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Genetic Variability and Multivariate Analysis in Mung bean (*Vigna radiata* L.)

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Abstract

In order to analyse and find a diverse line for future hybridizing programmes for genetic improvements, address variability and genetic diversity. This research focused on multivariate analysis using indirect and direct traits attributing to seed yield for developing a superior cultivar from existing cultivars and the coefficient of correlation using PCV and GCV with high heritability. Twenty-four genotypes with thirteen quantitative characters were used and found to have significant analysis of variance. High heritability and genetic advances are observed, through which the HI and BYP are observed in all the phenotypic traits and two genotypic traits: PP and biological yield per plant. High-contribution divergence genotypes are ranked highly according to seed weight and the highest intra-cluster distance. Highest seed weight and intra-cluster distance were observed in clusters IV and VII, indicating that genotypes Gujarat 4, MH 88, Tilak, and SML 688 were expected to have better performance and were therefore proposed for the hybridizing programme.

Keywords: *Vigna radiata*; Genetic variability; PCA and multivariate analysis

1.0 INTRODUCTION

Popularly known as mungbean or golden grams, green gram (*Vigna radiata* L., 2n=22, Fabaceae) is a significant pulse crop that is grown and consumed widely in India. High in nutrients, green gram is a significant source of protein (23.6%), along with carbohydrates (58 percent). The self-pollinating, diploid *Vigna radiata* is an important source of dietary protein for India's largely vegetarian population low day length, warm season crop most green gram is cultivated in semiarid to sub humid tropics and suvbtropics, where there is 600–1000 mm of annual rainfall, a mean crop temperature of 22–35°C, and elevations no more than 1800–2000 metre above mean sea level. **(Varma *et al.*, 2022).** As a result of its ability to adapt to short

growth cycles, low water needs, fertile soil, ease of digestion, and low flatulence production, green gram is one of the most significant pulse crops. India produces more green gram than any other country in the world, with an output of 24.48 lakh tonnes per year at an average productivity of 531 kg per hectare (Annual report, Directorate of Pulses Development 2021-22). India also produces the most green gram of any country in the world.

An important pulse crop and significant source of protein in India is the green gram. In addition to offering nutrition, pulse crops are a significant source of cash for small-scale farmers **(Kaur *et al.*, 2022).** One of the most extensively used fallow crops in the cultivation of green gram and rice, green gram is one of the most widely adapted drought-tolerant, versatile, and nutrient legume crops **(Varma *et al.*, 2022).** Additionally, it provides details on the nature of gene activity and the relative size of genetic variations that can be fixed and those that cannot, which can be utilised to choose superior parents for breeding programmes and create superior varieties with desirable traits **(Kohakade *et al.*, 2021).** Mahalanobis D^2 statistic is an effective instrument for measuring the extent of divergence at the genotypic level. **(Jadhav *et al.*, 2021).** The considerable diversity in the yield and yield components was noted by **(Hozayn *et al.*, 2013).** For the majority of the phenotypes, the phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) were about identical. On the other hand, path coefficient analysis is a powerful statistical method created specifically to measure the interactions between different elements and their direct and indirect effects on seed production. Principal component analysis (PCA) and cluster analysis assist in selecting significant features that contribute to the overall variation as well as genotype identification from remote clusters. Therefore, new mungbean types that are appropriate for a variety of environmental circumstances must be developed in order to boost the production of green gram. Hybridization between parents with the highest genetic divergence is an alternative possibility to release new genetic variation for genetic improvement when the simple genetic variation approaches exploitation by selection (**Jakhar and Kumar, 2018). Omima *et al.*, (2018)** suggested that having information on the magnitude of genetic variability is the number one criterion for successful breeding. The capacity of breeders to choose attractive superior individuals from a genetically varied base population is one of the factors that determine the successful of a plant breeding programme **(Partap *et al.*, 2019).** When used in a crossing programme, identified genetically dissimilar parents are anticipated to produce superior and desired segregates in the

segregating generations. This crop has a limited genetic variability as a result. The PCA has been referred by various researchers for the decrease of multivariate data into a biplot which can be additionally utilized for grouping material. This approach is particularly significant for screening a large number of genetic resources by a large number of descriptor variables. As a result, the need for the collection, preservation, and application germplasm in current breeding programmes has considerably increased. The evaluation of germplasm accessions is the most important step in effectively utilizing the variety that is already there. The green gram germplasm utilized in this study was evaluated for key agro-morphological and yield-related traits. Crop development efforts may benefit from the findings, which also include information on the extent of genetic variety, genetic progress, and germplasm lines suitable for specific qualities.

2.0 Material and Method

2.1 Experimental site

The study was conducted at the Research Farm at Lovely Professional University, Jalandhar, and Punjab during the 2022 *Kharif* season. The experimental location is in the district of Kapurthala. It has a subtropical climate and is located 225 metres above mean sea level at 31.24N latitude and 75.69E longitude.

2.2 Experimental material

The Department of Genetics and Plant Breeding at the Lovely Professional University in Jalandhar, Punjab, provided the 24 genotypes of green gram (*Vigna radiata* L.) cultivars that were utilised in the experiment. These cultivars are listed below.

