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Genetic Diversity for Quantitative Characters in Green Gram (*Vigna Radiata* (L.) *Wilczek*)

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A wide genetic variability among the types was revealed by the D^2 analysis and the canonical analysis wherein the forty five types formed as many as sixteen clusters. The types chosen from the same eco-geographic regions were found scattered in different clusters. The clustering together of types from same eco-geographic region into one cluster was also observed. Based on average inter-cluster distances, the clusters XV, XVI and XIII were found to be highly divergent from all the other clusters. Among them, the D^2 distance between Mutant 5 and AC. 263 was the maximum. The mutants namely Mutant. 1, Mutant 3 and Mutant. 5 which have the common parent (CO1) were distributed in three seperate clusters. in the selected materials yield/plant contributed maximum towards the genetic divergence.

The plant breeder is always interested tknow to he genetic divergence among the types or varieties available due to reasons that crosses between genetically diverse plants are likely to produce high heterotic effect (Ramanujam *et al*, 1974) and the crosses involving distantly related parents within the same species produce a wide spectrum of variability. The Mahalanobis D^2 statistic has found faavour as a tool for estimating such genetic divergence in the base population for use in the plant breeding. In this present study Mahalanobis D^2 analysis and canonical analysis were used to find out the genetic distance between forty five green gram types and also to identify the promising types among them.

MATERIAL AND METHODS

Materials for the present study consisted of forty five types of green gram of diverse origin. Selfed seeds of green gram types were sown in randomised block design with three replications in the Agricultural College and Research Institute, Coimbatore during the month of March, 1980. Each type was raised in 4 metres long row adopting a spacing of 45x10 cs. During the harvesting stage, observations were made on the height of the plant number of branches, number of clusters. pods/cluster, pod length, pod width, seeds/pod, single plant yield and 100 seed weight from ten randomly selected plants in each type in each replications. Mahalanobis D^2 analysis was used for estimating the genetic divergence among the types. The method suggested by Rao (1952) was followed for computing D^2 values and also for detertmining the group constellations. The canonical analysis as suggested by Arunachalam and Ram (1967) was also used for estimating the genetic divergence.

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RESULTS AND DISCUSSION

Significant differences were observed among the types for all the nine characters indicating the presence of high variability among the materials. By the application of clustering technqiue, the forty five genotypes were grouped into sixteen different clusters (Table 1). This did not conform to the groupings based on the geographic origin.

Among the clusters, cluster VII was the largest with eight types followed by cluster VI, while the cluster XIV, XV and XVI consisted of only one Type. the cluster XII contained the types from the Tamil Nadu regions showing the similar genetic architecture among the types of these clusters. Such a parallelism was also reported by Dhawan and Singh (1961) in maize, Singh and Joshi (1966) in linseed Nagesha (1976) in rice and Singh and Singh (1976) in chilli. Each of the other clusters contained types from different geographical regions. The clustering pattern thus failed to indicate any relationship between geographic divergence and genetic divergence. This is in consonance with the findings of Murthy and Anand (1966) in linseed, Gupta and Singh (1970). in green gram, Verma (1970) in soy bean, Mehndiratta and Singh (1971) in cowpea, Shwe *et al.* (1972) in Soybean and groundnuta, Malhotra *et al.* (1974) in green gram. Chaùdhary *et al.* (1975) in cluster bean, Paramasivam (1979) and Boomikumar (1980) in green gram.

Another feature which come to light was, the types from Tamil Nadu were distributed in different clusters indicating the presence of wide genetic variability in the material chosen from the same region. This may be due to the wide soil and climatic difference in the region. In the same way, Mutant 1, Mutant 3 and Mutant 5 which have the common parent (CO1) were distributed in three separate clusters namely XII, VIII and XVI and the inter-cluster D^2 distances were also moderately high This indicated that the mutations have got a very good effect in creating variability which result in genetically divergent mutants. The intra-cluster D^2 ranged from 2.24 to 14.79 (Table 2). The lowest intra-culster distance was shown by the clusters V and VI indicating the strains of these clusters resemble one another genetically and appeared to have evolved from the common gene pool.

Based on the inter-culster D^2 distance, the clusters XV, XVI and XIII were found to be highly divergent from all the other clusters. Among them, the inter-cluster distance between XV and XVI was the maximum followed by the distance between XII and XVI. All the types of these clusters belong to the Tamil Nadu region. The types in these clusters may serve as potential parents and the crossing between the types of these clusters may result in high heterosis for both the qualitative and the quantitative characters. Heterosis can also be exploited by using the genetic diversity of the germ

plasm (Wilcox and Wilsie, 1964 and Ramanujam *et al.*, 1974)

In the canonical analysis the first two canonical roots together accounted for 76.6% of the total variability. Hence, the two dimentional representation of the relative position of the types was found adequate and it again conform the clustering pattern of the D^2 analysis. In the present materials yield/plant contributed the maximum towards the genetic divergence followed by number of clusters and pods/cluster. (Table 3)

The present study thus indicated that the geographical diversity need not necessarily be related to genetic divergence. The desirable diverse plants need not be selected for hybridisation from distant geographical regions. Locally adopted diverse plants may as well be exploited furitfully.

