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GENETIC DIVERGENCE OF GREEN GRAM [*VIGNA RADIATA* (L.) WILCZEK] GROWN IN COASTAL SALINE LOW LAND OF TAMIL NADU, INDIA

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Abstract

An investigation is carried out with twenty green gram genotypes to study the nature and magnitude of genetic divergence using D^2 statistics. Ten yield traits were recorded on the genotypes raised in RBD design with two replications. The twenty genotypes were grouped into seven clusters based on hierarchical cluster analysis with cluster I containing the maximum of nine genotypes. The maximum Intra cluster distance was observed in cluster I (16.62) and minimum of 0.00 in cluster VI and VII respectively. The maximum inter cluster distance was between clusters III and cluster VII (118.43) followed by cluster II and cluster IV (112.07) indicating wide genetic diversity and it may be used in hybridisation programme for improving yield. The characters like days to first flowering, plant height, number of seeds per pod and number of pods per plant had contributed 77.32 per cent of total divergence. So direct selection of these characters is made among the concerned genotypes.

Key words : D^2 analysis, inter and intra cluster distance, character contribution.

Introduction

Pulses are extensively grown in tropical region of the world as a major protein rich crop bringing considerable improvement in human diet. The green gram (*Vigna radiata*) is one of the important pulse crops because of its adaptation to short growth duration, low water requirement and soil fertility and is favoured for consumption due to its easy digestibility and low production of flatulence. It is said to have originated in India where it is widely cultivated and a highly esteemed grain legume (Chatterjee and Battacharya, 1986). Average protein content in seeds is 24 per cent and is rich in lysine and amino acid predominantly deficient in cereal grains.

Genetic variability is the important food in the hands of plant breeder in choosing the elite type of parents for hybridization programme. The divergence can be studied by using D^2 statistics developed by Mahalanobis (1936). It is based on multivariate analysis and grouped into various clusters as given by Spark (1973). This is considered as the most effective method for qualifying degree of genetic diversity among different genotypes. The present investigation is about estimation of magnitude of genetic divergence of twenty green gram genotypes and to identify diverse genotypes for the future study.

Materials and Methods

Twenty green gram genotypes collected from different places were sown at Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar (T.N.), India; in a randomised block design with two replications each with spacing of 45×10cm. The observations were recorded on single plant basis in five randomly selected plants of each genotype for days to first flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, pod length, hundred seed weight and seed yield per plant. The analysis of genetic divergence was done using Mahalonobis (1936) D^2 statistics. The genotypes were grouped into different clusters, inter and intra cluster distances and mean performances for characters were also computed.

Result and Discussion

The analysis of variance gives the significant differences among the genotypes for all the characters (table 1). Mahalanobis D^2 statistic is a potential tool for estimating genetic diversity, as has been emphasised by many workers (Tawar *et al*., 1988; Raje and Rao, 2000; Manivannan, 2002; Patel *et al*., 2003; Venkatesan *et al*., 2003). Based on the D^2 values, twenty genotypes were grouped into seven clusters using the hierarchical cluster analysis. The genotypes in each cluster are closer than genotypes in different cluster.

Cluster I comprised of largest number with nine genotypes followed by cluster IV with three genotypes. Cluster II, III and V comprised of two genotypes each followed by clusters VI and VII were solitary clusters. The clustering pattern indicated that there is no parallelism between genetic and geographical diversity (Manikannan *et al*., 2000; Suganthi, 2000; Manivannan, 2002; Kumar

Table 1 : Analysis of variance of twenty green gram genotypes for ten characters.

Source	df	MSS									
		Days to first flowering	Plant height	No. of branches /plant	No. of clusters /plant	No. of pods per cluster	No. of pods/ plant	No. of seeds/ pod	Pod length	100 seed weight	Seed yield / plant
Replication	1	0.16	0.29	0.13	0.58	0.73	1.02	0.02	0.01	0.03	12.39
Genotypes	19	14.29**	99.30**	1.51**	3.45**	2.32**	15.22**	5.87**	5.29**	3.14**	9.28**
Error	19	0.54	3.99	0.05	0.24	0.37	1.87	0.06	0.03	0.02	1.54

** Significant at 1% level.

Table 2 : Mean performance of twenty green gram genotypes for ten characters.