Table 1 Details of twenty four green gram genotypes

Genotype code	Genotypes	Genotype code	Genotypes
G1	Moong 1312	**G13.**	G 65
G2.	Moong 757	**G14.**	WGG 37
G3.	Moong 1011	**G15**	MGG 336
G4.	Moong 987	**G16.**	LGG 465
G5.	Moong 0809	**G17.**	TILAK
G6.	Vijeta Srpm 26	**G18.**	TILAK GOLD
G7.	Moong 0808	**G19.**	BANSI

G8.	Gujarat 4	**G20.**	MGG 347
G9.	MH 88	**G21.**	MGG 348
G10.	Jackson	**G22.**	VIRAT GOLD
G11.	Virat	**G23.**	SML 688 **(Check)**
G12.	MGG 295	**G24.**	RAJ 3

2.3 Experimental Design

The experiment used twenty four genotypes with three replications and randomised complete block design (RCBD). All genotypes were sown on June 4, 2022, having five rows, a length of two meters, a plant to plant distance of 10 cm and a row to row distance of 30 cm. To cultivate the crop properly, all cultural practises were used.

2.4 Morphological data collection

The morphological data observation was recorded on five randomly chosen genotypes of plants in each replication on various characters, such as days to 50% flowering (DFF) in days, days to maturity (DM) in days, plant height (PH) in cm, number of primary branches (PB), number of secondary branches (SB), number of clusters per plant (CP), number of pods per plant (PP), PP(PL) in cm, number of seeds per pod (NSP), biological yield per plant (BYP) in gm.

2.5 Statistics analysis of data

The Panse and Sukhatme (1969) proposed a model which was used to perform the analysis of variance using the treatment means for all characters. The methods provided are used to determine the genotypic coefficient of variability (GCV) and the phenotypic coefficient of variability (PCV) **(Burton, 1952).** Estimating heritability combined with genetic advance are often more accurate than heritability estimates alone. **(Burton and Devane, 1953).** The formula proposed by calculated genetic advancement and genetic advancement as a proportion of the mean **(Johnson *et al.*, 1955).** The measure of genetic gain through selection, genetic advance describes the increase in the genetic worth of the chosen plant over the base population.

3.0 Result and Discussion

Genetic variability

3.1 Analysis Of Variance

All treatments are significant, according to the results of the analysis of variance (ANOVA). Main branches had the smallest error, which showed that the treatment's data were the least variable. On the other side, PH had the highest error, indicating that the treatment's statistics were the most variable.

These findings suggest that the various treatments significantly impacted the study's conclusion. Now, more investigation may be carried out to ascertain the precise impacts of each treatment on the response variable. Investigating the causes of the variation in the PH therapy may potentially be beneficial and offer important insights for next research. Overall, the ANOVA outcomes offer significant. There a mentioned in **(Table 2).**

Table 2 Analysis of variance for seed yield and other characters in green gram genotypes

Traits	Replication	Treatment	Error
DFF	16.78	63.77**	8.57
DM	9.28	56.84**	6.70
PH	38.59	144.78**	54.28
PB	0.01	0.32**	0.05
SB	0.05	3.06**	0.66
CP	1.46	10.94**	2.36
PP	4.07	28.26**	6.33
PL	3.00	9.89**	2.14
NSP	1.79	9.39**	2.25
BYP	27.95	87.06**	38.31
SW	0.28	0.81**	0.45
HI	31.02	45.92**	42.35
SYP	3.31	15.02**	3.18

Whereas DFF- Days to 50% flowering, DM-Days to maturity, PH- Plant height, PB- Number of primary branches, SB- Number of secondary branches, CP- Number of clusters per plant, PP- Number of pods per plant. PL-Pod Length in cm, NSP- of seeds per pod, BYP- Biological yield per plant and SYP- seed yield per plant.

3.2 Genetic variability

The outcomes of basic descriptive statistics, including means, maximums, minimums, SD, and CV for the thirteen quantitative characteristics examined in green gram genotypes. There genotypes list is presented in (**Table 1).** Among all quantitative characters have observed mean data their genotype G15 (52.30) had taken maximum number of DFF, while the genotypes G3 (37.50) reached a short DFF. In case of maturity of the genotypes G12 matured an early while G15 had 73.63 days to complete the maturation process. PH was ranged from 67.31 to 43.07. The PB per plant mean varied from 0.86 to 2.26 while maximum branches was observed

in G2 genotypes. There SB had recorded the minimum secondary branches are 3.82 in G24 and maximum branches per plant mean was recorded in 7.27 had G8 genotypes. The genotypes G20 (7.43) was produced a less CP while G10 (14.13) was produced a CP to all among genotypes. On average PP recorded in G24 (25.11) genotypes had a maximum number of pods while G23 (13.00) check variety recorded a minimum number of PP among all genotypes and as well average length of pods among the genotypes average was 11.00 cm was recorded. NSP mean had a high number of seed was recorded in G10 (13.55) genotypes while low number of seed recorded in G23 (9.07) genotype. The mean of BYP was recorded a 53.63g in G8 and minimum BYP was recorded in G11 (35.95). The average mean of SW among the genotypes was 4.90g with respect to SYP the genotype G17 (17.84) and G8 (17.86) produced a higher level of seed yield of plant, while the genotype G22 produced a 10.28g with an average of 13.34g while check variety perform a SYP a 15.76g there was high among to all genotypes mean. Similarly harvest index per plant was recorded a G1 was observing a high percentage but G7 was recorded a low percentage among all genotypes mean studied. The character under study with the greatest fluctuation was harvest index percentage of 21.7 percent while lowest variation among all traits had a maturity was recorded on 3.95 percent and the majority of the characteristics had variance of between 13 and 14 percent. This suggests a these personalities were influenced by their environment in some way. In summary, the study provides information on the genetic variability among different green gram genotypes in terms of multiple quantitative traits during *Kharif* season, including DFF, DM, PH, and PB, SB, CP, PP, PL, NSP, BYP,HI and SYP The data shows that the genotypes have a high degree of variation, which is beneficial for green gram or green gram breeding.

