



Multivariate Analyses and Genetic Divergence in Pigeonpea (*Cajanus Cajan* (L.) Millsp.).

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ABSTRACT

Forty one genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp.] collected from different research centres across the country were subjected to Mahalanobis' D^2 Statistic, cluster analysis and principal component analyses based on 13 traits. Considerable genetic divergence among the 41 genotypes resulted into six clusters as per D^2 analysis and seven clusters in the case of cluster analysis. The grouping of genotypes into clusters was at random which suggested that geographical isolation might not be the only factor causing genetic diversity. Out of thirteen characters studied, number of pods per plant contributed maximum towards divergence followed by grain protein content. Principal component analysis identified four principal components (PCs) which explained 77.65% of the variability. The genotypes SM 13, SM 114, Perennial 1 and TT 02 showed maximum inter-cluster distance and wide genetic distance with each other in all the three divergence methods. So they can be exploited in hybridization programme for identification of desirable segregants.

Key words : Cluster analysis, D^2 analysis, Pigeonpea, Principal Component Analysis.

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is second most important pulse crop after chickpea. Though 80 per cent of our pigeonpea requirement is normally met from domestic production, 20 per cent has to be imported. In order to reduce imports and to save foreign exchange, our production has to be increased to meet our total requirement for which yield enhancement is essential. Understanding genetic divergence in available germplasm is pre-requisite to plan crossing programme. Traditionally, Tocher's method, Ward's minimum variance method and Principal component analyses are being followed for estimating genetic divergence (Rao, *et al.*, 2010). Hence the present investigation was taken up with the objective to estimate genetic divergence in the available germplasm.

MATERIAL AND METHODS

Forty one genotypes of pigeonpea were sown in randomized block design with three replications at the Regional Agricultural Research Station, Lam, Guntur, during *kharif*, 2010-11. Each genotype was represented by six rows of four meter length in each replication with a spacing of 90 cm between rows and 20 cm within row. Crop

was managed as per recommendations. Observations were recorded on ten randomly selected plants without border effect of each genotype in each replication and the average values were subjected for statistical analysis except for days to 50% flowering, days to maturity, 100 seed weight and protein content which were recorded on plot basis. Observations on 13 characters, *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, shelling percentage (%), 100 seed weight (g), seed yield per plant (g), grain protein content (%) and harvest index were subjected to multivariate analyses following the procedures adopted by Rao, *et al.* (2010).

RESULTS AND DISCUSSION

The per cent contribution towards genetic divergence by all the 13 contributing characters is given in Table 1. The maximum contribution towards genetic divergence is by number of pods per plant (60.73%) followed by grain protein content (20.73%) indicating possibility of genetic improvement of these characters in the genotypes studied.

Table1. Contribution of different characters towards genetic divergence in Pigeonpea [*Cajanus cajan* (L.) Millsp.].

S. No.	Character	Contribution towards divergence (%)	Times ranked first
1	Days to 50% flowering	4.02	33
2	Days of maturity	0.12	1
3	Plant height (cm)	4.51	37
4	Primary branches/ plant	2.32	19
5	Secondary branches/plant	1.83	15
6	Pods/ plant	60.73	498
7	Pod length (cm)	0.12	1
8	Seeds/pod	0.00	0
9	Shelling percentage	0.00	0
10	100 seed weight (g)	1.10	9
11	Harvest index	1.46	12
12	Grain protein content (%)	20.73	170
13	Seed yield per plant (g)	3.05	25

Table 2. Clustering pattern of 41 pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes by Tocher's method and Ward's minimum variance method.

