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# Multivariate Analysis in Pigeonpea {*Cajanus cajan* (L.) Millsp.} Advanced Lines

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**ABSTRACT**

Forty nine genotypes of Pigeonpea were assessed for genetic divergence for 13 characters during Kharif 2010. The multivariate analysis revealed considerable genetic divergence and grouped into four clusters as per $D^2$ analysis and eight clusters in case of cluster analysis. Grouping of genotypes was at random suggesting no role of geographical isolation. Mahalanobis' $D^2$ statistic inferred that number of primary branches/plant contributed maximum towards divergence followed by days to 50% flowering. Based on the intra and inter-cluster distances among the clusters, crosses between the genotypes of cluster III and II followed by cluster II and IV will give new desirable recombinants. First five Principal Components (PCs) contributed 75.04 per cent of cumulative variance. The first principal component explained 31.71% of total variability and was characterized by plant height, number of primary branches/plant, number of secondary branches/plant and shelling percentage. Agglomerative cluster analysis showed wide genetic distance between clusters II and III followed by clusters I and II. Selection of parents from these clusters will produce superior segregants. Dendrogram obtained by cluster analysis sub-grouped the genotypes. The genotypes LRG-97, LRG-61, BRG-2 and BDN 2010 with maximum inter-cluster distance and wide genetic distance in all the three divergence methods, can be exploited in hybridization.

**Key words :** Cluster analysis, $D^2$ analysis, Pigeonpea, Principal component analysis.

Pigeonpea commonly known as redgram or arher or tur is a diploid (2n=22) and often cross pollinated (0-70%) crop (Sexena 2006). It is one of the major grain legume crops of the tropics and sub tropics, which belongs to family Papilionoideae and genus *Cajanus.* Its genetic improvement is essential to the food and nutritional security of many people, vegetarians in particular. The diversity of parents is of prime importance, since the crosses made between the genetically divergent parents are likely to throw desirable recombinants in the progenies. Traditionally, Mahalanobis' $D^2$ statistic to measure genetic divergence as suggested by Rao (1952) has been used by different workers in pigeonpea. The present study was carried out with different methods of clustering based on $D^2$ analysis, hierarchical cluster analysis and principal component analysis.

## MATERIAL AND METHODS

Forty nine Pigeonpea {*Cajanus cajan* (L.) Millsp.} genotypes obtained from different Research Centres across the country were sown in a randomized block design with three replications at Regional Agricultural Research Station, Lam, Guntur during *Kharif* 2010 – 11. The inter and intra- row spacing adapted was 90cm x 20cm. Each genotype was sown in six rows of 4m length and observations were recorded on five randomly selected plants without border effect of each genotype in each replication for characters viz., days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of secondary branches/ plant, number of pods/plant, pod length, number of seeds/pod, shelling percentage, 100 - seed weight, harvest index, seed yield/plant and grain protein content. The data were statistically analyzed to study the diversity by Mahalanobis' $D^2$ 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 furnished in the Table 1 revealed significant differences for all the characters, indicating considerable variation among the genotypes.

The magnitude of $D^2$ values suggested that there was considerable variability in the material studied, which led to genetic diversity. The per cent contribution towards genetic divergence by all the

Table 1. Analysis of variance for yield and yield component characters in pigeonpea.

| Source | d.f | Days to 50% flowering | Days to maturity | Plant height (cm) | Primary branches/ plant | Secondary branches/ plant | Pods/ plant | Pod length (cm) | Seeds/ pod |
|---|---|---|---|---|---|---|---|---|---|
| | | | | Mean squares | | | | | |
| Replications | 2 | 56.423 | 10.3673 | 996.426 | 13.367 | 35.7919 | 494.8903 | 0.0810 | 0.0734 |
| Treatments | 48 | 204.256** | 68.8070** | 4456.9951* | 419.9658** | 176.032** | 15087.8564** | 0.3352** | 0.1547** |
| Error | 96 | 14.2292 | 31.8257 | 218.580 | 4.9910 | 12.4907 | 1810.1323 | 0.0995 | 0.0612 |

| Source | d.f | Shelling percentage | 100 seed weight (g) | Harvest index | Grain protein content (%) | Seed yield/ plant (g) |
|---|---|---|---|---|---|---|
| | | | Mean squares | | | |
| Replications | 2 | 1.5147 | 4.4395 | 14.2443 | 2.5017 | 192.534 |
| Treatments | 48 | 16.6882** | 3.1816** | 15.2989** | 7.5145** | 675.2032** |
| Error | 96 | 7.3402 | 1.3223 | 4.1950 | 0.8300 | 56.2126 |