3.2. Genetic Parameter

Descriptive data, including GCV, PCV, Broad sense heritability, genetic advance 5%, and genetic advance mean 5%, were analysed in 24 green gram genotypes among the 13 characters that were subjected to all genetic parameters. While GCV had highest recording to primary branches (19.78) and lowest are recorded to harvest index per plant percentage (3.65). Similarly PCV was recorded to highest PB but lowest was recorded to DM. Among the broad sense heritability was highest recorded in DM of 88.20 % and lowest heritability was record in HI percentage 7.80. Therefore DM was recorded to high genetic advance in 5 % is 8.95, while 100seed weight was recorded to lowest percentage of genetic advance 5% is 0.48. Similarly

primary branches was recorded to high genetic advance mean in 5% is 37.41 while harvest index was recorded to lowest genetic advance mean in 5%and 1% is 2.10 and 2.70. Their descriptive study was present in (**Table 3)** The greatest PCV and GCV values were found in SYP, indicating that this characteristic contributes substantially more to genotypic variability. Direct selection based on this feature would thus be successful. This outcome correlated with those of **Pinchhyo*et al.*, (2016)** ***et al.*, (2018)**. Evidently, previous reports on the involvement of additive gene action for SYP were supported by high heritability and strong genetic progress. simmilarly result observed by **Keerthiga*, et al.*, (2018), Raturi *et al.*, (2015); Mariyammal *et al.*, (2019).**

Table 3 Estimation of genetic components for its yield and yield components

TRAIT	ECV	GCV	PCV	h^2 (Broad Sense)	Genetic advance 5%	Genetic advance mean 5%
DFF	6.56	9.61	10.33	86.60	8.22	18.42
DM	3.95	6.23	6.64	88.20	7.91	12.06
PH	13.64	10.17	12.87	62.50	8.95	16.57
PB	14.83	19.79	21.56	84.20	0.56	37.41
SB	14.07	15.47	17.47	78.40	1.63	28.21
CP	13.76	15.13	17.09	78.40	3.08	27.60
PP	13.59	14.60	16.58	77.60	4.91	26.49
PL	13.29	14.62	16.51	78.40	2.93	26.66
NSP	13.68	14.08	16.15	76.10	2.77	25.31
BYP	13.62	8.87	11.85	56.00	6.21	13.68
SW	13.64	7.07	10.59	44.60	0.48	9.73
HI	21.78	3.65	13.09	7.80	0.63	2.10
SYP	13.38	14.90	16.78	78.80	3.63	27.25

3.3 Genotypic and Phenotypic correlation coefficient analysis

Seed yield is a complex feature that is challenging to improve by selecting genotypes for yield, identifying the traits that contribute to and are closely related to seed yield that helps correlation. There a mentioned in (**Table 4**) is a genotypic coefficient of correlation and **(Table 5)** is a phenotypic coefficient of correlation. The findings demonstrated that greater genotypic correlation coefficients than phenotypic correlation coefficients were observed; showing that genetic variation mostly influenced how the features manifested. One cannot simply improve the complex characteristic of seed yield by selecting genotypes. It is therefore essential to identify the characteristics that were strongly connected to one another and affected the result. A statistical technique for determining the strength of a relationship among two or more variables is the correlation analysis. The correlation coefficient in plant breeding assesses the relationships

between various plant characteristics and identifies the specific factors that selection might use to genetically boost output. Genotypic correlation coefficient effect on seed yield has PH, PB, and SW showing a negative effect, while DFF, DM, SB, CP, PP, PL, NSP, BYP, and HI are showing a positive effect. Phenotypic correlation coefficient is to be similarly result observed, but phenotypic correlations are higher than genotypically observed. Details of the results revealed that NSP, BYP, and HI are highly significant positive genotypical coefficient correlations for SYP characters, along with significant SB and CP, while BYP and HI are highly significant positive phenotypic correlations, along with significant positive correlations for PL and NSP. The observed result to justify are highly significant and significant value are highly related to SYP that's character are collected to improvement of seed yield similarly result are observed in **Bhanu *et al.*, (2016); Manivelan *et al.*, (2019) and Muthuswami *et al.*,(2019). (Kritika and Yadav 2017)** are observed days to maturity on previous studies, have a near outcome reported. As well **(Dhoot et al., 2017)** was to be reported on earlier research work is similarly findings.

