Original Research Article

STUDYONGENETICDIVERGENCEUSINGD^2ANALYSISINGREENGRAM (*Vignaradiata*(L.)Wilczek)

ABSTRACT

The purpose of the present study was to evaluate the genetic variability parameters such as genotypiccoefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance, aswellastostudygeneticdivergenceandidentifysuitableparentsfordivergenceamong53differentGreengramgenotypes,includingonecheckvariety.Theexperimentwasconductedduringthekharifseason of 2022-23 at the experimental farm of the Department of Genetics and Plant Breeding, NainiAgriculturalInstitute,SamHigginbottomUniversityofAgriculture,Technology,andSciencesinPrayagraj, Uttar Pradesh. A randomized block design with three replications was employed for the study.Thirteen characteristics were observed and recorded, which include: days to 50% flowering, days to 50%pod initiation, days to maturity, plant height, number of primary branches per plant, number of clusters perplant, pod length, number of seeds per pod, biological yield, harvest index, seed index, seed yield per plant.IPM-2-14 exhibited the highest meanperformance in terms of seed yield per plant, followed by MGG-385,among all the genotypes. The PCV values were consistently higher than the corresponding GCV values forall traits, indicating the influence of environmental factorson traitexpression. The number of podsperplantandnumberof clusters per plant recorded the highest GCV and PCV values. The numberof podsperplant exhibited both high heritability and genetic advance. 53 genotypes were categorized intosixclusters through D^2 analysis. Cluster I had the maximum number of genotypes, the maximum intra clusterdistance was observed in cluster IV, inter cluster distance between cluster III and cluster VI. The highestcluster mean was recorded by Cluster VI for plant height. The Percentage contribution of characters wasmaximum by seed yield per plant followed by the number of pods per plant andnumber of clusters perplanttowardsgeneticdivergence.

Keywords:Greengram,Phenotypic,Genotypic,Heritability,Divergence,Cluster

1.INTRODUCTION

Greengram [*Vigna radiata* (L.) Wilczek] is one of the important pulse crop because of itsshort growth duration, adaptation to low water requirement and soil fertility and is widelycultivated and consumed throughout India. Greengram is popularly known as moong orgreengram or golden gram, belongs to family Fabaceae and sub family Papilionaceae withdiploidchromosome number 2n=2x=22.

The importantgreengramgrowingstatesinthe countryare Orissa,Maharashtra,Andhra Pradesh, Madhya Pradesh, Gujarat, Rajasthan and Bihar. Green gram is an importantpulse crop which comes up well in humid tropics, semi-arid and arid regions. It is cultivatedworldwide,mainlyinAsiancountries,viz,Bang ladesh,China,India,Indonesia,andMyanmar. In global scenario, India contributes about 25 to 28 percent of total production inpulses.(**Kumar*etal*., 2019**).

Though greengram is considered as an important pulse crop in India, production andproductivity levels are very low to meet the nutrient status of people and the reason behindthis low production and productivity are sowing on marginal and sub-marginal land under therainfed situation, lack of high yielding genotypes, low seed replacement ratio of improvedhigh yielding varieties, imbalanced use of plant nutrients. Thus, the availability of pulses isquitelowerthantheactualrecommendationofWHO,whi chis29.2kg/capita/year.Hence,the production and productivity potential of pulses must be increased substantially. Amongthe pulses, green gram plays a vital role to meet these demands since its short growth periodandsuitability tovarious niche andcropping systems.The cropisself-pollinatedandfullyself-fertile.Itisasmallherbaceousannualplant growing to a height of 30 to 120 cm with a slight tendency to twining in the upperbranches.Thecentralstemsareerectwhilethesidebr anchesaresemi-erect.Theleavesare5-10cmlong trifoliatewith long petioles.

Both the stems and leaves are covered with short hair. The pods are linear, sometimescurved, round and slender with short pubescence. The seeds are small and nearly globular.The colour of seed is usually green. Mungbean is a short-day, warm- season crop, grownmainly in the semi-arid to sub humid tropics and tropics with 600 to 1000 mm of annualrainfall. It requires 22 to 35 degree celsius mean temperature during crop production andelevations not exceeding 1800 to 2000 m above mean sea level. For a high yield, a warmclimateand deep, welldrainedloam orsandy loam soilsare desired.

