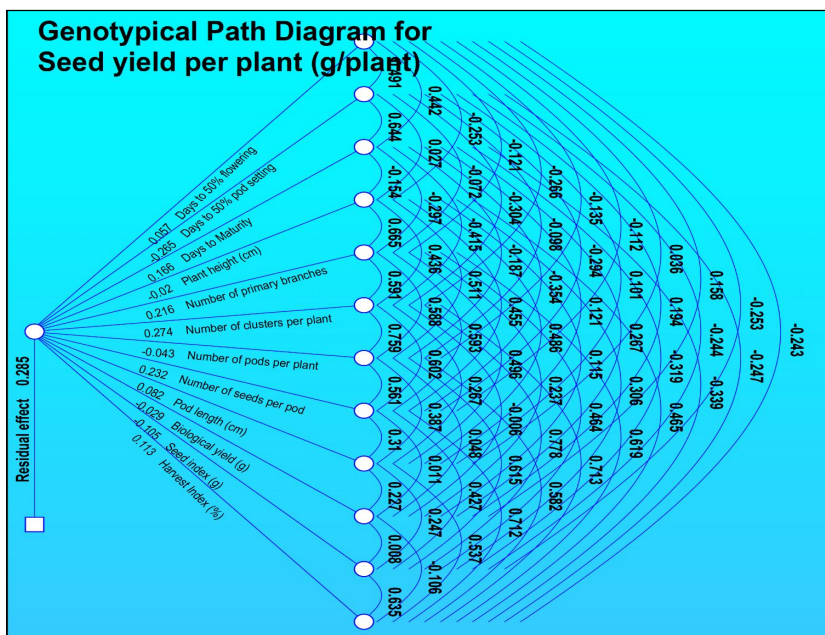


Fig. 2 : Genotypical path diagram for seed yield per plant.

with heritability would give a better idea about the efficiency of selection. Thus, a character with high GCV and high heritability will be more valuable in selection programme. As demonstrated by Johnson *et al.* (1955), heritability can be categorized as low (0-30%), moderate (30-60%) and high (60% and above). In the present investigation, high heritability estimates have been observed for high heritability (broad sense) was recorded for harvest index, number of seeds per pod, seed index, number of pods per plant, biological yield, days to maturity, plant height, number of primary branches, number of clusters per plant, pod length in green gram germplasm. Similar results for high heritability for plant height was reported earlier by Begum *et al.* (2013), Das and Barua

(2015) and Garg *et al.* (2017). High heritability for harvest index and number of pods per plant was concluded earlier by Tiwari *et al.* (2014), Garg *et al.* (2017) and Pulagampalli and Lavanya (2017). Biological yield and number of pods per plant also had high heritability and similar results were concluded by Hozayn *et al.* (2013), Tiwari *et al.* (2014) and Garg *et al.* (2017) in their work. Seed index with high heritability and similar investigation was reported by Muhammad *et al.* (2006) and Garg *et al.* (2017). Table 3 illustrates the genetic variability parameters.

In the current study, high genetic progress as a percentage of mean, high GCV and a high estimate of heritability were found for the harvest index only. For number of primary branches per plant, biological yield and seed index high genetic advance as a percentage of mean was observed along with moderate GCV and high heritability. These traits are governed by additive gene effects and therefore, may be improved through direct selection. Similar findings for harvest index were reported by Choudhary *et al.* (2017) and Pulagampalli and Lavanya (2017). High heritability coupled with high genetic advance as percent of mean for harvest index was reported by Pathak *et al.* (2014) and Choudhary *et al.* (2016). High heritability coupled with high genetic advance as percent of mean for number of primary branches per plant was reported by Pathak *et al.* (2014), Choudhary *et al.* (2017) and Abdus *et al.* (2021). High heritability coupled with high genetic advance as percent

Table 3 : Correlation coefficient between yield and its attributing traits in 20 green gram genotypes at genotypic level.