Table 4 Estimates of Correlation coefficients at Genotypic of 13 characters in green gram germplasm

Traits	DFF	DM	PH	PB	SB	CP	PP	PL	NSP	BYP	SW	HI	SYP
DFF	**1.000**	0.993**	-0.290	-0.399	0.332	0.010	0.175	-0.324	-0.363	0.282	0.140	-0.528	0.026
DM		**1.000**	-0.252	-0.426*	0.296	0.031	0.118	-0.206	-0.236	0.435	0.055	-0.814	0.049
PH			**1.000**	-0.519**	-0.343	-0.368	-0.324	0.003	0.003	0.367	-0.832	-0.832	-0.044
PB				**1.000**	-0.075	-0.136	-0.267	-0.286	-0.393	-0.282	-0.353	0.334	-0.073
SB					**1.000**	0.184	-0.312	-0.156	-0.246	0.406**	-0.479**	1.085	0.505*
CP						**1.000**	-0.155	-0.064	-0.112	0.686**	-0.705**	0.288	0.475*
PP							**1.000**	-0.123	-0.217	0.252	0.023	-0.018	0.150
PL								**1.000**	0.982**	0.971**	-0.742**	-0.172	0.664**
NSP									**1.000**	0.937**	-0.796**	-0.106	0.675**
BYP										**1.000**	-0.109	0.942**	0.984**
SW											**1.000**	-0.563**	-0.259
HI												**1.000**	0.9298**
SYP													**1.000**

Table 5 Estimates of Correlation coefficients at Phenotypic of 13 characters in green gram germplasm

Traits	DFF	DM	PH	PB	SB	CP	PP	PL	NSP	BYP	SW	HI	SYP
DFF	**1.000**												
DM	0.979**	**1.000**											
PH	-0.231	-0.213	**1.000**										

PB	-0.340	-0.385	-0.188	**1.000**									
SB	0.246	0.216	0.021	0.059	**1.000**								
CP	-0.015	-0.004	0.021	0.031	0.344	**1.000**							
PP	0.144	0.095	0.005	-0.086	-0.094	0.049	**1.000**						
PL	-0.276	-0.189	0.270	-0.098	0.067	0.153	0.073	**1.000**					
NSP	-0.309	-0.214	0.297	-0.170	0.016	0.136	0.012	0.977**	**1.000**				
BYP	0.248	0.344	0.018	-0.274	0.138	0.305	0.047	0.641**	0.607**	**1.000**			
SW	0.065	0.004	0.011	0.009	0.033	-0.077	0.290	-0.113	-0.107	-0.300	**1.000**		
HI	-0.214	-0.252	-0.191	0.063	0.253	0.063	-0.033	-0.058	-0.032	-0.170	-0.104	**1.000**	
SYP	0.007	0.045	-0.158	-0.126	0.300	0.275	0.026	0.426**	0.420*	0.590**	-0.301	0.693**	**1.000**

(*and **at 5% and 1% probability level respectively)

Figure 1 heat map chart of phenotypic correlation coefficients

3.4 Estimates of the direct and indirect impacts of 12 characteristics on the amount of seeds produced per plot in green gram at the genotypic and phenotypic levels

A correlation study's findings do not accurately depict the contributions made by each component character. Path coefficient analysis allows us to examine the causative factors according to their respective contributions and pinpoint both partially direct and indirect causes of link. The correlation coefficient was invented since it is insufficient to describe real relationships and allow for a character's manipulation to succeed. The maximum number of positive phenotypes in the current study are showing a HI (0.69) with SYP followed by BYP(0.59) as well as PP(0.43), NSP (0.42), SB (0.30), CP (0.28), DM (0.04), PP (0.03), and DFF (0.01) whereas SW (-0.30) was followed by PH (-0.16) and PB (-0.13). There is evidence that suggests that the seed weight, PH, and PB do not have an impact on the number of seeds yield per plant, however the remaining characteristics do. Since fertilisers and other components

have a modest impact on this study's phenotypic residue effect, which averages 0.0639, selecting these features should be prioritized in order to enhance green gram production. Similar result are observed a **Prajapati *et al.,* (2022) ; Hemavathy et., al (2015**) for 100 seed weight and number of seed per pod as well **Garg *et al.,* (2017)** for 100 SW.

Table 6 Estimates of direct and indirect effects at genotypic levels of 12 traits on seed yield per plot in green gram

	DFF	DM	PH	PB	SB	CP	PP	PL	NSP	BYP	SW	HI
DFF	**0.4**	0.3972	-0.1161	-0.1597	0.1326	0.004	0.0698	-0.1297	-0.1452	0.1129	0.0559	-0.2113
DM	-0.3543	**-0.3569**	0.09	0.1522	-0.1055	-0.011	-0.0423	0.0735	0.0842	-0.1553	-0.0197	0.2907
PH	-0.0034	-0.0029	**0.0117**	-0.0061	-0.004	-0.0043	-0.0038	0.001	0.001	0.0043	-0.0097	-0.0097
PB	-0.025	-0.0267	-0.0326	**0.0627**	-0.0047	-0.0085	-0.0168	-0.0179	-0.0246	-0.0177	-0.0221	0.0209
SB	-0.0062	-0.0056	0.0065	0.0014	**-0.0188**	-0.0035	0.0059	0.0029	0.0046	-0.0076	0.009	-0.0204
CP	0.0002	0.0006	-0.0071	-0.0026	0.0036	**0.0193**	-0.003	-0.0012	-0.0022	0.0133	-0.0136	0.0056
PP	0.001	0.0007	-0.0018	-0.0015	-0.0018	-0.0009	**0.0057**	-0.0007	-0.0012	0.0014	0.0001	-0.0001
PL	-0.0007	-0.0004	0.001	-0.0006	-0.0003	-0.0001	-0.0002	**0.002**	0.002	0.0023	-0.0015	-0.0003
NSP	-0.0252	-0.0164	0.0002	-0.0273	-0.0171	-0.0078	-0.0151	0.0683	**0.0696**	0.0819	-0.0554	-0.0074
BYP	0.173	0.2666	0.2246	-0.1728	0.249	0.4205	0.1542	0.7176	0.7215	**0.6128**	-0.0671	0.9802
SW	0.0012	0.0005	-0.0074	-0.0031	-0.0043	-0.0063	0.0002	-0.0066	-0.0071	-0.001	**0.0089**	-0.005
HI	-0.1346	-0.2076	-0.2122	0.085	0.2765	0.0734	-0.0046	-0.0439	-0.0271	0.4077	-0.1434	**0.2549**
SYP	0.0259	0.049	-0.0442	-0.0725	0.5053	0.475	0.1502	0.6642	0.6745	1.055	-0.2586	1.298