Cluster No.	By Tocher's method		Ward's minimum variance method	
	No. of genotypes	Name of the genotypes	No. of genotypes	Name of the genotypes
I	12	JSMP 8, SM 54, SM 12, MAC 19, CORG 9701, SM 5, SM 108, SM8-1, SM 20, CHILKA 1, SM 67 and BWR 376.	9	BSMR 737, SM 30, SM 118, ICPL 13082, ICPL 96058, SM 97, LOCAL 2002-3, LRG 30 and LOCAL 2003-1
II	10	MRG 66, SM 8, LRG 38, ICPL 13082, ICPL 96058, SM 97, SM 118, WRG 17, WRP1- 2 and SM 146	6	GM 1, WRG 53, JSA 72-3, WRG 150, SM 1 and TT02.
III	2	SM 114 and TAT 96 - 29.	3	JKM 144, PERENNIAL 1 and MAHANANDI 2
IV	14	JKM 144, PERENNIAL 1, MAHANANDI 2, LOCAL 2003-1, LOCAL 2002-3, LRG 30, JSA 72-3, SM 1, WRG 53, GM 1, WRG 150, SM 30, TT 02 and BSMR 737.	12	BWR 376, SM 20, CHILKA 1, SM 67, SM 8-1, JSMP 8, SM 54, MAC 19, SM 12, CORG 9701, SM 108 and SM 5
V	1	SM 7	5	MRG 66, SM 8, LRG 38, SM 146 and WRP 1 -2
VI	2	SM 13 and WRG 47	4	SM 114, TAT 96 - 29, SM 7 and WRG 17
VII	-	-	2	SM 13 and WRG 47

Table 3. Average intra and inter cluster distance (D^2) values of six clusters and Euclidian² values of seven clusters (Wards values) in pigeonpea {*Cajanus cajan* (L.) Millsp.}

Cluster No.	I	II	III	IV	V	VI	VII
I	40.646	98.998	76.789	294.582	90.674	175.171	-
II	(169.353)	(225.543)	(414.637)	(536.795)	(262.368)	(398.235)	(1707.959)
III		54.500	90.099	135.299	104.719	396.575	-
IV		(109.140)	(310.863)	(799.583)	(457.261)	(548.746)	(2061.450)
V			18.907	250.128	92.042	237.595	-
VI			(67.408)	(1445.723)	(827.627)	(1135.679)	(525.533)
VII				73.002	221.647	758.408	-
				(121.939)	(219.518)	(252.992)	(3278.342)
					0	290.869	-
					(125.906)	(267.000)	(1040.007)
						57.380	-
						(168.836)	(818.620)
							-
							(172.145)

Note : Values in parenthesis indicate Ward's values

All genotypes were grouped into six clusters using the Tocher's method and seven clusters by Wards minimum variance method (Table 2). Cluster IV in the groups by Tocher's method got maximum number of genotypes (14) followed by clusters I (12), II (10), III & VI (2) and minimum genotypes (one) for cluster V (Fig. 1). In the case of the groups by Wards minimum variance method Cluster IV got maximum genotypes (12) followed by I (9), II (6), V (5), VI (4), III (3) and VII (2) (Fig. 2). The distribution of genotypes indicated that the geographical diversity based on agro climatic conditions and genetic diversity were not related and there are forces other than geographical separation which are responsible for diversity such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation. Similar results were reported by Ganesamurthy and Stephendorairaj (1990), Viramgama and Goyal (1994), Basavarajaiah *et al.* (1998), Kumar *et al.* (2005), Magar *et al.* (2008) and Rao *et al.*, (2010).

The average intra- and inter- cluster D^2 values and Euclidean² values by Wards minimum variance method are presented in Table 3. Intra-cluster D^2 values ranged from zero (cluster V) to 73 (cluster IV) while the inter-cluster D^2

values ranged from 76.79 (cluster I and III) to 758.41 (cluster IV and VI). Of the 7 clusters formed Wards minimum variance method, cluster III had minimum intra cluster Euclidean² distance value of 67.41 followed by cluster II (109.14), cluster IV (121.94), cluster V (125.91), cluster VI (168.84), cluster I (169.35) and cluster VII (172.15). The inter cluster Euclidean² distances (Fig. 3) varied from 219.52 (between cluster IV and cluster V) to 3278.34 (cluster III and VII). This suggested that there is wide genetic diversity between the clusters having more distances and crosses can be made between genotypes of these clusters to obtain better and desirable segregants. These results are in agreement with the previous reports by Ganesa Murthy and Stephendorairaj (1990), Thombre *et al.* (2000) and Vasantha Rao *et al.*, (2010).

