



Multivariate Analyses of Genetic Divergence Based on Metric and Physiological Traits in Pigeonpea (*Cajanus cajan* (L.) Millsp.).

Bhanu Prakash N, B Govinda Rao, V Satyanarayana Rao and Y Asoka Rani

Department of Genetics and Plant Breeding, Agricultural College, Bapatla-522 101, Andhra Pradesh

ABSTRACT

Forty five genotypes of pigeonpea collected from different research centres across the country were subjected to Mahalanobis' D^2 Statistic, cluster analysis and principal component analyses based on 21 metric and physiological traits. Considerable genetic divergence among the 45 genotypes resulted into seven clusters as per D^2 analysis and also in 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 21 characters studied, seed yield per plant contributed maximum towards divergence followed by grain protein content, relative water content at flowering stage, relative water content at vegetative stage, number of secondary branches per plant and specific leaf weight at flowering stage. Principal component analysis identified seven principal components (PCs) which explained 78.0% of the variability. The genotypes LRG-69, JSA-66, LRG-73, TAT 9629 and 11969 showed maximum inter-cluster distance and wide genetic distance in all the three divergence methods with each other and hence these genotypes could be exploited in hybridization programme for identification of desirable segregants.

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

Pigeonpea has been recognized as a valuable source of protein and its improvement paves the way for national nutritional security. Yield is a complex character and depends on number of component characters (metric traits) which are quantitatively inherited. In addition to the metric traits, thorough understanding of physiological parameters of immense help. Though considerable efforts were made on metric traits (Rao, *et al.*, 2010), work done on physiological traits is meagre. Hence the present investigation was taken up with the objective to estimate genetic divergence based on metric and physiological traits in the available germplasm.

MATERIAL AND METHODS

Forty five genotypes of pigeonpea were sown in a randomized block design with three replications at the Regional Agricultural Research Station, Lam, Guntur, during *kharij*, 2009-10. 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 the package of practices recommended by ANGRAU. Observations (21 characters) were recorded on ten randomly selected plants without considering the border plants in 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. The data was recorded on plant height (cm), days to 50% flowering, days to maturity, number of primary branches per plant per plant, number of secondary branches per plant 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 (%), harvest index, Leaf Area Index (LAI) at vegetative stage, LAI at flowering stage, Specific Leaf Area (SLA) at vegetative stage (cm^2/g), SLA at flowering stage (cm^2/g), Specific Leaf Weight (SLW) at vegetative stage (mg/cm^2), SLW at flowering stage (mg/cm^2), Relative Water Content (RWC) at vegetative stage (%) and RWC at flowering stage (%). The data were statistically

Table 1. Clustering pattern of 45 pigeonpea {*Cajanus Cajan* (L.) Millsp.} by Tocher's method and Ward's minimum variance method.

Cluster No.	Based on D ² value (Mahalanobis' analysis)		Based on cluster analysis (Ward's minimum variance method)	
	No. of genotypes	Name of the genotypes	No. of genotypes	Name of the genotypes
I	14	TRG 7, LRG-81, LRG-85, LRG 41, LRG-80, GRG 2009, CO 6, WRG 53, LRG-83, LRG-86, LRG 87, TRG 21, WRP 1, WRG 170	7	JSA 73-1, RPS 2007-105, SKNP 0740, VKT 235, LRG 52, VKT 244, RPS 2007-109
II	15	VKT 235, LRG 52, LRG-59, VKT 244, RPS 2007-105, JSA 73-1, RPS 2007-109, SKNP 0740, TTB 7, SKNP 0528, LRG-84, 11960, LRG-56, WRG 173, ARCC V2	5	SKNP 0528, 11960, ARCC V2, LRG-56, 11969
			5	WRG 173, LRG-84, LRG-59, LRG-86, LRG-70
			5	BRG 9-2, LRG-79, WRG170, LRG-61, GRG 2009
III	8	WRG 166, ICP 8863, BRG 9-1, WRG 75, BRG 9-2, LRG 61, LRG-82, LRG-79	10	CO 6, LRG 41, LRG-80, LRG-87, WRP 1, WRG53, TRG 7, LRG-81, LRG-83, LRG-85
IV	1	LRG-70	7	WRG 75, ICP 8863, BRG 9-1, WRG 166, LRG-82, TTB 7, TRG 21
V	1	LRG-50	6	JSA66, LRG-50, TAT 9629, LRG-73, SURYA, LRG - 69
VI	5	SURYA, LRG-69, JSA 66, LRG-73, TAT 9629		
VII	1	11969		

Table 2. Contribution of different characters towards genetic divergence in pigeonpea {*Cajanus cajan* (L.) Millsp.}.