The crop is popular because of its suitability for multiple cropping systems. Due to itsshort life cycle of 60-75 days, it fits well into the intensive cropping systems, inter cropping,rotationandmixture.Itisgrownmainlya sakharifseasoncrop.However,withthedevelopm entofearlymaturingvarieties,thereisagreatscope andpossibilityofincreasing area and production of spring and summer mung bean. However, the productivityofmungbeansisstillverylow.

There are three subgroups of *Vigna radiata* one is cultivated (*Vigna radita*genus*Vigna sp*. radiata), and two wilds (*Vigna radita*subsp. Sublobata and *Vigna radiata* subsp.glabara) (**Asari *et al.*, 2019**) The origin of greengram [*Vigna radiata* (L.) Wilczek] is Indiansubcontinent according to **De Candolle (1886), Vavilov (1926) and Zukoveskij (1962)**.Since India has a wide range of genetic diversity of cultivated, as well as of weedy wild typeof greengram, it is considered as the region of its first domestication. It is widely cultivatedthrough the Asia, including India,Pakistan, Bangladesh, Sri Lanka, Thiland, Cambodia,Vietnam,Indonesia,Malaysia and SouthChina.

Sprouts of greengram is equivalent to fresh fruit in respect of nutrient content as itcontains vitamins A, B, C, E and minerals such as iron, calcium, phosphorous. It is rich invitamin B and regarded as a remedy for Beriberi, whereas sprouts contain vitamin C and E.Besides, there is an increase in the thiamine, riboflavin, niacin content as ascorbic acid issynthesizedwithsprouting.Itishighlynutritiveandis consideredahealthyfood,itconstitutes an important place in vegetarian diets. The protein of greengram is rich in lysinewhich is deficient in most of the cereal grain. To improve the protein level and quality ofprotein, the genetics of protein or its constituents may provide useful clues for further desiredimprovement(**Kamble *et al.*, 2017**).

Yieldisacomplextraitanddependson various componentscharacters,whichhaveapositiveandnegative correlationwithyieldandamongthemselves.Itisgovernedbypolygenes,henceknownto be highly influencedby the environment (**Allard, 1960**).

Inanybreedingprogrammeaimedatgeneticamelioration ofyield,geneticdiversityisthebasicrequirement.Effectiveh ybridizationprogramsbetweengeneticallydiverseparents will cause a substantial amount of heterotic response in F1 hybrid and therefore thebroadspectrumofvariabilityinsegregatinggenerations .So,selectionofparentsforhybridization plays an important role in breeding. Evaluation of large number of germplasmsfor genetic diversity is of great importance in selection of parents for hybridization.Afterrealizing the importance of germplasm in the development of desirable varieties, breeders arenow interested in diverse forms from various sources to further improve the yield potential ofthegenotypes.Thequantificationofgeneticdiversitythr oughabiometricalprocedurelikeD^2statistics.

(**Mahalanobis, 1936**) has made it possible to choose genetically diverse parents. Principalcomponent analysis (PCA) is also a powerful tool to measure genetic variability and diversityamonggenotypeswith respectto charactersstudiedtogether.

Keepinginviewtheabove-mentionedfacts,thepresentexperiment"StudyonGenetic Divergence using D^2 analysis in Greengram (*Vigna radiata* (L.) Wilczek)" wascarried outwith thefollowing

OBJECTIVES:

1.Toevaluategeneticvariabilityandheritabilitya monggreengramgenotypes

2. Tostudyaboutgeneticdiversityformorphologica lcharacters

3. Toidentifydivergenceparentforfuturehybridizat ionprogram

MATERIALSANDMETHODS

The investigation on **"Study on Genetic Divergence using D^2 analysis in Green gram(*Vignaradiata*(L.)Wilczek)"** was carried out at Crop Research Farm, Department of Geneticsand Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture,Technology and Sciences, Prayagraj, Uttar Pradesh during *Kharif*, 2022. The spacing adoptedwas 30 x 10 cm. Observations on Days to 50% flowering, Days to 50% pod initiation, Days tomaturity, Plant height (cm),Number of primary branches per plant, Number of clusters perplant, Number of pods per plant, Pod length (cm), Number of seeds per pod, Biological yieldper plant (g), Harvest Index (%), Seed Index (%), Seed yield per plant (g). The experimentalfieldwaslaidoutinRandomizedBlockD esign(RBD).Theexperimentcomprisedof3Replicati onswith53genotypes

Chart1 : List of the genotypes.