The cluster mean values, by both the methods, for all the thirteen characters are given in Table 4. Cluster I recorded high mean values for harvest index (26.22); cluster II recorded high mean for pod length (4.53); cluster III recorded high mean for days to 50% flowering (151.5), days to maturity (190.33) and grain protein content (25.09); cluster V recorded high mean for 100 seed weight (12.8) and seed yield per plant (90.33); and cluster VI

Table 4 . Mean values of six/seven clusters estimated by Tocher's / Ward's minimum variance method from 41 genotypes of pigeonpea { *Cajanus cajan* (L.) Millsp. } genotypes.

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Secondary branches/plant	Pods/plant	Pod length (cm)	Seeds/pod	Shelling Percent- age	100 seed weight (g)	Harvest index	Grain protein content (%)	Seed yield/ plant (g)
I	141.028 (144.519)	188.833 (189.519)	243.028 (229.148)	15.636 (13.537)	17.050 (12.811)	276.358 (195.911)	4.351 (4.435)	3.753 (3.804)	67.156 (67.294)	9.834 (9.681)	26.221 (24.955)	19.959 (22.566)	73.194 (57.037)
II	148.067 (144.833)	189.267 (190.611)	233.322 (224.911)	14.773 (17.539)	15.577 (16.944)	224.440 (177.822)	4.529 (4.206)	3.777 (3.706)	67.485 (67.317)	9.707 (10.378)	25.515 (21.216)	21.298 (25.393)	63.133 (45.722)
III	151.500 (143.667)	190.333 (187.111)	243.933 (198.800)	10.833 (13.256)	15.150 (17.311)	284.133 (119.689)	4.447 (4.396)	3.917 (3.689)	64.821 (66.596)	9.417 (9.089)	26.027 (26.788)	25.087 (22.951)	72.167 (41.667)
IV	143.238 (141.028)	189.429 (188.133)	217.095 (243.028)	14.721 (15.636)	15.721 (17.050)	168.805 (276.358)	4.284 (4.351)	3.724 (3.753)	66.878 (67.156)	9.879 (9.834)	23.441 (26.221)	23.888 (19.959)	47.429 (73.194)
V	140.667 (147.533)	189.000 (189.133)	197.867 (227.591)	14.067 (14.113)	20.867 (17.780)	271.200 (234.120)	4.227 (4.425)	3.800 (3.720)	65.966 (66.861)	12.800 (9.640)	25.331 (25.022)	24.163 (19.434)	90.333 (61.800)
VI	140.000 (147.833)	187.333 (189.500)	272.200 (228.033)	18.967 (13.042)	21.367 (17.308)	360.400 (271.833)	4.403 (4.483)	3.833 (3.850)	68.925 (65.779)	9.500 (10.533)	25.380 (25.834)	21.535 (25.071)	85.333 (77.083)
VII	(140.000)	(187.333)	(272.200)	(18.967)	(21.367)	(360.400)	(4.403)	(3.833)	(68.925)	(9.500)	(25.380)	(21.535)	(85.333)

Note : Values in parenthesis are of Ward's minimum variance method.

recorded high mean values for plant height (272.2), number of primary branches per plant (18.97), number of secondary branches per plant (21.37), pods per plant (360.4) and shelling percentage (68.93). Cluster mean values by Ward's method (Fig. 3) ranged from 140(cluster VII) to 147.83 (cluster VI), 187.11 (cluster III) to 190.61 (cluster II), 198.8 (cluster III) to 272.2 (cluster VII), 13.04 (cluster VI) to 18.97 (cluster VII), 12.81 (cluster I) to 21.37 (cluster VII), 119.69 (cluster III) to 360.4 (cluster VII), 4.21 (cluster II) to 4.48 (cluster VI), 3.69 (cluster III) to 3.85 (cluster VI), 65.78 (cluster VI) to 68.93 (cluster VII), 9.09 (cluster III) to 10.533 (cluster VI), 21.216 (cluster II) to 26.788 (cluster III), 19.434 (cluster V) to 25.993 (cluster II), 41.67 (cluster III) to 85.33 (cluster VII) for Days to 50% flowering, Days to maturity, Plant height, Number of primary branches per plant, Number of secondary branches per plant, Number of pods per plant, Pod length, Seeds per pod, Shelling percentage, 100 seed weight, Harvest index, Grain protein content and Seed yield per plant, respectively.

