Genetic correlation and path analysis among diverse genotypes of Green gram [*Vigna radiate* (L.) Wilczek]

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ABSTRACT

Green gram (*Vigna radiate* L.Wilczek) is an annual, erect or semi-erect plant. It is a high source of protein and included in the day today diet of human mostly in developing countries. Twenty two Green gram (*Vigna radiata* L. Wilczek) genotypes were used for studying the dynamics of genetic divergence by Mahalanobis's D^2 Statistics and the association among different character using Heritability, Path and Correlation coefficient analysis. The data of fourteen quantitative characters observed from the selected genotypes were raised in (RBD) Randomized Block Design, under field condition of Lovely Professional University, Punjab, India. Our results revealed genotypes diverse in nature significantly for all characters under study. Analysis of Variance showed mean square values that specified a significant genetic difference within genotypes used in present study. Variations were observed for 75% maturity and days to flowering. Cluster analysis based on Hierarchical analysis on 14 morphological characters gathered all 22 genotypes into 5 different clusters. Three characters i.e. plant height (cm), days to 75% flowering and seed yield per plant (g) contributed maximum in presence of genetic diversity. In terms of variance, close proximity among PCV & GCV values for most of the traits showed there is significant variation due to environment on the expression of the traits under experimental. Hence, we were able to identify characters that should be given more weightage in selection programme of high yielding Green gram genotypes.

KEYWORDS: Green Gram, Genetic divergence, Heritability, Cluster Analysis, Path Analysis

INTRODUCTION

Pulses are mostly growing tropical region as a major source of protein which brought a considerable improvement in the human diet system (Tateishi and Maxted, 2002; Tomooka et al., 2002b).Green gram (*Vigna radiata* L. Wilczek) belongs to the family leguminacea commonly known as Mungbean and also known as green bean, mash bean, golden gram and green soy in different parts of the world for its excellent source of easily digestible proteins. Moreover, due to wider adaptation for short duration, minimum water requirement and soil fertility is most suitable pulse crops grown in tropics (Tomooka et al., 2002a). The grains contain approximately 3.5-4.5% fibre, 4.5-5.5% ash 1.0-1.5% oil, 62-65% carbohydrates and 25-28% protein, on dry weight basis (Katiyar, 2009).Despite being enriched in protein and nutrients still pulse production is lagging in tropics. Therefore, present study evaluates different germplasm of green gram using effective selection methods for desirable traits present which can further use in crop improvement programmes (Venkata krishna et al., 2000). Furthermore, deep understanding towards variability in different quantitative characters available in the breeding material may help the plant breeders to select superior genotypes based on different genetic parameters such as heritability, genotypic variation, genetic gain etc. to observe and understand the magnitude and understand the nature of variability for the desirable plant characters (Tabasum, *et al*., 2010).Therefore , it is essential to study association of characters among themselves for yield and yield related components (Sangiri *et al*., 2008). This can be achieved by character association studies under different environmental conditions. Moreover, different methods ex. Genotypic correlation provides an idea about measure of genotypic association between two or more characters which can be suitable methods to identify the relationship between the characters. However, indirect associations are more complex and become important when a number of variables are present in the study for correlation (Zong *et al*., 2003). Present studies suggested that some depended and independent traits also positively correlated with yield and yield related components. Direct and indirect independent traits associated with dependent traits mainly involve for yield and yield related path coefficient analysis. It was also showed that the correlation is because of direct effect, it shows true and positive relation in which selection is done for such characters for improving the yield of the desired genotypes. (Kumar *et al*., 2002a, 2002b).The data that were collected were used to study more on cluster and principal component analysis. Different cluster were grouped which showed the variation levels in the different genotypes which will help us further in future breeding programmes. Moreover, availability of high percentage of protein is also valuable marker for varietal selection in breeding program. Therefore, our study was conducted to identify superior cultivar based on variability and diversity which will enhance productivity and stabilize the yield for local benefit of farmers.