** = significance at 1% level, d.f = Degrees of freedom

Table 2. Contribution of different characters towards genetic divergence in Pigeonpea.

| S. No. | Character | Times ranked first | Contribution towards divergence (%) |
|---|---|---|---|
| 1 | Days to 50% flowering | 107 | 9.10 |
| 2 | Days of maturity | 18 | 1.53 |
| 3 | Plant height (cm) | 63 | 5.36 |
| 4 | Primary branches/ plant | 639 | 54.34 |
| 5 | Secondary branches/plant | 48 | 4.08 |
| 6 | Pods/ plant | 50 | 4.25 |
| 7 | Pod length (cm) | 14 | 1.19 |
| 8 | Seeds/pod | 7 | 0.60 |
| 9 | Shelling percentage | 10 | 0.85 |
| 10 | 100 seed weight (g) | 15 | 1.28 |
| 11 | Harvest index | 15 | 1.28 |
| 12 | Grain protein content (%) | 91 | 7.74 |
| 13 | Seed yield per plant (g) | 99 | 8.42 |

Table 3. Genotypes included in each cluster based on Mahalanobis 's $D^2$ analysis and Ward's minimum variance method.

| Cluster No. | Based on D2 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 | 22 | LRG96, LRG41, RGT4, LRG106, LRG99, TRG38, LRG105, LRG90, LRG103, WRG179, LRG101, LRG93, LRG100, WRG180, LRG104, LRG92, LRG102, LRG91, LRG52, LRG95, LRG98, LRG94. | 9 | JKM 250, NTL 520, SKNP 0845, RVSA 07-24, GRG 2010, GJP 2010, GJP 0902, JKM 249, LRG89, RVSA 07 – 31 |
| II | 25 | SKNP 0845, RVSA 07-24, GJP 0902, AKT 08-2, GAUT 2003 – 1, PT 00 – 012-1, JKM 249, WRG 173, CO-6, RVSA 07-31, LRG89, LRG88, GRG 2010, NTL 554, WRP -1, AKT – HR 2001 -18, PT04 – 149, ICP 8863, GAUT 93-17, JKM 250, NTL 520, GJP 0901, BDN 2010, BRG-2.RSVA 7031. | 2 | WRG 168, GJP 0901 |
| III | 1 | LRG61 | 1 | BDN 2 |
| IV | 1 | LRG97 | 13 | ICP 8863, WRP – 1, NTL 554, AKT –HR 2001-18, PT 00- 012-1, GAUT 2003-1, AK 8-2, CO-6, LRG88, WRG 173, GAUT 93-17, PT04-149, BDN 2010 |
| V | | ——— | 18 | WRG180, LRG104, WRG179, LRG 103, LRG41, LRG101, LRG 96, LRG105, RGT4, TRG38, LRG 93, LRG 92, LRG100, LRG99, LRG106, LRG90, LRG102 |
| VI | | ——— | 2 | LRG94, LRG95 |
| VII | | ——— | 3 | LRG91, LRG98, LRG61 |
| VIII | | ——— | 1 | LRG 97 |

13 contributing characters is presented in Table 2. The maximum contribution towards genetic divergence is by number of primary branches /plant (54.34%).

The 49 genotypes were grouped into four clusters using the Tocher's method and eight clusters by Ward's method (Table 3). 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 Hamid *et al.,* (2011).