In the present study, the first four principal components with eigen values more than one contributed 77.65 per cent towards the total variability (Table 5). The principal component with eigen values less than one *i.e.*, fifth (0.77) was considered as non-significant. The first principal component contributed maximum towards variability (44.58%). The characters viz. shelling percentage (-0.4), number of pods per plant (-0.39), pod length (-0.36), 100 seed weight (-0.35), number of seeds per pod (0.32) and protein content (0.32) explained the maximum variance in the first principal component (PC1). The second principal component (PC2) described 14.42 per cent of total

Table 5. Eigen values, proportion of the total variance represented by first five principal components, cumulative percent variance and component loading of different characters in {*Cajanus cajan* (L.) Millsp.].

Character	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector
Eigen Value (Root)	5.796	1.874	1.389	1.035	0.767
% Var. Exp.	44.582	14.416	10.687	7.961	5.897
Cum. Var. Exp.	44.582	58.998	69.685	77.647	83.544
Days to 50% flowering	0.031	0.326	0.668	0.264	0.068
Days to maturity	0.029	-0.248	0.482	-0.604	0.352
Plant height (cm)	-0.297	0.048	0.306	-0.103	-0.303
Primary branches/ plant	-0.012	-0.548	0.162	0.538	0.153
Secondary branches/ pant	-0.269	-0.092	0.073	-0.387	-0.083
Pods/ plant	-0.394	0.025	-0.046	-0.047	-0.049
Pod length (cm)	-0.356	0.081	-0.114	0.092	-0.100
Seeds/ pod	0.321	0.022	-0.317	-0.276	0.162
Shelling percentage	-0.397	-0.043	0.069	0.038	-0.072
100 seed weight (g)	-0.346	-0.229	-0.203	-0.013	0.028
Harvest index	-0.050	0.663	-0.029	0.054	0.196
Grain protein content (%)	0.316	-0.134	0.159	0.097	-0.060
Seed yield per plant (g)	-0.270	0.033	-0.095	0.122	0.814

Fig 1. Dendrogram showing relationship among 41 genotypes {*Cajanus cajan* (L.) Millsp.}