Genotypes	Days to first flowering (days)	Plant height (cm)	No. of branches /plant	No. of clusters /plant	No. of pods per cluster	No. of pods/ plant	No. of seeds per pod	Pod length (cm)	100 seeds weight (g)	Seed yield per plant(g)
VGG4	35.84	55.37	2.35	5.70	3.10	18.35	10.30	7.58	2.82	5.47
GPLM 163	36.29	45.85	2.15	6.25	3.65	18.55	8.55	7.64	2.93	7.16
EC 16708	35.69	47.50	2.50	5.65	2.72	20.30	9.35	7.60	3.10	7.16
VRM GG Local	32.14**	55.37	4.20**	6.60	5.50*	29.10**	13.70**	8.72**	5.75**	9.49
PDM 89-226	34.57	29.30**	1.25	4.15	2.65	19.20	12.10*	7.28	3.22	4.72
WGG 42	33.03*	47.75	2.55	6.25	4.45	20.60	10.25	7.32	3.22	6.17
VBN 1	30.04**	33.76**	3.80**	7.70**	5.85*	22.80	14.60**	11.60**	7.30**	12.38**
PLM 696	36.80	4625	1.50	5.10	4.50	21.35	11.05	8.05*	2.89	6.13
CO – 4	34.80	48.12	1.70	6.20	4.35	17.50	10.40	5.17	2.80	6.25
CDM Local	42.36	36.37**	3.45**	6.50	5.40	21.90	11.20	7.20	2.65	1.70
LGG450	33.01*	50.85	3.10*	6.65	3.45	18.35	11.60	8.72**	3.80	8.10
WGG 17	35.30	50.35	2.90	6.30	5.75	19.35	10.30	4.11	3.20	6.56
VRMGG 1	30.54	55.12	4.35**	8.40**	3.90	24.45**	14.50**	11.19**	5.85**	11.53**
EC 314292	34.60	45.10	1.85	6.55	4.35	17.80	11.60	7.39	3.30	7.55
WGG 48	33.67	48.41	2.55	6.25	3.50	20.15	10.35	7.30	3.20	7.35
GPLM 136	35.06	48.80	2.45	6.30	5.15	21.70	10.45	7.25	3.50	7.10
EC 30072	33.02*	53.25	3.35**	7.56**	2.30	20.35	13.30**	8.00	3.95*	8.71
ADT 3	37.80	53.37	2.70	3.35	2.30	17.75	10.55	7.13	3.15	6.15
VGG7	36.35	51.50	2.45	6.35	1.50	19.00	13.05**	7.64	2.75	4.40
KM 2	34.95	48.72	1.60	3.10	4.65	22.35	13.45**	7.15	2.43	4.60
General mean	34.79	47.55	2.63	6.04	4.26	20.55	11.53	7.69	3.59	7.06
CD(p=0.05)	1.48	4.01	0.46	0.99	1.22	2.75	0.50	0.36	0.30	2.49
CD(p=0.01)	2.10	5.94	0.64	1.42	1.74	3.88	0.69	0.49	0.40	3.52

* Significant at 5% level, ** Significant at 1% level.

Table 3 : Composition of D^2 clusters for twenty green gram genotypes.