S. No.	Character	Contribution towards divergence (%)	Times ranked first
1	Plant height (cm)	0.20	2
2	Days to 50% flowering	0.00	0
3	Days to maturity	0.00	0
4	Primary branches/ plant	0.20	2
5	Secondary branches/ pant	2.73	27
6	Pods/ plant	0.61	6
7	Pod length (cm)	0.00	0
8	Seeds/ pod	0.00	0
9	Shelling percentage	0.00	0
10	100 seed weight (g)	0.40	4
11	Seed yield per plant (g)	46.97	465
12	Grain protein content (%)	33.13	328
13	Harvest index	0.00	0
14	LAI at vegetative stage	0.10	1
15	LAI at flowering stage	0.10	1
16	SLA at vegetative stage (cm ² /g)	0.30	3
17	SLA at flowering stage (cm ² /g)	0.00	0
18	SLW at vegetative stage (mg/cm ²)	0.00	0
19	SLW at flowering stage (mg/cm ²)	1.11	11
20	RWC at vegetative stage (%)	3.74	37
21	RWC at flowering stage (%)	10.40	103

Table 3. Average intra-and inter-cluster distance and Euclidian² (ward) values of seven clusters in Pigeonpea {*Cajanus cajan*_(L.) Millsp.}.

Cluster No.	I	II	III	IV	V	VI	VII
	70.73	185.26	116.48	144.45	122.83	215.10	516.52
I	(146.99)	(354.11)	(311.68)	(804.98)	(516.28)	(406.72)	(1366.18)
II		87.48	232.46	171.06	302.11	458.51	191.19
III		(271.19)	(501.3)	(1480.66)	(1024.58)	(773.68)	(1812.05)
IV			128.81	221.89	158.19	293.31	528.50
V			(153.59)	(620.28)	(329.04)	(418.3)	(724.44)
VI				0.00	83.72	176.23	461.83
VII				(189.84)	(281.45)	(422.77)	(592.01)
					0.00	93.41	722.64
					(182.13)	(386.2)	(584.30)
						111.49	995.09
						(254.48)	(947.1)
							0.00
							(316.4)

Note : Values in Parenthesis are of Ward's method.

analyzed to study the diversity by Mahalanobis' D² statistic as per Rao (1952), Principal Component Analysis (PCA) as described by Morrison (1976) and cluster analysis as described by Anderberg (1993).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences for all the characters studied. The 45 genotypes were grouped into seven clusters using the Tocher's method as well as Wards minimum variance method (Table 1). Cluster II in the groups by Tocher method got maximum number of genotypes (15) followed by clusters I (14), III (8), VI (5) and minimum genotypes (one each) for clusters IV, V and VII. In the case of the groups by Wards minimum variance method Cluster V got maximum genotypes followed by I & VI (7), VII (6) and II III & IV each with 5 genotypes. 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 also reported by Garten *et al.* (1989), Ganesa Murthy and Stephen

Dorairaj (1990), Viramgama and Goyal (1994), Basavarajaiah *et al.* (1998), Katiyar *et al.* (2004), Kumar *et al.* (2005), Firoz Mahamad *et al.* (2006), Magar *et al.* (2008) and Vasantha Rao, *et al.* (2010).

The per cent contribution towards genetic divergence by all the 21 contributing characters is given in Table 2. The maximum contribution towards genetic divergence is by seed yield per plant (46.97%) followed by grain protein content (33.13%), RWC at flowering stage (10.40%), RWC at vegetative stage (3.74%), number of secondary branches per plant per plant (2.73%) and SLW at flowering stage (1.11%) indicating possibility of genetic improvement of these characters in the genotypes studied.

The average intra- and inter- cluster D² values and those by Wards minimum variance method are presented in Table 3. Intra-cluster D² values ranged from zero (cluster IV, V, and VII) to 128.81 (cluster III) while the inter-cluster D² values ranged from 83.72 (cluster IV and V) to 995.09 (cluster VI and VII). Of the 7 clusters formed Wards minimum variance method, cluster I had minimum intra cluster Euclidean² distance value of 146.985 followed by cluster III (153.591), cluster V (182.133), cluster VI (189.844), cluster VI (254.482), cluster II (271.191) and cluster VII

Table 4. Mean values of seven clusters estimated by Tocher's and Ward's methods from 45 genotypes of pigeonpea *{Cajanus cajan (L.) Millsp}*.