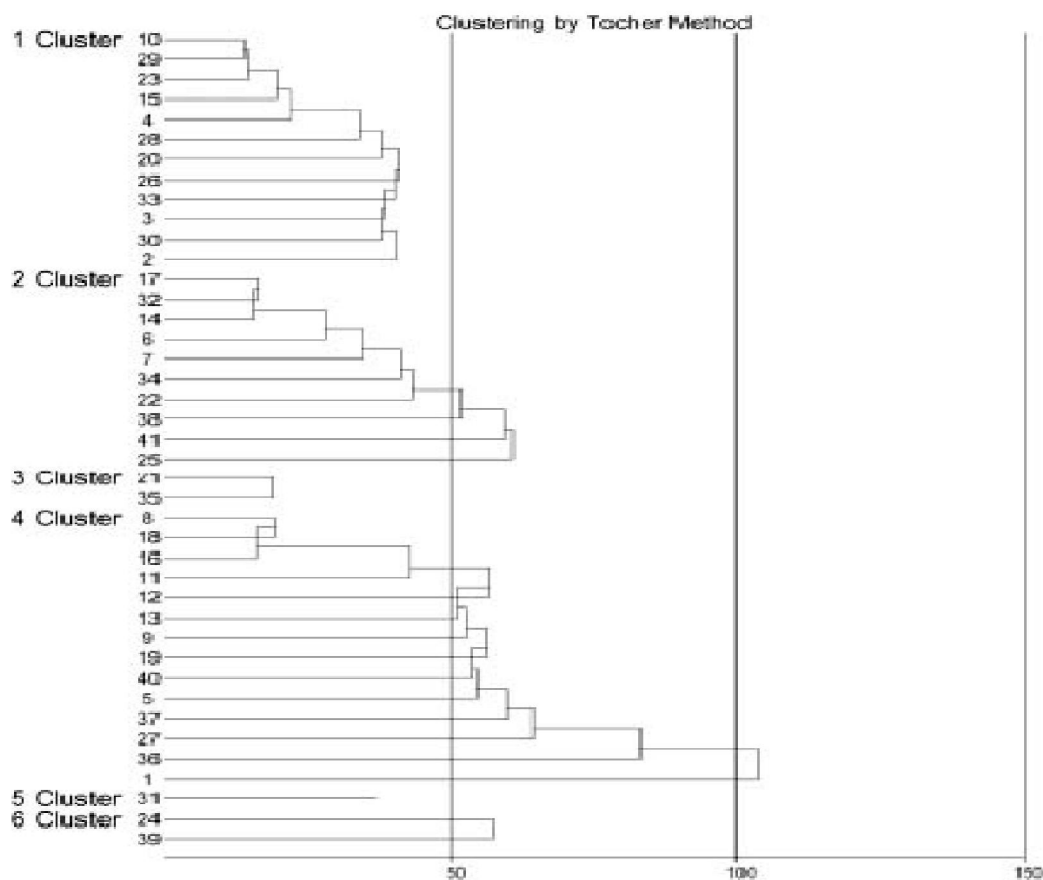


Fig 2. Dendrogram shoing relationship of 41 pigeonpea {*Cajanus cajan* (L.) Millsp.} genotypes in seven clusters

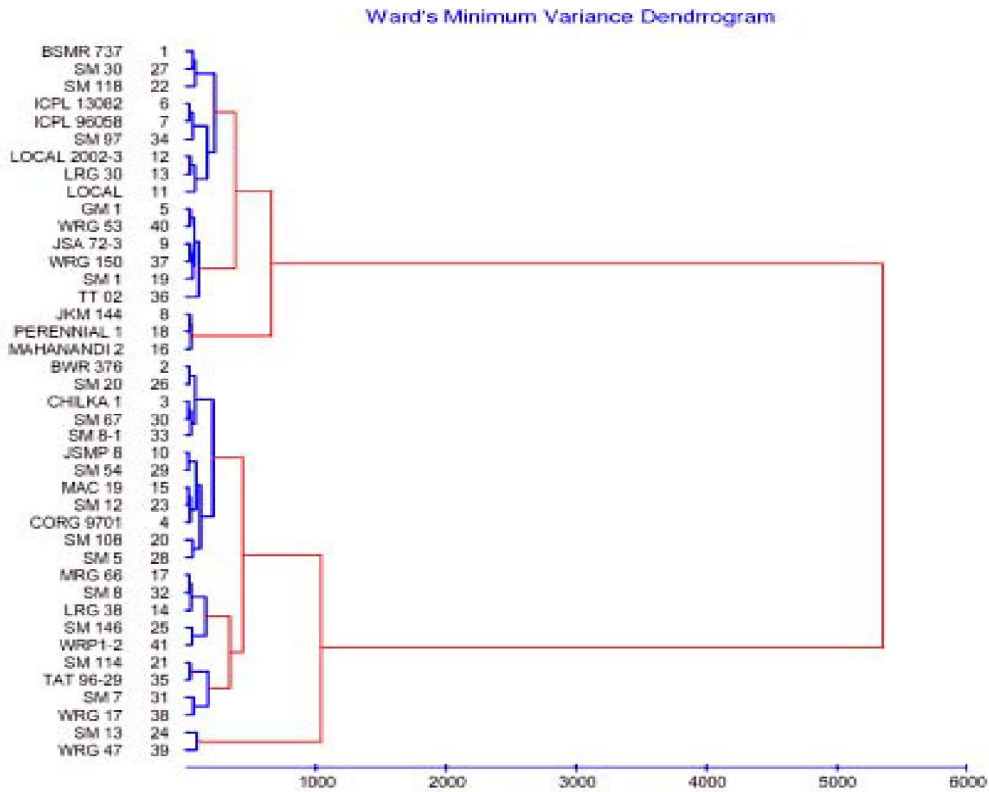


Fig 3. Intra and inter - cluster distance of 41 pigeonpea {*Cajanus cajan* (L.) Millsp.} genotypes in seven clusters based on Euclidean² distance.