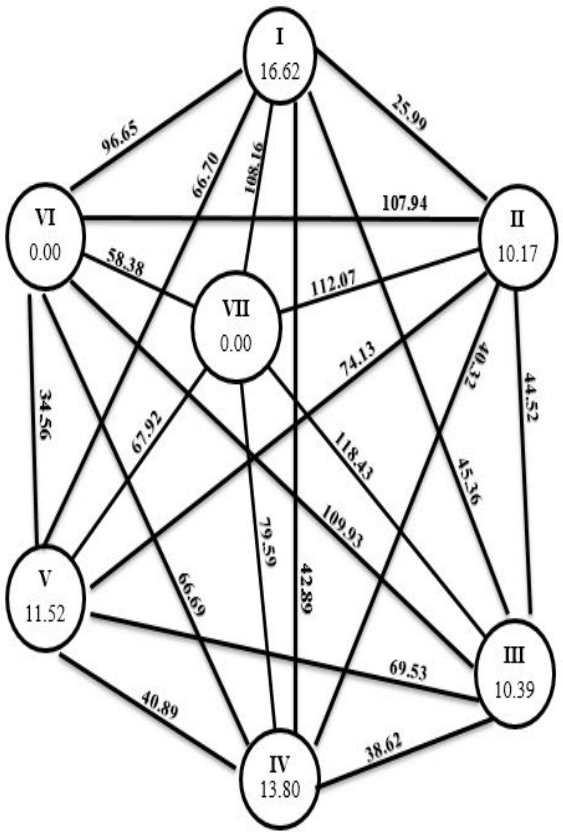
Clus-ters	Number of genotypes	Name of the genotypes
I	9	WGG 48, GPLM 139, VGG 4, EC 16708, IGG 450, KM 2, EC 30072, ADT 3, GPM 163
II	2	CO – 4, WGG 17
III	2	VRMGG Local, VRMGG 1
IV	3	VGG 7, EC 314292, PDM 89 – 226
V	2	WGG 42, PLM 696
VI	1	CDM Local
VII	1	VBN 1

et al., 2002; Patel, 2003; Haritha and Sekar, 2003).

The average inter and intra cluster distance have been shown in the table 4. The intra cluster distance varied from 0.00 (cluster VI and VII) to 16.62 (cluster I). Inter cluster distance was minimum between cluster I and II (25.99) followed by clusters V and VI (34.56) suggesting closer relationship. Maximum inter distance existed between cluster III and VII (118.43) followed by clusters II and VII (112.07). This indicated that genotypes included in these clusters are having broad spectrum of genetic diversity. The genotypes of clusters III and VII selected as parents for breeding programmes (Kumar *et al*., 2002; Venkatesan *et al*., 2003).

Table 4 : Average intra and inter cluster D^2 and D values for twenty green gram genotypes.

Cluster	I	II	III	IV	V	VI	VII
I	**276.33(16.62)**	675.39(25.99)	2057.41(45.36)	1840.21(42.89)	4449.16(66.70)	9341.42(96.65)	11698.99(108.16)
II		**103.49(10.17)**	198.15(44.52)	1626.10(40.32)	5495.83(74.13)	11651.13(107.94)	12560.71(112.07)
III			**107.51(10.39)**	1491.24(38.62)	4834.65(69.53)	12084.87(109.93)	14025.96(118.43)
IV				**190.45(13.80)**	1672.19(40.89)	4447.74(66.69)	6336.01(79.59)
V					**132.78(11.52)**	1194.37(34.56)	4613.33(67.92)
VI						**0.00(0.00)**	3408.71(58.38)
VII							**0.00(0.00)**



Cluster diagram.

A wide range of variation was observed in cluster means for all the ten characters studied (table 5) (Manivannan, 2002; Haritha and Sekar, 2003). The cluster VII showed high mean values for seed yield per plant followed by cluster III, for the characters like plant height, number of branches per plant, number of cluster per plant, number of pods per cluster, number of pods per plant, cluster III showed highest mean value and while cluster VII registered maximum mean value for number of seeds per plant and pod length. The minimum mean value for days to first flowering was observed in cluster VII, which may be suitable source for earliness.

The results indicated that among twenty genotypes studied VBN 1 and VRMGG 1 showed better performance for seed yield per and hundred seed weight, number of pods per cluster and pod length. The genotype VRMGG Local showed better performance for plant height and number of pods per plant.

The contribution of individual traits to the divergence among genotypes is presented in table 6. The trait plant height contributed maximum towards divergence (30.88 per cent) followed by days to first flowering (23.85 percent) and number of pods per plant (14.31 per cent) and number of seeds per pod (8.08 per cent). The characters, pod length, seed yield per plant, number of

Table 5 : Cluster means of twenty green gram genotypes for ten characters.