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TABLE 1 COMPOSITION OF D^2 CLUSTERS

Cluster	No. of types	Designation and origin
I	3	LM58(p), LM251(P), AC266 (M)
II	4	PS10(D), LM220(P), LM294(D), NP36(D)
III	3	LM197(P), LM205(P), PLS308(P)
IV	2	LM215(P), CO2(C)
V	2	PLS291(P), PLS318/2 P)
VI	5	LM314(P), LM360(P), LM388(P), 1781/3(A), PLS41 (P_e)
VII	8	LM66(P), LM197(P), LM220(P), LM304(P), AC42(M), PLS271(P), PLS308(P) 1725/1-1 (A)
VIII	2	LM85(P), Mutant3 (C)
IX	4	LM25(P), LM105(P), LM229(P), L306(P)
X	3	MS9723(C), LM391(P), 1790/4(A)
XI	2	PLS267/2(P), LM406(P)
XII	2	Mutant 1 (C), MS8909 (C)
XIII	2	MS9331(C), LM275(P)
XIV	1	MS9724(B)
XV	1	Mutant 5 (C)
XVI	1	AC263 (M)

P = Punjab; M = Madurai; D = Delhi; C = Coimbatore

A = Annamalai University

P_e = Periyanaickenpalayam

B = Bihar

TABLE 2. Inter and intra cluster D^2 and D (within parenthesis value)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	35.0 (5.9)	219 5 (14.8)	73.3 (8,6)	455.9 (21.4)	859.5 (29.3)	305.7 (17.5)	399.3 (20.0)	1385.6 (37.2)	729.5 (27.0)	518 4 (22.8)	85.1 (9.2)	1368.0 (37.0)	2267 5 (47.6)	1193.0 (34.5)	1905 0 (43.6)	1212.5 (34.8
II		35.6 (6.0)	189.1 (13,8)	654.2 (25.8)	412.2 (20.3)	457.8 (21.4)	595.7 (24.4)	733.4 (27.1)	745.1 (27.3)	791.6 (28.1)	277.0 (16.6)	1497.1 (38.7)	1621.1 (40.3)	1263.3 (35.5)	3403.1 (58.3)	1215.0 (34 9)
III			8.02 (2.8)	290.3 (17.0)	1022.5 (32.0)	111.6 (10 6)	576.5 (24.0)	1275 3 (35.7)	911.1 (30.2)	312.8 (17.7)	34 4 (5.9)	1334.7 (36.5)	1518.6 (39.0)	1184 9 (34.4)	1703.2 (41.3)	1812 2 (42.6)
IV				5 0 (2.2)	1998.1 (44.7)	149.4 (12.2)	479.2 (21.9)	1594.4 (39.9)	626.1 (25.0)	321.4 (17.9)	260.9 (16.2)	361.7 (19.0)	1057.2 (32.5)	609.2 (24 7)	1307 4 (36.2)	3673.5 (60.6)
V					5.21 (2.3)	1751.1 (41.8)	1494.4 (38.6)	291.4 (17.1)	761.9 (27.6)	1887.2 (43.4)	1147.4 (33.9)	4510.6 (67.2)	2965.9 (54.5)	2690.5 (51.9)	5743.2 (75.8)	234.4 (15.3)
VI						53.11 (7.3)	737 1 (27.2)	2184.4 (46.7)	851 4 (29.2)	506.7 (22.5)	187.2 (13.7)	687.4 (26.2)	1387.3 (37.2)	998.7 (31.6)	966.4 (31.1)	2664.9 (51.6)
VII							93.9 (9.7)	797.6 (28 2)	948.6 (30.8)	491.4 (22.2)	457 6 (21.4)	1585.2 (39.8)	1960.0 (44.3)	434 8 (20.9)	2720.5 (52.2)	3102.9 (55.7)
VIII								18.6 (4.3)	603.6 (24.6)	1156.8 (34.0)	1599.7 (40.0)	3282.4 (57.3)	1672.5 (40.9)	838 8 (28.9)	3832.8 (61.9)	1939 3 (44.0)
IX									75.5 (8.7)	1244 3 (35.3)	442.0 (21.0)	1943.9 (44.1)	813.8 (28.5)	855 8 (29.3)	4934.4 (70.2)	2098.3 (45.8)
X										65.5 (8 1)	524.9 (22 9)	765.1 (27.7)	1926.8 (43,9)	837.3 (28,9)	768.1 (27.7)	3183.9 (56 4)
XI											39.6 (6 3)	1304 7 (36 1)	1304.7 (36.1)	631 8 (25 1)	1812 8 (42 6)	1723.6 (41.5)
XII												69 3 (8.3)	2016.1 (44 9)	1291 0 (35 9)	173.2 (13 2)	6493.1) (80,6)
XIII													218.80 (14.8)	5243 7 (72.4)	5477 6 (74.0)	1183.5 (34.4)
XIV														—	4072.3 (63.8)	6125.4 (78 3)
XV															—	7261.7 (85.2)
XVI																—

Table 3 Co-efficients of first two canonical vectors in 45 types of greengram

Characters	Canonical vectors Z1	Z2
Days to first bloom	.0450	—.0465
Plant height	.0177	—.0031
Number of branches	.1280	—.0387
Pod length	.1001	.0302
Pod width	—.0139	.1715
Seeds/pod	—.0064	.1578
Number of clusters	.7782	—.5246
Pods/clusters	.2846	—.0492
100 seed weight	.0300	.1637
yield/plant	.5324	.7979