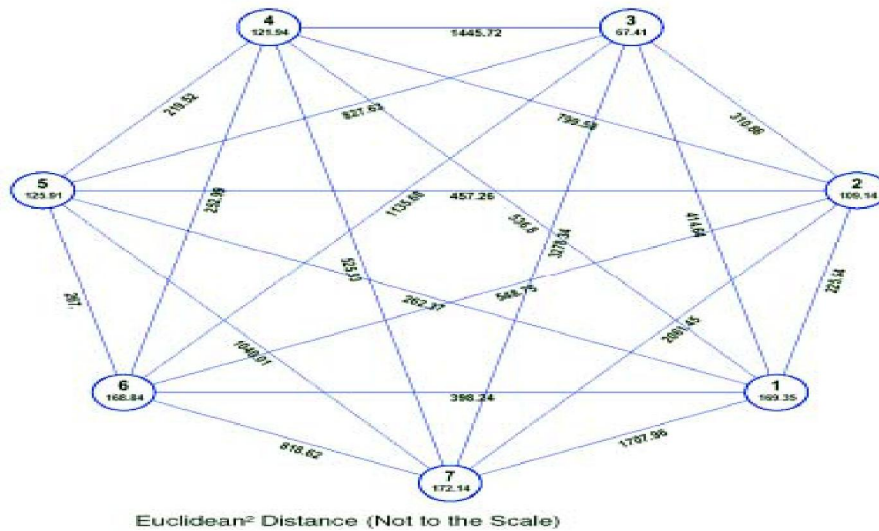


Fig 4. Two dimensional graph showing relative positions of 41 pigeonpea {*Cajanus cajan* (L.) Millsp.} genotypes based on PCA scores.

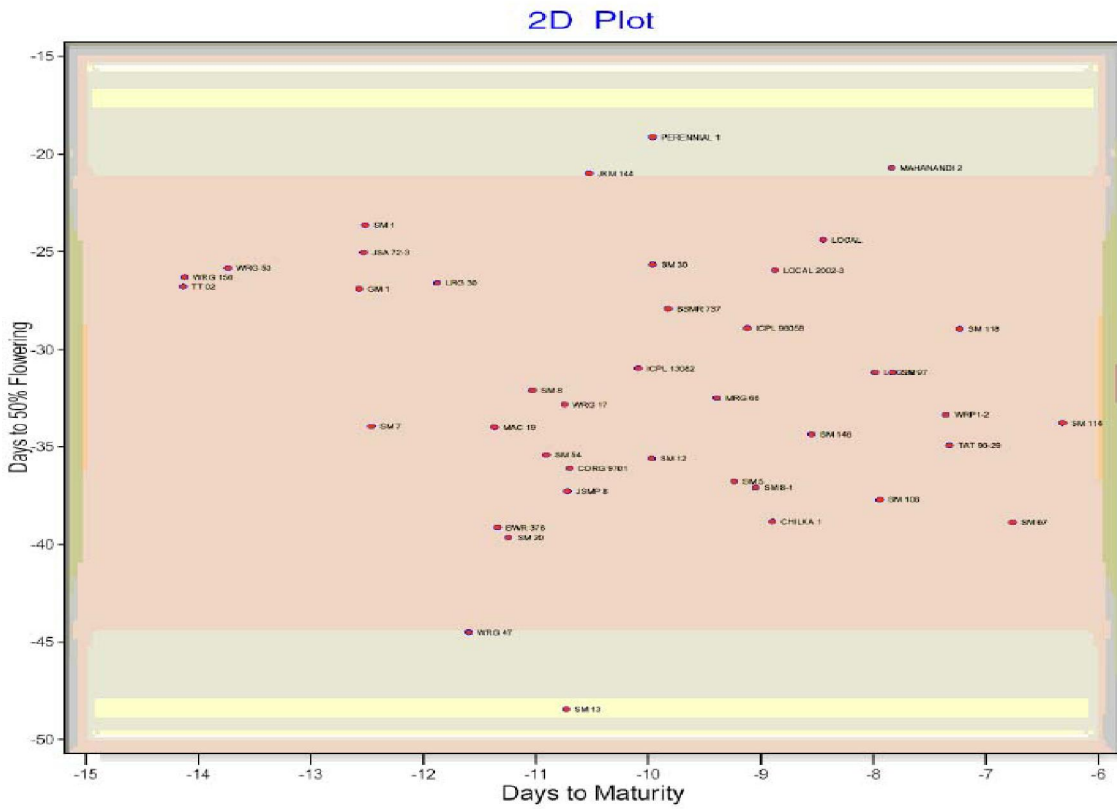
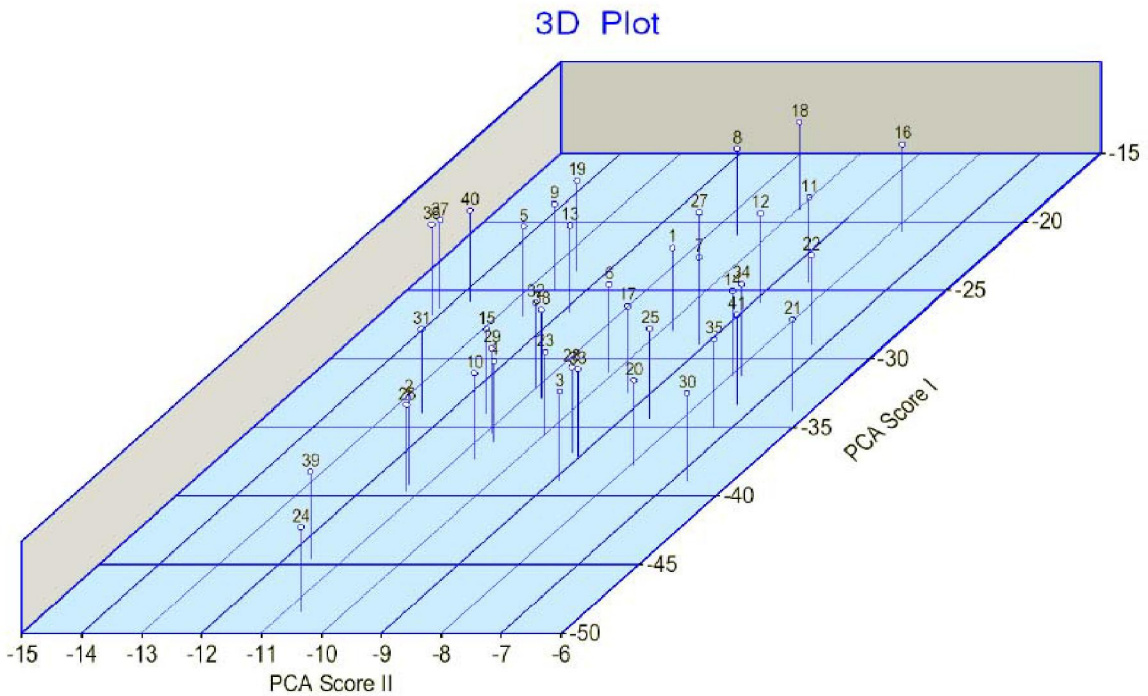