Table 7 Estimates of direct and indirect effects at phenotypic levels of 12 traits on seed yield per plot in green gram

TRAITS	DFF	DM	PH	PB	SB	CP	PP	PL	NSP	BYP	SW	HI
DFF	**-0.011**	-0.0108	0.0025	0.0038	-0.0027	0.0002	-0.0016	0.003	0.0034	-0.0027	-0.0007	0.0024
DM	0.0311	**0.0318**	-0.0068	-0.0123	0.0069	-0.0001	0.003	-0.006	-0.0068	0.0109	0.0001	-0.008
PH	0.0024	0.0022	**-0.0104**	0.0019	-0.0002	-0.0002	-0.0001	-0.0028	-0.0031	-0.0002	-0.0001	0.002
PB	-0.0097	-0.011	-0.0054	**0.0286**	0.0017	0.0009	-0.0025	-0.0028	-0.0049	-0.0078	0.0003	0.0018
SB	-0.003	-0.0026	-0.0002	-0.0007	**-0.012**	-0.0041	0.0011	-0.0008	-0.0002	-0.0017	-0.0004	-0.003
CP	-0.0001	0.001	0.0001	0.0002	0.0018	**0.0053**	0.0003	0.0008	0.0007	0.0016	-0.0004	0.0003
PP	0.0027	0.0018	0.0001	-0.0016	-0.0018	0.0009	**0.0189**	0.0014	0.0002	0.0009	0.0055	-0.0006
PL	-0.008	-0.0054	0.0078	-0.0028	0.0019	0.0044	0.0021	**0.0289**	0.0282	0.0185	-0.0033	-0.0017
NSP	0.0014	0.0009	-0.0013	0.0007	-0.0001	-0.0006	-0.0001	-0.0043	**-0.0044**	-0.0027	0.0005	0.0001
BYP	0.1765	0.2442	0.0125	-0.195	0.0977	0.2166	0.0333	0.4555	0.4318	**0.7109**	-0.2135	-0.1207
SW	-0.0002	0.001	0.001	-0.001	-0.0001	0.0003	-0.001	0.0004	0.0004	0.001	**-0.0035**	0.0004
HI	-0.1751	-0.2065	-0.1565	0.0515	0.2069	0.0516	-0.0273	-0.0478	-0.0258	-0.1391	-0.0852	**0.8195**
SYP	0.0069	0.0445	-0.1576	-0.1258	0.3	0.275	0.0263	0.4256	0.4196	0.5897	-0.3008	0.6925

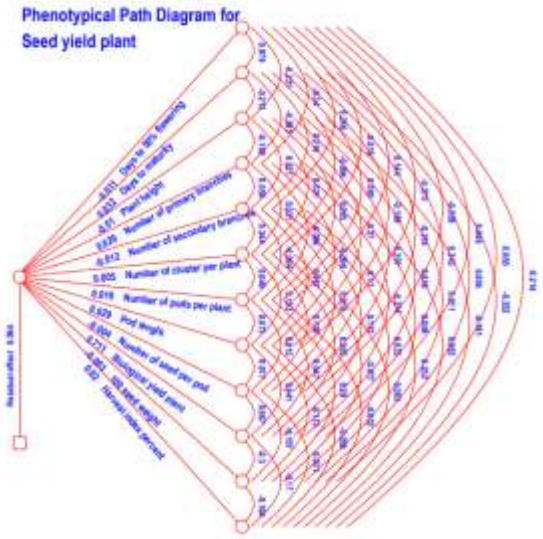

Figure 2 Figure of direct and indirect effects at phenotypic levels of 12 traits on seed yield per plot in green gram.

3.5 D^2 matrix

D^2 matrix it is statistic tool that quantify the individual or population based on multiple quantitative traits they can descried a how much contribution are contribute an each traits. There a result are revealed a highest ranking and greatest number of contributions were found in the seed weight categories (90, 0.33), cluster size (87, 0.32), and number of seeds per plant (68, 0.25). While BYP and BYP are ranked, the remaining characters are observed below 10, with contributions below 20. On character, a similar contributing proportion is seen. As a similar result was observed in **Singh et al., (2015)** was a contribution of BYP, SYP and CP showed the contribution.