Materials and methods

Study sites

The present experimental research was done during the Summer season of 2017, at main experimental farm in Lovely Professional University, Phagwara, Kapurthala (district), Punjab at the latitude and longitude range of 31.2554° N and 75.7058° E respectively, to evaluate the genetic diversity between the selected Green gram genotypes. The area of experimentation was quite uniform with regards to topography and fertility with sandy loam soil. The material used for the experiment consists of 22 genetically diverse genotypes were collected from different sources mention on Table (1)and the field experiment was conducted using Randomized Block Design (RBD) three replications. The row to row spacing within the ridges containing same germplasm was 50 cm and interspacing between two rows containing different germplasm was 100 cm. The spacing within plant to plant was 10 cm. Seeds were sown with a depth of 4-5 cm with maximum of 5 seeds/hill and length of 200cm for each row. All the recommended practices are agronomic and some plant protection measures were used to ensure a healthy crop growth and yield.

Phonological study

Morphological traits were recorded for flowering (75%), Period of maturity (DOM), no. Of branches/plant (PBPB), duration of reproductive phase (DORP), no. of flower clusters each plant (FC), plant height (PH) (cm), no. of secondary branches each plant (SBPB), no. of pods per plant (PPP), length of the pod (PL) (cm), no. of grains per pod, pod density (PD) , 100 seed weight (SW) (g), yield per plant (YPP) (g) and yield per plot (g).

Statistical analysis

The data based on phenological traits was further utilized for ANOVA analysis as per described by Panse (1954) for individual characters. Correlation coefficient and path coefficient was worked out as method given by Dewey and Lu (1959). The replicated data were used for genetic divergence analysis using Mahalanobis's D^2 - statistic (Mahalanobis 1936).

Seed protein analysis

Total protein was isolated from seeds of all genotypes used in the study using standard Bradford methods (Bradford, 1976). Quantification of protein was done using spectrophotometer and total protein percentage was calculated using standard curve of Bovine serum albumin (BSA) suggested by Canas et al., (2007).

Table 1: List of Green gramgermplasm used in present study

S.no.	Name of Variety/Inbred line	Source	Characteristics
1	HUM-1	BHU, Varanasi	Spring and kharif season, Maturity time 60-65, Yield 9.4-16.0 q/ha
2	Gold	IIPR	Seeds are Green and bold, Maturity time65-64 days
3	Moongi	IIPR	Bushy plants, Maturity time 65-68 days, Yield7-11q/ha
4	HUM-1L	BHU, Varanasi	Summer season, Maturity time 60-62, Yield11.2 q/ha
5	PUSA-460	IARI, New Delhi	Kharif season, Golden green compact, Maturity time65-70 days, Yield 8-11q/ha
6	MLA 720	PAU, Ludhiana	Summer season, Maturity time 70-71days, Yield 6-8 q/ha
7	Kopergane	BHU, Varanasi	Solid and Green bold seeds, Maturity time 60-65, Yield 8-10q/ha

8	LM-5	BHU, Varanasi	Solid and light green, Maturity time 45-40 days, Yield 9-10q/ha
9	PUSA-Vishal	IARI, New Delhi	Summer season, bold seed, Maturity time 62, Yield 11.0 q/ha
10	LG-420	BHU, Varanasi	Summer season, Maturity time 50-55 days,Yield 5-7 q/ha
11	IPM-2	IARI, New Delhi	Large seed suitable for rainy season, Maturity time 62-68, Yield 11-12 q/ha
12	SML-668	PAU, Ludhiana	Spring-Summer season, Maturity time 60-63,Yield 11.3 q/ha
13	JAUM0936	KVK,Manipur	Seeds small in size,Maturity time 50-45,Yield 4-5q/ha
14	KM2241	KVK,Manipur	Summer crop, Maturity time 44-59 days, Yield 7-8q/ha
15	ML2479	KVK,Manipur	The short duration crops, Maturity time58-60 days, Yield 6-7q/ha
16	PUSA0672	KVK,Manipur	Summer crop, Maturity time 70-71 days, Yield 6-5q/ha
17	NVL855	KVK,Manipur	Dark green colour seeds, Maturity time 49-50 days, Yield 6-7 q/ha
18	SVM6133	KVK,Manipur	Summer and Winter season crop, Maturity time 65-67 days,Yield 8-9 q/hac
19	IPM512-1	KVK,Manipur	Summer crop, Maturity time 44-48 days, Yield 6-7 q/ha
20	MH1323	KVK,Manipur	Seeds small in size,plants had dark violet veins, Maturity time 65-75 days, Yield -10 q/ha
21	PUSAM 1772	KVK,Manipur	Summer crop, Maturity time 50-52 days, Yield 7-8 q/ha
22	IPM410-9	KVK,Manipur	Summer crop, Maturity time 69-70 days, Yield 6-7 q/ha