S.No.	Genotypes	S.No.	Genotypes	S.No.	Genotypes
1.	MGG-385	19.	SPM-20-47	37.	SML-1638
2.	KM-2	20.	GM-3	38.	TS-16
3.	MGG-295	21.	SM-20-103	39.	LGG-460
4.	ML-131	22.	SM-2029	40.	LGG-407
5.	VBN-3	23.	ML-337	41.	TM-96-2
6.	VEENA	24.	TYPE-51	42.	IPM-2-3
7.	RM-12-13	25.	PHULE MOONG-9339	43.	VIRAT
8.	MGG-347	26.	ML-331	44.	SHIKA
9.	R-288-8	27.	BM-2002-1	45.	MH-421
10.	IPM-2-14	28.	T-44	46.	SAKTHI
11.	WGG-42	29.	PDM-139	47.	AMULYA
12.	MGG-371	30.	SHWETA	48.	PUSABISAKHI
13.	IPM-205-7	31.	SPM-2040	49.	PUSA-105
14.	MGG-351	32.	CO-7	50.	SM-20-108
15.	MGG-348	33.	JALGOON-781	51.	SML-1668
16.	K-851	34.	VBN-2	52.	LGG-450
17.	MGG-2	35.	CO-8	53.	SAMRAT(CHECK)
18.	KM-11-564	36.	PHULEMOONG - 95418		

RESULTSANDDISCUSSIONS:

3.1Analysisofvariance

Analysisofvariancefor thethirteenquantitativetraitshasbeen presentedinTable. Aperusalof

Table 1. revealed that the lines exhibited highly significant differences among thirteen traits *viz*.,days to 50% flowering, days to 50% pod initiation, days to maturity, plant height (cm), numberof primary branches, number of clusters per plant, number of pods per plant, pod length, numberof seeds per pod, biological yield per plant, harvest index, seed index (g), seed yield per plant(g).

3.2. GENETICVARIABILITY

The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation(GCV)fromexperimentweregiven belowinTable2.

1 PhenotypicCoefficientofVariation

TherangeforPhenotypicCoefficientofVariation(PCV)variesfrom25.994%innumberof pods per plant to 3.703 % in the case of days to 50 % pod initiation. The PCV estimates in allthe characters indicated that the phenotypic variability was low (<10%) for days to 50%podinitiation (3.703), days to maturity (4.08), pod length (8.204), number of seeds per

pod (9.208),biological yield (9.697), seed index (8.972) and zyield per plant (8.984).

The phenotypicvariability was moderate (10-20%) in the case of days to 50 % flowering (10.056), Plant height(16.145), number of primary branches per plant (15.468), number of clusters per plant (18.899)and harvest index (12.637). The phenotypic variability was high (>20%) in the case of number ofpodsperplant (25.994).Similarresultsarereporedby**Anonymous(2019)**fornumberofpodsperplant,daystomaturity, biological yield, seed yield per plant , plant height, number of cluster per plant while**Divya Ramakrishnan (2018)**for number of primary branches, days to 50% pod initation,harvestindex, days to 50%flowering,number of primary branches, pod length.

1 GenotypicCoefficientofVariation(GCV)

The range for Genotypic Coefficient of Variation (GCV) varies from 25.019 % in number ofpods per plant to 1.728 % in case of days to 50 % pod initiation. The GCV estimates in all thecharacters indicated that the genotypic variability was low (<10%) for days to 50% pod initiation(9.635), days to 50 % pod initiation (1.728), days to maturity (2.99), pod length (3.289), number ofseeds per pod (5.535), biological yield (5.867), seed index(5.694) and seed yield per plant (5.374).The phenotypic variability was moderate (10-20%) in the case of plant height (14.102), number ofprimarybranchesperplant(14.128), numberofclustersperplant(17.38)andharvestindex(10.281). The phenotypic variability was high (>20%) in the case of number of pods per plant(25.019).

Similar results are repored by **Garje, U. A., (2011)**.days to 50% pod initiation, number ofseed per plant, biological yieldd, pod length,harvesting index, days tomaturity,seed index,numberof cluster per plant

3.3 Heritability

The heritability for all 13 characters were estimated. The heritability in broad sense (h^2) ranged from92.634%inthecaseofnumberofpodsperplantto16.072%inthecaseofpodlength.Themagnitude of heritability was found to be moderate (30-60%) for number of seeds perpod (36.126),biological yield per plant (36.601), seed index (40.278) and seed yield per plant (35.788).Highheritability (>60%) wasfound for daysto 50%flowering(91.803),daystomaturity (53.967), plant height (76.293), number of primary branches per plant (83.427), number of clusters per plant(84.571),numberofpodsper plant (92.634),andharvestindex(66.192).