Genotypic Correlation Matrix													
Characters	DF50	DPS50	DM	PH	NPB	NCPP	NPPP	NSPP	PL	BY	SI	HI	SYPP
DF50	1.000	0.491**	0.442**	-0.2534	-0.1214	-0.266*	-0.1347	-0.1116	0.0364	0.1581	-0.2527	-0.2429	-0.1163
DPS50		1.000	0.644**	0.0273	-0.0718	-0.304*	-0.0976	-0.294*	0.1007	0.1944	-0.244	-0.2474	-0.293*
DM			1.000	-0.1536	-0.297*	-0.415**	-0.1868	-0.355*	0.1208	0.267*	-0.320*	-0.339*	-0.2313
PH				1.000	0.665**	0.436**	0.511**	0.455**	0.486**	0.1151	0.306*	0.465**	0.337*
NPB					1.000	0.591**	0.588**	0.593**	0.496**	0.2369	0.464**	0.619**	0.495**
NCPP						1.000	0.759**	0.602**	0.267*	-0.0064	0.778**	0.713**	0.518**
NPPP							1.000	0.561**	0.387*	0.0484	0.615**	0.582**	0.431**
NSPP								1.000	0.310*	0.0106	0.428**	0.712**	0.565**
PL									1.000	0.2272	0.2471	0.537**	0.332*
BY										1.000	0.0082	-0.1062	0.0263
SI											1.000	0.635**	0.364*
HI												1.000	0.549**
SYPP													1.000

Residual: 0.285

Abbreviations: - DF50:-Days to 50% flowering, DPS50:-Days to 50% pod setting, DM:-Days to maturity, PH:-Plant height (cm), NPB:-Number of primary branches per plant, NCPP:-Number of clusters per plant, NPPP:-Number of pods per plant, NSPP:-Number of seeds per pod, PL:-Pod length (cm), SI:-Seed index (G), BY:- Biological Yield (g), HI:- Harvest index (%), SYPP:- Seed yield per plant (g).

*,** at 5% and 1% Level of Significance

of mean for biological yield was reported by Pathak *et al.* (2014), Choudhary *et al.* (2017), Wesly *et al.* (2020) and Abdus *et al.* (2021). High heritability coupled with high genetic advance as percent of mean for seed index was reported by Pathak *et al.* (2014), Choudhary *et al.* (2017) and Abdus *et al.* (2021).

Character associations

Seed yield per unit area is essentially used to determine a crop's potential productivity. Its polygenic character, which primarily depends on a variety of attributing characters and environmental factors, makes direct selection a difficult method for improving it. Therefore, estimating the relationship between seed yield and attributed characteristics as well as among themselves becomes crucial. Therefore, by practicing selection simultaneously for character attributes that are correlated with yield, selection efficiency can be increased. Regarding the quantitative traits, the environment has an impact on the genotype, which in turn influences the phenotypic expression, association and direction of association between the characters. By dividing the correlation coefficient into components of direct and indirect effects, path coefficient analysis offers a comprehensive understanding of the contribution of different characters and aids breeders in identifying the yield components (Wright, 1921). In the current study, the analysis's goal was to show how important path coefficient analysis is for figuring out the real nature of character association. To ascertain the contribution of various characters to the seed yield per plant, path coefficient analysis was performed using the dependent variable of seed yield per plant to divide the correlation coefficient into direct and indirect effects. There is agreement between the direction and magnitude of the direct effects of the various characters and their correlation with seed yield, according to the direct and indirect effects of the characters on seed yield. Thus, selection for the contributing traits with a high positive direct effect should result in a notable increase in seed yield. Tables 3 and 4 illustrates the correlation and path coefficient analysis for seed yield characters studied in green gram.

Genotypic correlation coefficient analysis revealed that seed yield per plant exhibited highly significant and positive correlation with number

Table 4 : Direct and Indirect effects of yield attributing traits on seed yield at genotypic level.

Genotypic Path Matrix												
Characters	DF50	DPS50	DM	PH	NPB	NCPP	NPPP	NSPP	PL	BY	SI	SYPP
DF50	0.057	0.028	0.0252	-0.0144	-0.0069	-0.0152	-0.0077	-0.0064	0.0021	0.009	-0.0144	-0.1163
DPS50	-0.1298	-0.2647	-0.1705	-0.0072	0.019	0.0804	0.0258	0.0777	-0.0267	-0.0515	0.0646	-0.293*
DM	0.0732	0.1066	0.1656	-0.0254	-0.0492	-0.0687	-0.0309	-0.0587	0.02	0.0442	-0.0529	-0.2313
PH	0.005	-0.0005	0.003	-0.0197	-0.0131	-0.0086	-0.0101	-0.009	-0.0096	-0.0023	-0.006	0.337*
NPB	-0.0262	-0.0155	-0.0641	0.1434	0.2158	0.1275	0.127	0.128	0.1071	0.0511	0.1002	0.495**
NCPP	-0.073	-0.0833	-0.1139	0.1196	0.1621	0.2743	0.2081	0.1651	0.0734	-0.0018	0.2134	0.518**
NPPP	0.0058	0.0042	0.008	-0.0218	-0.0251	-0.0324	-0.0427	-0.024	-0.0165	-0.0021	-0.0263	0.431**
NSPP	-0.0259	-0.0682	-0.0823	0.1057	0.1377	0.1397	0.1302	0.2321	0.0719	0.0025	0.0992	0.565**
PL	0.003	0.0083	0.0099	0.0399	0.0407	0.0219	0.0317	0.0254	0.0821	0.0186	0.0203	0.332*
BY	-0.0046	-0.0056	-0.0077	-0.0033	-0.0068	0.0002	-0.0014	-0.0003	-0.0065	-0.0288	-0.0002	0.0263
SI	0.0266	0.0257	0.0337	-0.0323	-0.049	-0.082	-0.0649	-0.0451	-0.0261	-0.0009	-0.1054	0.364*
HI	-0.0275	-0.028	-0.0383	0.0526	0.07	0.0805	0.0658	0.0804	0.0606	-0.012	0.0718	0.549**