Results and Discussion

Present investigation revealed high genetical variance among traits used under study. Data obtained from ANOVA analysis showed that the selected genotypes were genetically diverse and significant amount of variability present within them. Similar results were obtained by Reni and Rao (2013) and Garg *et al.,* (2017) shown in the Table (2). PCV and GCV were recorded using traits used in present study (Table 3). The PCV was higher than GCV for all the characters showing that the visible variation in the expression of traits was mostly because of environment. High PCV was recorded for no. of flower cluster per plant (30.238), followed by no. of pods per plant (25.602), RP (21.411), 100 SW (21.365), seed yield per plot

(19.797), pod density (19.104), PH (cm)(18.391), yield/plant(17.751) and PBPP (16.901). Present study also suggested high GCV for no. of cluster per plant (24.380), after that PPP (23.756), RP (20.335), 100 SW (19.703), yield/plot (13.706), yield/ plant (13.459) and plant height (cm) (11.928). Similar finding was found by Osekita and Ajayi (2013) suggested high GCV and PCV for no. of seeds per plant and seed yield per plant. These data not independently suggested for heritable traits as heritability states the fraction of gene which is transmitted from parents to all springs (Makeen *et al*., 2007). Therefore, present study estimated heritability among selected genotypes varied from 25.66% for PBPP to 90.202% DORP. Similarly, heritability for duration of RP (90.202%) was recorded highest among all the characters used in present study followed by PPP (86.095%), PD (cm) (77.979 %), total protein percent (71.916%), CPP (65.009%), PD (63.537%), no. of grain per pod (63.069 %) , yield/ plant (57.490) and DOM (56.862%). These findings were similar to Okonkwo and Idahosa (2013) who recorded high heritability estimates for days to 50% flowering, days to maturity. While, low heritability was reported for yield/plot (47.929%), PH (cm)(42.064%), SBPP (39.048%) PBPP (25.660%). Like findings were reported by Osekita and Ajayi (2013) for 100 seed weight and no. of branches. Percentage of mean calculated Genetic advance value and concluded maximum for no. of pods per plant (45.407) after that FC (40.494), DORP (39.785), 100 SW (g) (37.431) and PD (25.005). The estimations of high broad sense heritability and high genetic advance indicate that improvement in these traits could be possible by direct selection. High heritability with moderate genetic advance was recorded for CPP, DORP and PD indicating presence of G x E interaction. This indicated that simple selection may not be rewarding for these traits. The present findings corroborate the earlier report of Okonkwo and Idahosa (2013) and Bhat and Basavaraja (2011).Present study record correlation coefficient estimated positive and significant genotypic and phenotypic correlation in PD (0.509, 0.337), days to 75% Flowering (0.409,0.349), PBPP (0.312, 0.419), SBPP (0.277, 0.267) with seed yield per plant. Similarities were revealed by Ghodrati et al., (2013) that harvest index and no. of pods per plant showed positive association with seed yield /plant. Correlation coefficient analysis measure natural relation between 22 genotypes for different plant traits showing in Table (4). Selected traits can be allowed for selection process in crop improvement program. When characters having direct effect on yield are selected, their association with other character are to be considered simultaneously as they will indirectly affect the yield. Days to 75% flowering implied positive significant correlation at both levels with Seed yield per plant (0.409, 0.278), seed yield per plot (0.409, 0.349), while negatively associated with duration of RP (-0.679, -0.569), PH (-0.589, -0.301). PBPP in this experiment directly correlated with SBPP (0.557, 0.251), however seeds/plant positively correlated with phenotypic and genotypic level (0.896, 0.483). Moreover, study showed significant and not positive correlation with number of CPP (-0.580, -0.299), at both genotypic and phenotypic level and 100-seed weight (-0.233) at the genotypic level. Data suggested plant height significantly positive correlated with PBPP (0.495, 0.395). However, PPP (0.349, 0.331) in present study both PCV and GCV are negatively correlated for traits seed yield per plant (-0.282, -0.451). Our study revealed PBPB have positive and significant correlation with total protein content (0.483, 0.716) and number of seed yield per plot (0.312, 0.419) while negative and significant correlation with number of seed yield per plant (-0.409, -0.338) at both phenotypic and genotypic level whereas with SBPP (-0.251) at Phenotypic level alone. These results displayed close resemblance with the report of Siahbidi *et al.