Similar results are reported by **Degefa, I., Petros, Y.,(2014)** biological yield per plant,days to 50%flowering, plant height, number of pods per plant, seed index,days to maturity, numbers of cluster perplant.

3.4 Geneticadvance

The expected genetic advance for different characters ranged from 16.403% in the case ofplantheight to 0.203% in the case of pod length. Lowest to moderate values of expectedgenetic advance(<20) were found for all the characters; days to 50% flowering (7.151), days to 50% pod initiation(0.923),daystomaturity(3.058),plantheight (16.403),numberofprimarybranchesper plant(1.983), number of clusters per plant (1.872), number of pods per plant (4.003), pod length (0.203),number of seeds per pod (0.42), biological yield per plant (2.376), harvest index (3.435), seed index(0.3)andseed yield per plant (0.423).

Similar results are reported by**Mishra, S. P., (2018)** seed yield per plant, number of primarybranchesperplant,plantheight,harvestindex, while**Ramachandra,P.(2017)**numberofpodsperplan t ,biologicalyield,daystomaturity,podlength.

3.4. D^2AnalysisforGeneticDivergence

Simultaneousvariationinall13charactersof53gree ngramgenotypeswasverified forevaluatingthenatureofgeneticdivergenceamongt hemfollowingMahalanobisD^2statistics.

IntraandInter-clusterdistance

Average intra- and inter-cluster distances (D^2) values among the six clusters were calculated andare presented in Table 1. The lowest intra-cluster distance was associated with cluster I (14.98)followedbyclusterII(21.93)and the highestintra-cluster distance was associated withclusterIV(24.47).ClusterIII,VandVIhadnointra - clusterdistancesincethosethreewererepresentedbya singlegenotypeeach.

From the average inter-cluster distance, it was evident that the most divergent clusters were IIIand VI (279.51) followed by clusters I & VI (176.69), cluster II & III (125.25), cluster V & VI(116.56), and cluster IV & VI (106.19). On the other hand, the least inter-clusters distance wasobservedbetween clustersI&V(32.46)followedby clustersI& III(35.46).

Table1.Analysisofvariancefor13morphologicalcharacters inGreengram

Sl.No.	Source	MeanSumofSquares(MSS)		
		Replication	Treatment	Error
	Degreesoffreedom	2	52	104
1.	Daysto50% flowering	2.717	40.552**	1.172
2.	Daysto50% podinitiation	10.063	6.079**	3.313
3.	Daystomaturity	11.679*	15.848**	3.538
4.	Plantheight(cm)	11.999	275.124**	25.823
5.	Numberof primarybranchesperplant	0.198	3.551**	0.221
6.	Numberofclustersperplant	0.379	3.109**	0.178
7.	Numberofpodsperplant	0.018	12.552**	0.324
8.	Podlength(cm)	0.06	0.497*	0.316
9.	Numberofseedsperpod	0.186	0.548**	0.203
10.	Biologicalyieldperplant(g)	5.357	17.207**	6.298
11.	HarvestIndex(%)	3.183	14.75**	2.146
12.	SeedIndex(%)	0.018	0.236**	0.078
13.	Seedyieldperplant(g)	0.107	0.566**	0.212

Table2.GenotypicParametersfor13QuantitativetraitsinGreengramgenotypes

S.No.	Characters	GCV(%)	PCV(%)	h^2 (Broad Sense)	GeneticAdvance	Gen.Advas%ofMean
1	Daysto50%flowering	9.635	10.056	91.803	7.151	19.017
2	Daysto50%pod initiation	1.728	3.703	21.771	0.923	1.661
3	Daystomaturity	2.99	4.08	53.697	3.058	4.513
4	Plantheight	14.102	16.145	76.293	16.403	25.374
5	Numberofprimarybranchesperplant	14.128	15.468	83.427	1.983	26.583
6	Numberofclustersper plant	17.38	18.899	84.571	1.872	32.925
7	Numberofpodsperplant	25.019	25.994	92.634	4.003	49.604
8	Podlength	3.289	8.204	16.072	0.203	2.716
9	Numberofseedsperpod	5.535	9.208	36.126	0.42	6.853
10	Biologicalyieldperplant	5.867	9.697	36.601	2.376	7.311
11	HarvestIndex	10.281	12.637	66.192	3.435	17.231
12	SeedIndex	5.694	8.972	40.278	0.3	7.444
13	Seedyieldperplant	5.374	8.984	35.788	0.423	6.623