Residual: **0.285**

Abbreviations:- DF50:- Days to 50% flowering, DPS50:- Days to 50% pod setting, DM:- Days to maturity, PH:- Plant height (cm), NPB:- Number of primary branches per plant, NCPP:- Number of clusters per plant, NPPP:- Number of pods per plant, NSPP:- Number of seeds per pod, PL:- Pod length (cm), SI:- Seed index (g), SYPP:- Biological Yield (g), HI:- Harvest index (%), SYPP:- Seed yield per plant (g).

*,** at 5% and 1% Level of Significance.

of primary branches (0.495**), number of clusters per plant (0.518**), number of pods per plant (0.431**), plant height (0.337*), number of seeds per pod (0.565**), pod length (0.322*), seed index (0.364*) and harvest index (0.549**). Negative significant correlation was noted between seed yield per plant and days to 50% pod setting (-0.293*). While, seed yield per plant showed non-significant correlation with remaining characters. Genetic correlation coefficient was higher than their corresponding phenotypic correlation coefficient for many characters was similarly reported earlier by Khanpara *et al.* (2012). Similarly, for genotypic correlation coefficient, Kousar *et al.* (2007), Tabasum *et al.* (2010), Garg *et al.* (2017) reported significant and positive correlation with seed yield per plant for number of primary branches. Ahmad and Belwal (2020) and Dhunde *et al.* (2021) concluded seed yield per plant to be significantly and positively correlated with number of clusters per plant. Seed yield per plant had positive and significant correlation with number of seeds per pod and seed index, similar results were also reported by Tabasum *et al.* (2010), Ahmad and Belwal (2020) and Dhunde *et al.* (2021). Das and Barua (2015) and Garg *et al.* (2017) came up with similar conclusion earlier that seed yield per plant was positively and significantly correlated with harvest.

At genotypic level the highest positive direct effects on seed yield at genotypic level was depicted by days to maturity (0.1656), harvest index (0.1130), number of seeds per pod (0.2321), number of clusters per plant (0.2743), number of primary branches per plant (0.2158), pod length (0.0821), while negative direct effects were due to days to 50% pod setting (-0.2647) and seed index (-0.1054). The residual component of genotypic path analysis indicated that 71.50% of variability of seed yield was accounted for by these thirteen characters. Similar results have been reported from earlier researchers. Tabasum *et al.* (2010), Vinay *et al.* (2010), Das and Barua (2015) and Garg *et al.* (2017) reported that harvest index had maximum positive direct effect on seed yield per plant. Vinay *et al.* (2010), Das and Barua (2015) reported number of primary branches per plant had positive direct effect on seed yield. Seed index and number of seeds per pod had positive direct effect on seed yield, similar conclusion was also drawn by Vinay *et al.* (2010), Garg *et al.* (2017) and Ahmad and Belwal (2020). Hence, selection based on these

characters would bring an improvement in seed yield in green gram. Plant height also exhibited positive direct effect on seed yield was earlier reported by Tabasum *et al.* (2010) and Garg *et al.* (2017) too.

Conclusion

Harvest index exhibited high estimates of GCV and PCV. Genetic parameters also revealed that high heritability (broad sense) was observed for days to maturity, plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, seed index, biological yield and harvest index. Correlation coefficient analysis revealed that seed yield per plant exhibited significant and positive association with plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, seed index and harvest index at both genotypic level. Path coefficient analysis revealed that characters like days to maturity, number of primary branches per plant, number of seeds per pod, number of clusters per plant and harvest index exhibited direct positive effect at genotypic level. This indicated that seed yield was mainly a product of direct and indirect effects of above attributing characters and priority should be given to these characters during selection for improvement in green gram.

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