* (2013).Path coefficient analysis is more useful for separating of direct and indirect effect of correlation and also allows comparing the component factors on the basis of their relative contributors. The path coefficient analysis in Table 5 exhibited that highest positive direct effects was noted for Days to 75% Flowering (3.24264) after that Days to Maturity (0.93768), PH (0.07704), no. of Grain per pod (0.05361) on the dependent character *i.e.,* seed yield per plant. Similar result obtained by Arshad *et al.,*(2014) who found seed yield /plant provide greater input towards number of branches per plant. Hence, these specific traits could be used as selective marker for future breeding program. Data revealed highest negative direct effect for DORP (-3.1258), PBPP (-1.03082), SBPP (-0.03959), PPP (0.8963), CPP (-0.03317), PL (-0.84792), PD (-0.5768), 100 SW (-0.01345), Total Percent Protein (-0.11094). Similar investigation by Arshad *et al.,* (2014) found that DOM and days to 50% flowering have direct but negatively correlated with yield per plant. Days to 50% flowering had medium positive indirect effect via 100 SW (0.1251).Moderate indirect effect of no. of primary PBPP was positive via Duration of RP (0.29967), DOF (0.28385) and PH (0.03812). SBPP showed high positive indirect effect via number of Cluster per plant (1.49608). no. of pods per plant had high positive indirect effect via no. of Cluster per plant (2.85167), Days of RP (1.49608), Plant height (0.01968), PBPP (0.34077),PPP had high positive indirect effect via PBPP (0.57941), SBPP (0.08708), CPP (2.85167), PL (0.0219), no. of grain per Pod (0.25689), Total Protein percent (0.03321). No. of cluster per plant imposed high indirect effect via PD (2.27549), Days to 75% Flowering (0.50632), no. of grain per Pod (0.45508), PH (0.02847).PL had moderate positive indirect effect via PH (0.04538), number of PBPP (0.01316), no. of pods CPP (0.72513).100SW imposed moderate positive indirect effect via PD (0.2513), (.0.14424), Plant height (0.01254), DRP (0.55102),Days to 75% Flowering (0.5651).These results are in conformity with the work of Abady *et al.* (2013).The residual effect (0.83659) on seed yield per plant was negligible, which suggest that most of the yield component was included in the study. The method recommended by Tocher (Rao, 1952) was taken for grouping the genotypes into diverse clusters using D^2 values. 5 clusters are formed with 21 genotypes. Among the cluster, cluster I and III were the largest having 10 and 9 genotypes respectively and Cluster II, IV, V were having single genotype in each. The distribution and clustering pattern of genotypes are shown in Table (7).The average D^2 value of inters and intra cluster distances are shown in Table (4). Genetical distance between the within genotypes were calculated by cluster III (153.064) after that cluster I (57.038). Solitary clusters II, IV, V showed zero intra-cluster distances. Diversity within the clusters varied from 82.608 to 204.730 inter-cluster distances. Cluster I and V showed highest inter cluster distance (204.730) after that between cluster I and IV (178.539), cluster I and III (153.064). The lower inter-cluster distance was recorded within cluster IV and II (150.177) after that between cluster V and IV (110.412). In present study showed that inter-cluster genetical distance were larger than intra-cluster distances deal substantial genetic divergence between the genotypes showing in Table (4). Study concluded genotypes fell in two distinct clustered with maximum genetical distance as compared with genotypes fell in same clustered. Therefore, these genotypes can be further used for future hybridization program (Gadakh *et al.*, (2013) and Payai *et al.*, (2015).The general mean values and cluster mean values for 14 characters of 22 genotypes have been represented in Table (5). The data showed Cluster I contain10 genotypes which were considered as having more than average values for, plant height, 100 seed weight, primary branches, days to 75% flowering, pod density. Cluster II had 1genotype that indicate the more than average values for days to 75% flowering, pods per plant, clusters per plant and pod density. Cluster III contain9 genotypes which were grouped as having more than average values for duration of reproductive phase, primary branches per plant, days to maturity, plant height pod length, grains per pod, 100 seed weight and yield per plot. Cluster IV and V consisting of 1 genotype each showed above average values for days to 75% flowering, SBPP, PPP, CPP, grains per plant, yield per planting and yield per plot. Similar study by Singh *et al.,* (2009) and Ahmad *et al.*, (2013).In terms of protein content, the analysis showed highest total protein content in cultivar IPM410-9 (22%) followed by Gold 21% than MLA 270 (20.28%) and least was observed HUM-1 (15%).