Cluster No	Plant height (cm)	Days to 50% flowering	Days to maturity	Primary branches/ plant	Secondary branches/ Plant	Pods / plant	Pod length (cm)	Seeds/ pod	Shelling percentage	100 seed weight (g)	Seed yield/ plant (g)
I	163.595 (181.571)	121.167 (119.667)	176.024 (175.810)	22.452 (15.190)	59.071 (65.667)	598.286 (503.429)	4.908 (4.867)	3.819 (3.619)	51.917 (54.204)	10.287 (11.534)	125.761 (148.070)
II	175.844 (171.733)	121.578 (122.533)	176.911 (179.400)	18.133 (20.733)	61.000 (59.467)	550.311 (615.067)	4.939 (4.771)	3.756 (3.840)	54.488 (58.251)	11.184 (11.377)	150.569 (176.635)
III	166.292 (148.533)	123.792 (124.600)	179.083 (177.400)	18.625 (21.733)	66.542 (55.333)	649.458 (624.200)	5.128 (5.013)	3.992 (3.893)	49.572 (52.799)	11.582 (10.623)	143.738 (138.090)
IV	142.000 (168.867)	124.000 (124.000)	176.000 (181.000)	22.333 (19.000)	62.333 (79.267)	653.333 (678.933)	4.433 (4.913)	3.667 (3.800)	52.573 (48.443)	9.227 (11.539)	119.553 (135.887)
V	148.333 (157.300)	124.000 (120.067)	175.000 (173.900)	25.000 (23.067)	44.667 (51.267)	749.667 (539.800)	5.453 (4.972)	3.733 (3.867)	47.917 (50.393)	12.923 (9.981)	128.920 (110.939)
VI	161.600 (178.667)	121.400 (123.286)	179.067 (178.000)	19.867 (19.476)	54.200 (65.714)	809.400 (647.333)	4.940 (5.915)	3.853 (3.981)	46.567 (53.218)	10.549 (11.160)	121.397 (155.698)
VII	140.000 (159.389)	122.667 (121.833)	178.000 (178.389)	23.000 (20.722)	66.000 (52.611)	564.667 (799.444)	5.387 (5.026)	4.133 (3.833)	60.040 (46.792)	12.707 (10.944)	200.173 (122.651)

Table 4 cont.....

Cluster No	Grain protein content (%)	Harvest index	LAI at vegetative stage	LAI at flowering stage	SLA at vegetative stage (cm ² /g)	SLA at flowering stage (cm ² /g)	SLW at vegetative stage (mg/cm ²)	SLW at flowering stage (mg/cm ²)	RWC at vegetative stage (%)	RWC at flowering stage (%)
I	24.779 (22.470)	44.978 (45.600)	3.036 (3.168)	4.876 (5.122)	208.345 (224.674)	239.705 (253.664)	4.826 (4.157)	4.377 (4.053)	62.210 (59.356)	76.090 (76.467)
II	21.740 (19.848)	47.809 (54.795)	3.133 (3.217)	5.114 (5.037)	225.202 (225.733)	254.561 (259.273)	4.540 (4.666)	4.077 (4.171)	63.382 (71.389)	72.290 (64.583)
III	26.181 (21.749)	42.479 (49.095)	3.020 (2.985)	4.629 (4.941)	230.373 (217.046)	250.054 (249.861)	4.520 (4.742)	4.123 (4.059)	65.380 (56.254)	61.595 (69.361)
IV	21.120 (26.813)	51.137 (42.879)	2.923 (3.158)	5.153 (4.950)	220.997 (235.447)	258.710 (250.223)	4.527 (4.580)	3.917 (4.519)	53.723 (64.623)	54.617 (74.417)
V	24.620 (24.665)	44.970 (43.581)	2.907 (3.017)	5.060 (4.910)	231.623 (201.262)	267.583 (238.082)	4.223 (4.939)	3.797 (4.451)	54.223 (60.905)	50.027 (78.926)
VI	23.558 (25.430)	44.043 (43.378)	3.715 (2.950)	5.537 (4.581)	224.524 (227.185)	253.413 (249.273)	4.733 (4.392)	3.989 (4.078)	64.444 (68.333)	70.288 (55.716)
VII	20.420 (23.735)	54.707 (44.197)	3.203 (3.580)	4.517 (5.458)	207.920 (225.707)	264.747 (255.774)	5.337 (4.648)	4.127 (3.957)	65.770 (62.741)	59.363 (66.911)

Note : Figures in parentheses are of Ward's method.