.Table3.Distribution of53GreengramGenotypesintodifferentClustersbasedonD^2Statistic

ClusterGroup	No.ofgenotypes	ListofGenotypes
ClusterI	36	MH-421, PDM-139, SML-1638, PUSA-BAISAKHI, SHWETHA, SHIKHA, MGG-2, PHULE MOONG - 95418,PUSA-105,SAMRAT(CHECK), T-44, MGG-371,BM-2002, LGG-460, VIRAT, SPM-2040,SHAKTI, IPM-2-3,KM-11-564,SM-20-108,AMULYA,KM-2,SM-20-103,JALGAAN-781,K-851,TS-16,MGG-351,MGG-295,VBN-3,MGG-348,CO-7,VBN-2,ML-337,CO-8,VEENA&MGG-385
ClusterII	9	MGG-347,SM-2029,SPM-20-47,R-288-8,LGG-450,SMl-1668,RM-12-11,WGG-42&GM-3
ClusterIII	1	ML-131
ClusterIV	5	LGG-407,PHULEMOONG-9339,TYPE-51,TM-96-2&ML-331
ClusterV	1	IPM-2-14
ClusterVI	1	IPM-205-7

Table4..InterandIntraclusterdistanceof53GenotypesofGreengram

ClusterDistances						
	ClusterI	**ClusterII**	**ClusterIII**	**ClusterIV**	**ClusterV**	**ClusterVI**
ClusterI	**14.98**	58.33	35.46	71.59	32.46*	176.69
ClusterII		**21.93**	125.25	64.05	51.21	66.26
ClusterIII			**0.00**	90.14	69.21	279.51**
ClusterIV				**24.47**	70.04	106.19
ClusterV					**0.00**	116.56
ClusterVI						**0.00**