Conclusion

Present study concluded that environmental effects played a profound role in causing all the characters variance as the magnitude of phenotypic is more than genotypic variance. Characters like days to maturity and 75% flowering showed positive direct effects which showed that this character should be selected for modern breeding programme for higher seed yield. Moreover, when we observed the cluster means the highest were observed in cluster III (HUM-1L, LM-5, Kopergane, Moongi, KM2241, PUSA-460, HUM-1, Gold, PUSA-Vishalso the genotypes from cluster III the genotypes from cluster III should be selected for the hybridization programme for the betterment of those selected traits.

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Table 2: **Analysis of variance for various yield contributing characters in Green gram**

Characters	Mean Sum of Squares		
	Replication (d.f=2)	**Treatments (d.f=21)**	**Error (d.f=42)**
Days to 75% Flowering	4.424	15.724***	2.773
Duration of Reproductive Phase	3.591	76.874**	2.686
Days to Maturity	13.818	46.284**	9.342
Plant height(cm)	7.961	101.463**	31.926
No. of primary branches	0.065	0.592**	0.291
No. of secondary branches	0.396	0.886 **	0.303
No. of pods per plant	41.523	137.461**	7.022
No. of cluster per plant	0.520	1.623**	0.247
Pod length (cm)	0.046	1.243**	0.107
No. of grain per pod	0.073	3.415**	0.558
Pod density	0.010	0.047*	0.008
100 seed weight (g)	0.321	3.356**	0.186
Yield/ plant	0.859	2.97**	0.588
Yield/plot	433.126	979.717**	260.471

Table3.Genotypic (G) andphenotypic (P) coefficient of correlation among different character in Green Gram genotypes used for study.

Characters		X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15
	G	-0.679**	0.047^{NS}	-0.589**	-0.335**	-0.163^{NS}	0.138^{NS}	0.085^{NS}	-0.156^{NS}	-0.443**	-0.168^{NS}	0.145^{NS}	-0.174^{NS}	0.409**	0.409**
X1	P	-0.569**	0.406*	-0.589**	0.406*	0.406*	0.406*	0.406*	0.406*	0.406*	0.406*	0.406*	0.406*	0.406*	0.406*
	G		-0.139^{NS}	0.204^{NS}	-0.096^{NS}	-0.170^{NS}	-0.134^{NS}	0.235^{NS}	0.175^{NS}	0.324**	0.095^{NS}	-0.169^{NS}	-0.176^{NS}	-0.096^{NS}	-0.194^{NS}
X2	P		0.336**	-0.571**	-0.068^{NS}	-0.118^{NS}	-0.130^{NS}	0.160^{NS}	0.163^{NS}	0.238^{NS}	0.076^{NS}	0.164^{NS}	-0.161^{NS}	-0.075^{NS}	-0.149^{NS}
	G			0.092^{NS}	0.303*	-0.128^{NS}	-0.562**	-0.184^{NS}	-0.386**	-0.240^{NS}	-0.124^{NS}	0.451**	-0.227^{NS}	-0.085^{NS}	-0.114^{NS}
X3	P			-0.248*	0.068^{NS}	-0.077^{NS}	-0.452**	-0.061^{NS}	-0.251*	-0.166^{NS}	-0.202^{NS}	0.331**	-0.176^{NS}	-0.128^{NS}	-0.244*
	G				0.495**	0.283*	0.255*	-0.226^{NS}	0.370**	0.589**	-0.037^{NS}	-0.087^{NS}	0.163^{NS}	-0.283*	0.206^{NS}
X4	P				0.194^{NS}	0.090^{NS}	0.149^{NS}	-0.142^{NS}	0.222^{NS}	0.244*	0.007^{NS}	-0.076^{NS}	0.049^{NS}	-0.182^{NS}	0.093^{NS}
	G					0.557**	-0.331**	-0.562**	0.235^{NS}	0.002^{NS}	-0.162^{NS}	0.423**	0.896**	-0.451**	0.240^{NS}
X5	P					0.251*	-0.053^{NS}	-0.120^{NS}	0.119^{NS}	-0.007^{NS}	-0.057^{NS}	0.230^{NS}	0.483**	0.142^{NS}	0.312*
	G						0.264*	-0.580**	0.208^{NS}	-0.141^{NS}	0.114^{NS}	0.336**	0.716**	-0.170^{NS}	0.419**
X6	P						0.250*	-0.299*	0.174^{NS}	0.049^{NS}	-0.062^{NS}	0.151^{NS}	0.421**	0.094^{NS}	0.277*
	G							0.525**	0.140^{NS}	-0.008^{NS}	-0.078^{NS}	-0.435**	0.215^{NS}	-0.230^{NS}	0.267*
X7	P							0.383**	0.137^{NS}	0.055^{NS}	-0.112^{NS}	-0.330**	0.228^{NS}	-0.068^{NS}	0.243*
	G								-0.012^{NS}	0.254*	-0.146^{NS}	-0.414**	-0.079^{NS}	0.090^{NS}	-0.186^{NS}
X8	P								-0.016^{NS}	0.193^{NS}	-0.132^{NS}	-0.285*	-0.015^{NS}	0.016^{NS}	-0.072^{NS}