Table 8 Percentage contribution of characters of genetic diversity

Source	Times Ranked 1st Contribution %	Contribution %
DFF	5	0.0021
DM	4	0.041
PH	7	0.032
PB	2	0.0072
SB	18	0.0652

CP	87	0.3152
PP	1	0.0036
PL	1	0.0036
NSP	68	0.2464
BYP	12	0.12
SW	90	0.3261
HI	8	0.029
SYP	1	0.0036

3.6 Principal component analysis (PCA)

Graphical presentation of the scree plot

According to the scree plot, PC1 had the highest percentage of variation (26.5%), PC2 had the second-highest percentage (17.5%), and PC3 to PC9 had the lowest percentages of variation (16.2%, 14.8%, 10%, 7.7%, 4.9%, 2.2%, and 0.2%, respectively). The importance of the top five PCs may be shown by the fact that they accounted for more than 80% of the overall variability. so they can demonstrate the importance of the first five PCs.

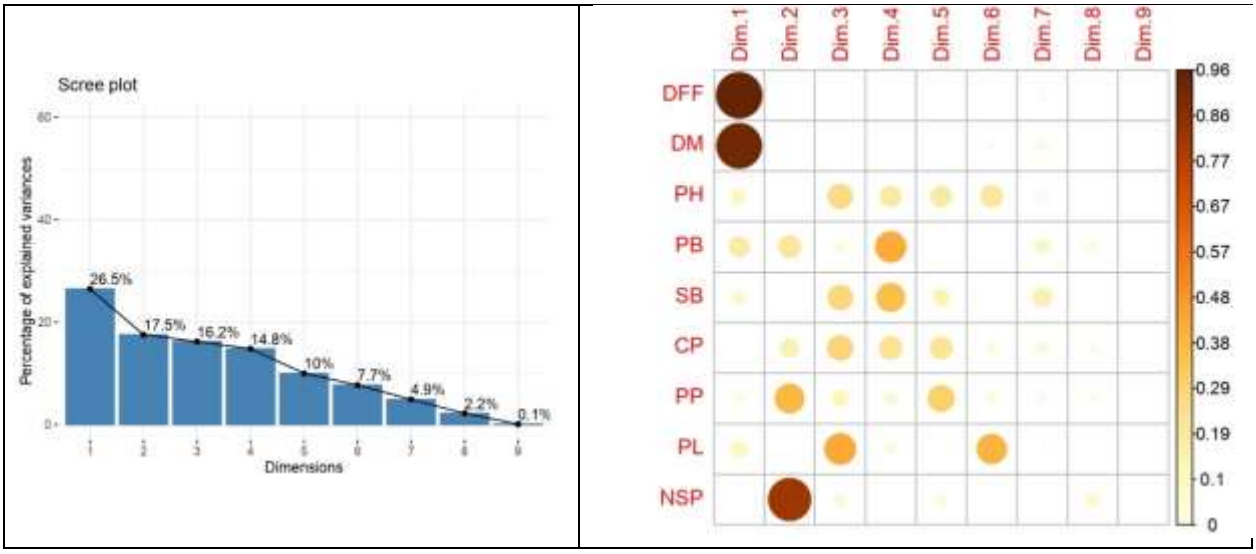

Figure 3 Dimensions of the scree plot and its graphic presentation

Biplot principal component analysis

The Biplot analysis, which shows the relationship between the many qualities and genotypes, focused on the first two main components, since the set of data showed a 45.5% divergence. Four coordinates along the x and y axes were used to indicate the biplot's two first main components. Coordinate -1 is made up of the five genotypes Gen1, Gen7, Gen12, Gen15,

and Gen16, with the first and second PCs having positive values. Significant variables including the DM and SB were associated to this location's genotypes. While other genotypes are located near to the origin, Gen 15, which is the most varied genotype, is positioned far from the origin after Gen 7, Gen 12, and Gen 1. The longest vector, which exhibits the greatest variation, Gen3, Gen4, Gen5, Gen6, Gen19, and Gen23, for Thus, are plotted in the direction of a negative PCA1 and a positive PCA2 in coordinate -2, where the PH and PP are connected to the genotypes there. The remaining genotypes are distributed close to the centre, except for Gen 23, which is positioned far from the core. In the seven genotypes assigned to coordinate 3, the first two main

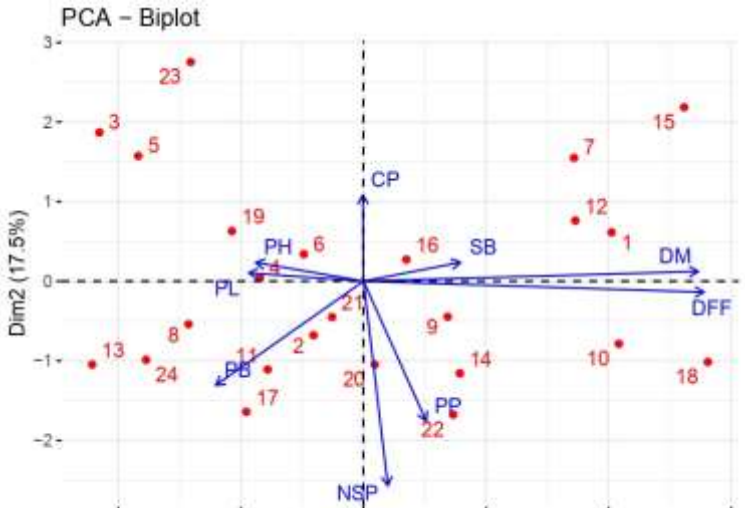

Figure 4 Different dimension coordinate biplot characters

components were negative. The coordinate with the most genotypes is -3, whereas the coordinate with the remaining six genotypes, which had positive and negative values for the first and second PCs, respectively, is 4. Six genotypes provide traits including Days of flowering, pods per plant, and the amount of seeds per plant. DFF displayed the longer line, which represented the larger variation, among the four variables. The genotype distribution in the biplot indicated that the several green gram breeding lines had some genetic variation.