Fig.1:DiagramshowingtheMahalanobisEuclideandistance

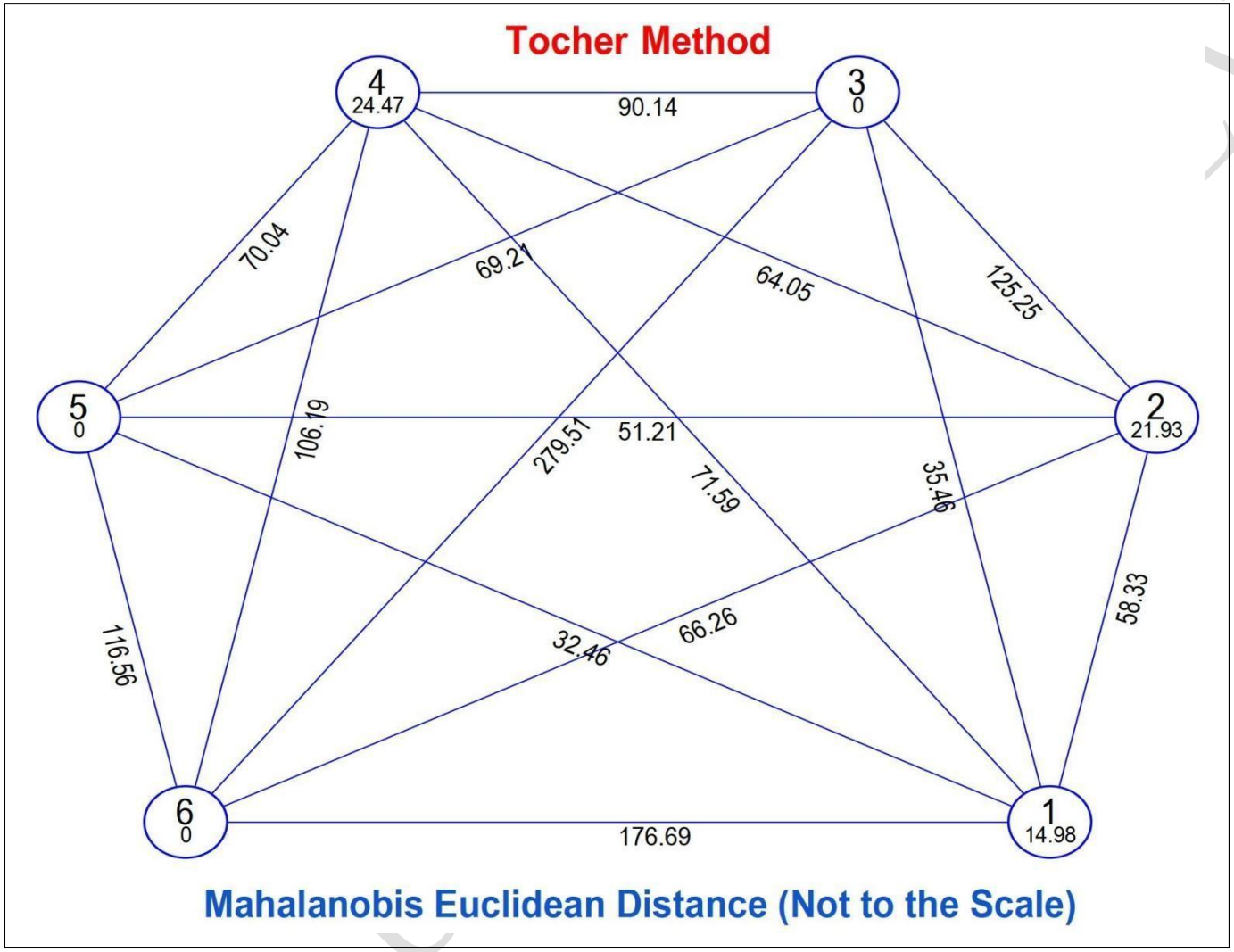

Table5.ClusterMeanof13BiometricalTraitsof53GreengramGenotypes

ClusterMeans:Tocher'sMethod													
	Days to50 % flowering	**Daysto50%podi nitiation**	**Days tomaturi ty**	**Plant height**	**Number ofprimary branchesp erplant**	**Number ofclusters perplant**	**Number ofpods perplant**	**Podl ength**	**Number ofseeds perpod**	**Biological yield perplant**	**Harvest Index**	**Seed Index**	**Seedyieldper plant**
Cluster I	36.00	55.72	68.01	62.27	7.09	5.35	7.28	7.38	5.97	32.40	19.90	4.05	6.36
ClusterII	38.37	54.74	66.19	60.88	8.76	6.82	11.34	7.51	6.47	33.09	19.04	3.97	6.20
ClusterIII	40.00	56.00	68.33	62.03	6.33	3.87	4.40	8.51	6.28	26.48	24.57	3.85	6.31
ClusterIV	46.60	56.00	68.73	82.92	6.99	5.58	8.08	7.85	6.47	33.10	20.36	4.08	6.73
ClusterV	36.67	58.67	70.67	70.60	9.33	6.93	6.34	7.48	6.39	33.18	21.87	3.75	7.26
ClusterVI	42.00	52.33	64.33	89.30	10.40	8.73	12.53	7.65	6.39	33.34	20.80	3.84	6.76

CONCLUSION

Onthebasisoffindinggeneratedfromthepresentinvestigation,followingconclusionscanbedrawn, which may be considered for improvement in greengram crop in future breedingprogrammes.The wide range of genetic variability observed for most of the characters asevidenced by significant variances due to genotypes signifying that, it could be helpful inselection of better germplasm. The phenotypic coefficients of variation were slightly higherthan genotypic coefficients of variation which suggest the role of environment in governingthese traits. Similarly, the magnitude of GCV andPCV was observed high for the charactersviz.,numberofpodsperplantandnumber ofclustersperplant.The genetic diversity assessedusing Mahalanobis's D^2 statistics among 53 greengram genotypes, which were grouped intosix clusters. From the studies of percent contribution of thirteen characters towards totaldivergence, it can be concluded that, seed yield per plant contributed highest for divergencefollowed by number of pods per plant, number of clusters per plant, number of seeds per pod,biological yield, number of primary branches per plant, pod length, harvest index, days tomaturity,seedindex,plantheight,daysto50%pod initiationanddasyto50%flowering.Theobjective of identifying divergence parents can be concluded by considering the genotypes ofcluster III andclusterVIforfurtherstudies.

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