	G	0.450^{**}	0.645^{**}	-0.323^{**}	0.207^{NS}	-0.117^{NS}	0.071^{NS}
X9	P	0.424^{**}	0.489^{**}	-0.258^{*}	0.139^{NS}	0.037^{NS}	0.096^{NS}
	G		0.053^{NS}	-0.562^{**}	0.143^{NS}	-0.057^{NS}	-0.199^{NS}
X10	P		-0.147^{NS}	-0.309^{*}	0.103^{NS}	0.074^{NS}	0.072^{NS}
	G			-0.163^{NS}	0.071^{NS}	-0.023^{NS}	-0.509^{**}
X11	P			-0.201^{N}	0.047^{NS}	-0.068^{NS}	-0.337^{**}
	G				-0.016^{NS}	-0.038^{NS}	0.025^{NS}
X12	P				0.015^{NS}	0.027^{NS}	0.066^{NS}
	G					0.025^{NS}	0.264^{*}
X13	P					0.093^{NS}	0.116^{NS}
	G						0.029^{NS}
X14	P						0.220^{NS}

X1=Days to 75%flowering,
X2= Duration of reproductive phase,
X3 = Days to maturity
X4= Plant height
X5= No. of primary branches
X6= No. of secondary branches
X7=No. of pods per plant
X8= No. of cluster per plant
X9=Pod length (cm)
X10= No. of grain per pod
X11=Pod density
X12=100 seed weight (g)
X13= Total protein percent
X14=Yield/ plant
X15= Yield/plot

Table4.Estimates of variability, heritability and genetic advance as per cent of mean in Green gram

Characters	Range		Mean	Coefficient of variation (%)		Heritability (bs)(%)	Genetic Advance	GA as 5 per cent of mean
	Min	Max		PCV	GCV			
Days to 75% Flowering	36.6667	44.6667	41.7121	6.384	4.981	60.883	3.340	8.006
Duration of Reproductive Phase	17.0000	36.6667	24.4545	21.411	20.335	90.202	9.729	39.785
Days to Maturity	61.0000	74.6667	68.4091	6.803	5.130	56.862	5.451	7.968
Plant height(cm)	34.0400	56.8867	40.8189	18.391	11.928	42.064	6.432	15.936
No. of primary branches	2.9967	4.6633	3.7005	16.901	8.561	25.660	0.331	8.934
No. of secondary branches	5.9600	8.1333	6.9477	10.149	6.342	39.048	0.567	8.164
No. of pods per plant	15.0267	38.8867	27.7573	25.602	23.756	86.095	12.604	45.407
No. of cluster per plant	1.6500	4.5500	2.8223	30.238	24.380	65.009	1.125	40.494
Pod length (cm)	5.4300	8.0400	7.0085	9.942	8.779	77.979	1.119	15.971
No. of grain per pod	6.3400	10.4633	8.4829	14.486	11.504	63.069	1.597	18.821
Pod density	0.4433	0.9633	0.7547	19.104	15.228	63.537	0.189	25.005
100 seed weight (g)	3.4767	6.8767	5.2176	21.365	19.703	85.049	1.953	37.431
Yield/ plant	4.9267	8.3100	6.6265	17.751	13.459	57.490	1.393	21.022

Table 5.Path coefficient showing direct (diagonal) and indirect effect (off diagonal) of different characters on seed yield plant^{-1} in Green gram (*Vigna radiata*)