Contribution along with the quality of variables and genotypes

The DFF makes up the largest proportion of the 9 variables, whereas the NSP makes up the most percentage of the dimension 2 variables. The DFF is followed by the principal components DM, NSP, PP, PB, CP, PL, PH, and SB. The 24 genotypes showed that genotype Gen 15 contributed the biggest proportion of the total diversity, followed by genotypes Gen 23, Gen 18, Gen 3, Gen 13, Gen 5, Gen 7, Gen 10, and Gen 1 are respectively high contribution.

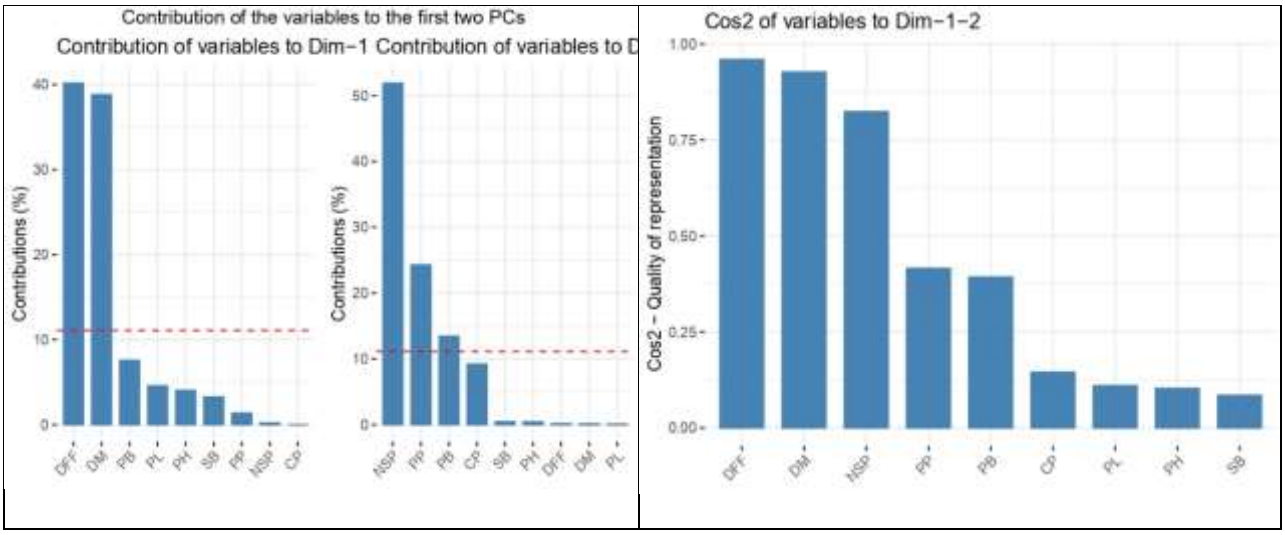

Figure 5 Contribution among different variables and dimension

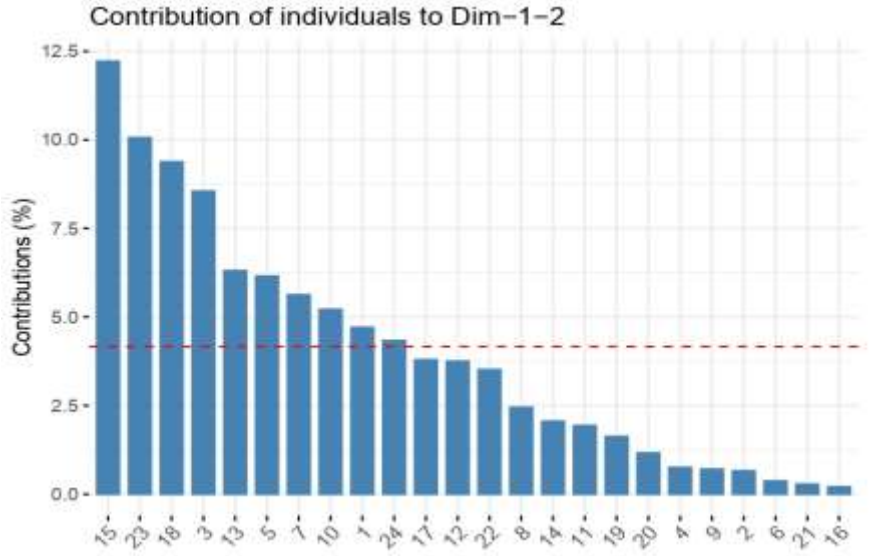

Figure 6 contribution individual genotypes

3.7 Cluster analysis by torcher's method

To understand the genetic relationships between the cultivar and identify the best genotypes for future efforts in breeding cluster analysis was performed. 10 quantitative characters for 24 genotypes were used in a cluster analysis, which separated the genotypes into seven distinct and well-defined clusters. The largest cluster, cluster II, has seven genotypes, compared to cluster I has six. Additionally, clusters III and IV each have four genotypes. It

should be observed that there is no correlation between genetic diversity and geographic variety, as shown by the grouping of genotypes from diverse geographic origins into the same cluster.