Fig 5. Three dimensional graph showing relative positions of 41 pigeonpea {*Cajanus cajan* (L.) Millsp.} genotypes based on PCA scores.



variance and it reflected significant loading of number of primary branches per plant (-0.55) and harvest index (0.66). The third principal component (PC3) was characterized by 10.69 per cent contribution towards the total variability and it reflected significant loading of number of seeds per pod (-0.32), days to 50% flowering (0.67), days to maturity (0.48) and plant height (0.31). The fourth principal component (PC4) was characterized by 7.96 per cent contribution towards the total variability and it reflected significant loading of days to maturity (-0.6), number of secondary branches per plant (-0.39) and number of primary branches per plant (0.54). Similarly, principal component five (PC5) contributed 5.9 per cent towards total variability. In PC5, plant height (-0.3), seed yield per plant (0.81) and days to maturity (0.35) reflected significant loadings towards variability.

The PCA scores for 41 genotypes in first three principal components were plotted in graph to get the 2D (PCA I as X axis and PCA II as Y axis) and 3D (PCA I as X axis, PCA II as Y axis and PCA III as Z axis) scattered diagram. The genotypes of divergent clusters like SM 13, SM 114, Perennial 1 and TT 02 were scattered far apart while genotypes of similar clusters were placed close to each other in the centre in the 2D (Fig.4) and 3D plots (Fig. 5).

The results of present study can be used as a stepping stone for evolving well defined approach based on evaluation and characterization of variation in red gram and can be utilized in various breeding programmes depending on their specific objectives. The genotypes SM 13, SM 114, Perennial 1 and TT 02 showed maximum inter-cluster distance and wide genetic distance with

each other in all the three divergence methods. So they can be exploited in hybridization programme for identification of desirable segregants.

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