Traits	DTF	DOR	DTM	PH	NBP	NBS	NPP	NCP	PL	NGPP	PD	100SW	TPP	SYP
DTF	**3.24264**	2.12299	-0.04398	-0.04539	0.345	0.02451	-0.22538	0.24287	0.29392	-0.44777	-0.59149	0.1251	0.07333	1.77798**
DOR	2.20234	**-3.1258**	0.38048	0.01575	0.09882	0.02545	0.21892	0.6699	-0.32889	0.3273	0.33385	-0.1459	0.07418	-0.84288**
DTM	0.1521	-1.26835	**0.93768**	-0.04403	-0.31204	0.01926	0.92092	-0.52398	0.7269	-0.24266	-0.43901	0.38902	0.09543	-0.49631
PH	1.91071	-0.63918	-0.53588	**0.07704**	-0.51013	-0.0424	-0.41864	-0.64539	-0.69566	0.59513	-0.13104	-0.07534	-0.06852	0.89664**
NBP	1.08525	0.29967	0.28385	0.03812	**-1.03082**	-0.0836	0.54166	-1.60289	-0.4425	0.00169	-0.57068	0.36503	-0.377	1.04121**
NBS	-0.44602	0.41764	-0.52701	0.01968	0.34077	**-0.03959**	-1.63854	1.49608	-0.26408	-0.00812	-0.2765	-0.37545	-0.09052	1.16124**
NPP	-0.27617	-0.73429	-0.17229	-0.01744	0.57941	0.08708	**-0.85963**	2.85167	0.0219	0.25689	-0.51563	-0.35729	0.03321	-0.8075
NCP	0.50632	-0.54615	-0.3621	0.02847	-0.24233	-0.03117	-0.22988	**-0.03317**	-1.88233	0.45508	2.27549	-0.27889	-0.08696	0.31047
PL	1.43724	-1.01268	-0.22523	0.04538	-0.00172	0.0211	0.01316	0.72513	**-0.84792**	1.01025	0.18732	-0.48537	-0.06008	-0.86382**
NGPP	0.54331	-0.29561	-0.11661	-0.00286	0.16664	-0.01714	0.12834	-0.41653	1.21332	**-0.05361**	3.53017	-0.14079	-0.02996	-2.21229**
PD	-0.46986	0.52822	0.42252	-0.00672	-0.43584	-0.05045	0.71255	-1.18013	0.60806	-0.56795	**-0.57568**	0.86335	0.00655	0.10697**
100SW	0.5651	0.55102	-0.21266	0.01254	-0.92352	-0.10744	-0.35245	-0.22509	-0.38897	0.14424	0.2513	**-0.01345**	-0.4208	1.14499**
TPP	1.32746	0.60663	-0.10715	0.0159	-0.24713	-0.06291	-0.4381	-0.5302	-0.13456	-0.20093	-1.79817	0.02126	**-0.11094**	4.34316**

Residual are 0.83659*,** significant at 5% and 1% level of significance. DTF: Days to 50% flowering, DOR : Duration of reproductive phase, DTM: Days to maturity, PH: Plant height, NBP: Number of primary branches /plant, NSP: Number of secondary branches /plant, NPP: Number of pods/plant, NCP: Number of cluster/plant,PL: Pod length, NGPP: Number of grain /pod,PL: Pod length, PD :pod density , 100SW: 100-seed weight, TPP:total protein percent, SYP: Seed yield per plant.

Table6. Cluster profile of 22 genotypes of Green gram

Sr. No.	Cluster	No. of genotypes	Name of genotypes
1	I	10	PUSaM1772, IPM410-9, ML2479,NVL855, PUSA0672, LG-420, MH1323, SVM6133, JAUM 0936, IPM512-1
2	II	1	MLA-720
3	III	9	HUM-1L, LM-5,Kopergane, Moongi,KM2241, PUSA-460, HUM-1,Gold, PUSA-Vishal
4	IV	1	IPM-2
5	V	1	SML-668

Table.7 Estimation of intra (diagonal) and inter- cluster distances in 22 genotypes of Green gram

Euclidean² : Cluster Distances : Ward

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster
1 Cluster	57.038	120.112	153.064	178.539	204.730
2 Cluster		107.089	106.769	150.177	121.617
3 Cluster		0	0	111.114	108.010
4 Cluster				82.608	110.412
5 Cluster					0.000

Fig.1: Dendrogram of 22 genotypes of Green gram using Tocher Method