The cluster means for the thirteen attributes studied likewise showed the presence of variability in the 24 genotypes. The maximum value seen for cluster I in terms of DM is 68.06g. Among clusters, the longest cluster distance III and VI is 35.54, whereas the highest value observed for clusters V, VI, and VII is zero. Furthermore, data from the same source were sorted into several clusters, showing that eco-geographic variety is not a reliable indicator of genetic diversity **(Vijaya and Shekhawat, 2012).**whereas (**Gupta et al.,**2023) to be recorded a similar cluster and genotypes distribution as well mean and distance are closely related to early researchers is **Kundagrami (2016) and Razzaque et al., (2016).**

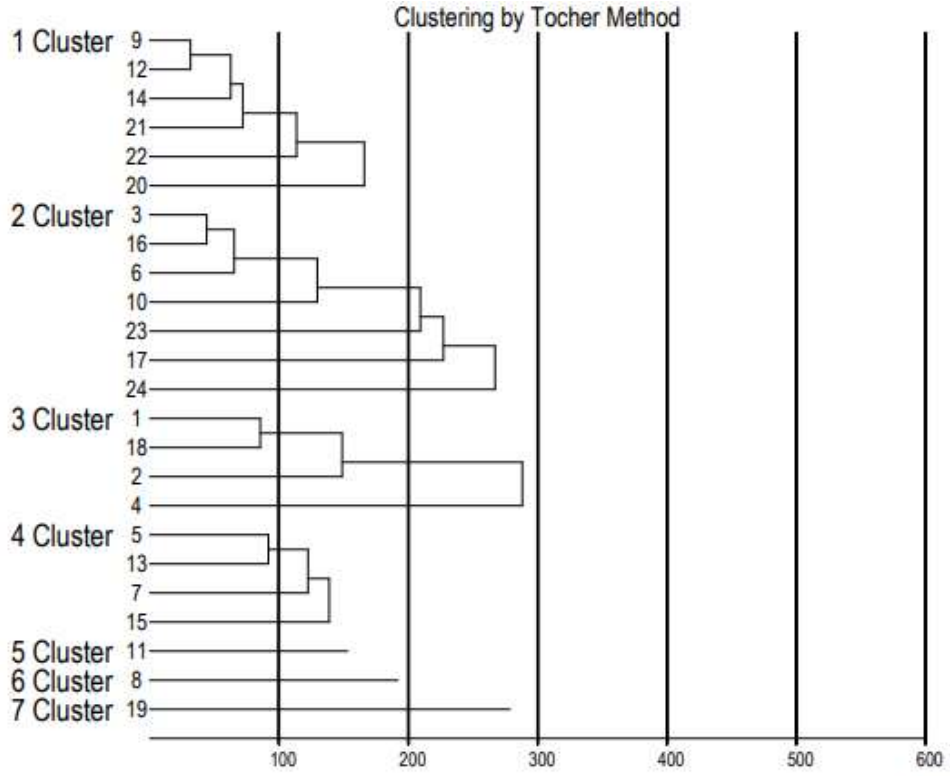

Figure 7 clustering by tocher's methods study in twenty four genotypes

Conclusion

The analysis of variance had a significant effect on the outcome of the study. The genetic variability among green gram genotypes for multiple quantitative traits increased during the Kharif season, with some genotypes exhibiting higher performance than others. Seed yield per plant may be an effective trait for direct selection in breeding programs, as it exhibited the

highest PCV and GCV values. Additionally, traits such as DM and primary branches showed a high genetic advance of 5%, suggesting that selection based on these traits may lead to a significant improvement in yield. Correlation analysis suggests that seed yield is influenced by multiple traits, both positively and negatively. Traits such as PH, PB, and SW showed a negative effect on seed yield, while DFF, DM, SB, NSP, PP, PL, BYP, and HI showed a positive effect on seed yield. The genotypic correlation coefficients were greater than the phenotypic correlation coefficients, indicating that genetic variation plays a more significant role in determining the relationship between traits and seed yield. It would be beneficial to focus on improving the traits with a positive effect on seed yield, such as NSP, BYP, and HI. These traits could be used as selection criteria in breeding programs. Focusing on improving traits with a positive effect, such as NSP, BYP, and HI, could be beneficial for breeding programs aimed at improving seed yield. Traits such as HI, BYP, and PP had a significant positive effect on SYP, while SW, PH, and PB had a negative effect. Seed weight, cluster size, and number of seeds per plant made the greatest contributions to the overall phenotype. These traits should be prioritized in breeding programs aimed at improving the overall yield. On the scree plot, the first five principal components (PC1 to PC5) are the most significant in explaining the variability. In the biplot, the first two principal components accounted for a significant amount of the total variance, and the genotypes were associated with important variables such as SB, PH, PP, and NSP. Days to 50% flowering are the most important variable in dimension 1, while NSP has the highest contribution in dimension 2. In terms of genetic diversity, Gen 15 was found to have the highest contribution among the 24 genotypes studied, followed by Gen 23, Gen 18, Gen 3, Gen 13, Gen 5, Gen 7, Gen 10, Gen 1, and Gen 24. The highest value for distance was observed in cluster I at 68.06g, and significant differences in quantitative traits were observed among the different clusters. This analysis provides valuable information for future breeding efforts, emphasizing the importance of selecting genetically diverse and distinct genotypes.

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