(316.397). The inter cluster Euclidean² distances varied from 281.45 (between cluster IV and cluster V) to 1812.049 (cluster II and VII). This suggested that there is a 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. Similar results were also reported by Ganesa Murthy and Stephen Dorairaj (1990), Thombre *et al.* (2000) and Vasantha Rao, *et al.*, (2010).

The clusters mean values, by both the methods, for all the 21 characters are presented in Table 4. High mean values by Tocher's method were recorded for SLW at flowering stage and RWC at flowering stage; plant height; days to maturity, number of secondary branches per plant and grain protein content; days to 50% flowering; days to 50% flowering, number of primary branches per plant, pod length, 100 seed weight, SLA at vegetative stage and SLA at flowering stage; number of pods per plant, LAI at vegetative stage and LAI at flowering stage; and number of seeds per pod, shelling percentage, seed yield per plant, harvest index, SLW at vegetative stage and RWC at vegetative stage for Clusters I to VII, respectively. Whereas high mean values for Clusters I to VII by Ward's method were for Plant height; Shelling percentage, Seed yield per plant, Harvest index, SLA at flowering stage and RWC at vegetative stage; Days to 50% flowering; Days to maturity, Number of secondary branches per plant, 100 seed weight, Grain protein content, SLA at vegetative stage and SLW at flowering stage; Number of primary branches per plant, SLW at vegetative stage and RWC at flowering stage; Pod length and Seeds per pod; and Number of pods per plant, LAI at vegetative stage and LAI at flowering stage, respectively.

In the present study, the first six principal components with individual percentage of variances of 22.629, 14.525, 12.711, 9.312, 8.497, 6.108 and 4.238, respectively, contributed 73.782 per cent towards the total variability. The PCA scores for 45 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 LRG-73, WRG-170, 11960, LRG-52 were scattered far apart in the 2D and 3D plots while genotypes of similar clusters were placed close to each other in the centre.

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 redgram and can be utilized in various breeding programmes depending on their specific objectives. The genotypes LRG-69, JSA-66, LRG-73, TAT 9629 and 11969 showed maximum inter-cluster distance and wide genetic distance in all the three divergence methods. So they can be exploited in hybridization programme for identification of desirable segregants.

LITERATURE CITED

- Anderberg M R 1993** Cluster analysis for application. Academic press, New York.
- Basavarajiah D, Byre Gowda M, Kulakarni R S and Loithaswa H C 1998** Genetics divergence studies in pigeonpea (*Cajanus cajan* (L.) Millsp.). *Mysore Journal of Agricultural Sciences*, 32: 111-115
- Firozmahamad, Gowda M B and Girish G 2006** Assessment of genetic divergence in vegetable pigeonpea germplasm. *Environment and Ecology*, 24S (Special 4): 1135-1139
- Samurthy G K and S Dorairaj 1990** Genetic divergence in pigeonpea. *Indian Journal of Genetics and Plant Breeding*, 50(3): 279-282
- Garten S L, Tomer Y S and Singh V P 1989** Genetic divergence in early maturing pigeonpea. *Indian Journal of Pulse Research*, 2(1): 25-31
- Katiyar P K, Dua R P, Singh I P, Singh B B and Singh F 2004** Multivariate analysis for genetic diversity in early pigeonpea accessions. *Legume Research*, 27(3): 164-170
- Magar N M, Mane L L, Gavit A F and Patil S S 2008** Genetic diversity in pigeonpea (*Cajanus cajan* (L) Millsp.). *Advances in Plant Sciences*, 21 (2): 679-681
- Morisson D F 1976** Statistical methods. Mac Graw Hill. Second edition, New York.

- Rao C R 1952** Advanced Statistical Methods in Biometric Research. John Willey and Sons Inc., New York: 390
- Kumar D S, Koteswararao Y, Ramakumar P V and Srinivasarao V 2005** Genetic diversity in pigeonpea (*Cajanus cajan* (L.) Millsp.). *The Andhra Agricultural Journal*, 52(1&2): 443-450
- Thombre B B, Aher R R and Dahat D V 2000** Genetic divergence in pigeonpea. *Indian Journal of Agricultural Research*, 34:126-129
- Vasantharao U, Govindarao B, Pandurangarao C and Srinivasarao V 2010** Multivariate analyses of genetic diversity in Pigeonpea [*Cajanus cajan* (L.) Millsp.] *The Andhra Agricultural Journal*, 57(2): 156-163
- Viramgama A V and Goyal S N 1994** Genetic divergence in pigeonpea. *Gujarat Agricultural University Research Journal*, 19(2): 65-71

(Received on 12.02.2013 and revised on 28.10.2013)