Characters / Cluster	Days to first flowering	Plant height (cm)	No. of branches per plant	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 seed weight (g)	Seed yield per plant(g)
I	35.04	50.42	2.64	5.96	3.81	19.30	10.10	7.65	3.30	7.24
II	35.05	49.23	2.30	6.25	3.90	18.42	10.35	4.64	3.00	6.40
III	31.34	55.24	4.27	8.05	5.67	26.77	13.70	8.28	5.80	10.12
IV	35.11	43.65	1.78	5.02	3.92	20.48	12.45	7.36	2.92	5.21
V	34.91	47.00	2.02	5.67	4.47	20.97	10.65	7.32	3.05	6.15
VI	42.36	36.37	3.45	6.50	5.40	21.90	11.20	7.20	2.65	4.70
VII	30.04	33.76	3.80	6.60	5.50	20.35	13.90	11.39	7.30	12.38

Table 6 : Percentage contribution of characters of genetic diversity.

S. no.	Characters	Values (%)
1.	Days to first flowering	23.85
2.	Plant height	30.88
3.	Number of branches per plant	1.98
4.	Number of clusters per plant	4.31
5.	Number of pods per cluster	3.21
6.	Number of pods per plant	14.01
7.	Number of seeds per pod	8.08
8.	Pod length	5.27
9.	100 seed weight	2.73
10.	Seed yield per plant	5.13

clusters per plant, number of pods per cluster, hundred seed weight and number of branches per plant contributed little bit to divergence, so it is considered less importance. Since varieties with narrow genetic base are more prone to diseases and adverse climatic changes, availability of genetically diverse genotypes for hybridization programme become more important. Since plant height and days to first flowering contributed maximum towards divergence, we go for direct selection for this traits for diversity purpose.

References

Chatterjee, B. N. and K. K. Bhattacharya (1986). Principles and practices of grain legume production. *Oxford and IBH Publ. Co*., New Delhi, pp: 434.

Haritha, S. and M. R. Sekar (2003). Comparison of cluster formation by Mahalanobis' D^2 and Meteroglyph analyses in mung bean [*Vigna radiata* (L.) Wilczek]. *Legume Res*., **26(2)** : 100-104.

Kumar, R., A. Singh, A. S. Rathi and R. Krishna (2002). Genetic divergence in relation to breeding for grain yield in urdbean (*Vigna mungo* L.Hepper). *Legume Res*., **25(2)** : 109- 112.

Mahalanobis, P. C. (1936). On the Generalized distance in Statistics. *Proc. Nat. Sci., India*, **2** : 49-55.

Manikannan, C., S. Jebaraj and S. Ashok (2000). Genetic divergence in urdbean [*Vigna mungo* (L.) Hepper]. *Madras Agric. J.*, **87(7-9)** : 520 – 523.

Manivannan, N. (2002). Genetic diversity in cross derivatives of greengram [*Vigna radiata* (L.) Wilczek]. *Legume Res*., **25(1)** : 50-52.

Patel, B. L., V. S. Hedge and P. M. Salimath (2003). Studies on genetic divergence over stress and non – stress environment in mungbean [*Vigna radiata* (L.)Wilczek]. *Indian J. Genet. Plant Breed*., **63(1)** : 77-78.

Raje, R. S. and S. K. Rao (2000). Multivariate linear regression analysis of yield and its components in mungbean (*Vigna radiata* L.Wilczek). *Legume Res*., **23(4)** : 268-270, 2000.

Spark, D. N. (1973). Euclidean cluster analysis. *Algorithm. As 58 App. Stat*., **22** : 126-130.

Suganthi, S. (2000). Studies on genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp]. *M.Sc. (Ag). Thesis*, Annamalai University, Tamil Nadu.

Tawar, M. L., A. K. Mishra, S. K. Rao and S. M. (1988). Genetic divergence environments in greengram. *Legume Res*., **11** : 109 – 115.

Venkatesan, M., M. Prakash and J. Ganesan (2003). Genetic divergence in blackgram [*Vigna mungo* (L.) Hepper]. *Legume Res*., **26(4)** : 268- 271.