Table 4. Average intra-and inter-cluster $D^2$ and Eucledian$^2$ values among four and eight clusters, respectively, based on cluster analysis.

| Cluster No. | I | II | III | IV | V | VI | VII | VIII |
|---|---|---|---|---|---|---|---|---|
| I | **14.514**<br>26.238 | **56.569**<br>67.116 | **36.652**<br>91.037 | **45.917**<br>48.367 | 169.794 | 82.139 | 293.517 | 277.163 |
| II | | **18.125**<br>53.543 | **135.319**<br>148.698 | **87.804**<br>105.443 | 173.964 | 100.703 | 264.756 | 273.032 |
| III | | | **0.000**<br>0.000 | **61.913**<br>130.124 | 243.094 | 161.379 | 364.656 | 448.678 |
| IV | | | | **0.000**<br>37.145 | 164.212 | 85.018 | 304.984 | 238.163 |
| V | | | | | 35.454 | 62.109 | 72.168 | 137.433 |
| VI | | | | | | 17.493 | 120.831 | 115.745 |
| VII | | | | | | | 59.054 | 170.330 |
| VIII | | | | | | | | 0.000 |

Note: Bold values are of $D^2$ method

The average intra- and inter- cluster $D^2$ values estimated as per the procedure given by Singh and Chowdhary (1977) are presented in Table 4. The maximum inter cluster distance (135.319) was observed between cluster III and II followed by clusters II and IV (87.804). Cluster I comprised 22 genotypes and was nearest to cluster III (36.65). Cluster II, comprised 25 genotypes was nearest to cluster I (56.56). Cluster III was monogenotypic which was closest to cluster I (36.65) Cluster IV was monogenotypic and closest to the cluster I (45.91). The highest intra-cluster distance in cluster II indicates the presence of wide genetic diversity among the 25 genotypes within the cluster. The maximum inter cluster distance (135.319) was observed between cluster III (LRG 61) and II (SKNP 0845, RVSA 07-24, GRG 2010, GJP 0902, AKT 08-2, GAUT 2003- 1, PT 00-012-1, JKM 249, WRG 173, CO-6, RVSA07-31, LRG 89, LRG 88, NTL 554, WRP-1, AKT- HR 2001-18, PT04-149, ICP 8863, GAUT 93- 17, JKM 250, NTL 520, GJP 0901, BDN 2010 and BRG-2) indicates the presence of wide diversity between two clusters. For successful breeding program selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants.

Similarly, the average intra- and inter- cluster Euclidean$^2$ distance were estimated based on Ward's minimum variance and are presented in the Table 4. Cluster I comprised nine genotypes and was closest to cluster IV (48.367). Cluster II consisted of two genotypes with proximity to cluster I (67.116). Cluster III was monogenic and was nearest to cluster I (91.037). Cluster IV was consisted of 13 genotypes with as the nearest. Cluster V comprised 18 genotypes and was proximal to cluster VI (62.109). Cluster VI comprised two genotypes with cluster V (62.109) as the nearest. Cluster VII comprised three genotypes and was closest to cluster V (72.168). Cluster VIII comprised one genotype (LRG 97) which was closest to cluster VI (115.745). The maximum inter cluster distance was observed between cluster II (WRG 168 and GJP 0901) and cluster III (BRG 2). This suggested that there is wide genetic diversity between these clusters. Based on these studies, crosses can be made between genotypes of these clusters to obtain better and desirable segregants. Utilization of principal component analysis combined with clustering by ward's method in genetic diversity studies was reported Brown (1991).

The clusters mean values for all the 13 characters by both the methods are presented in Table 5. Cluster I recorded high mean value for days

Table 5. Mean values of four and eight clusters estimated by Tocher's and Ward's methods, respectively, from 49 genotypes of Pigeonpea {*Cajanus cajan*(L.) Millsp.}

| Cluster No | Days 50% flowering | Days of maturity | Plant height (cm) | Primary branches/ plant | Secondary branches/ plant | Pods/ plant | Pod length (cm) | Seeds/ pod | Shelling percentage | 100 seed weight (g) | Harvest index | Protein content | Seed yield/ plant(g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | **140.667** | **193.227** | **262.024** | **27.456** | **29.702** | **267.360** | **4.537** | **4.032** | **65.343** | **11.384** | **25.977** | **24.035** | **76.636** |
| | 141.926 | 193.111 | 185.232 | 6.226 | 18.194 | 329.233 | 4.748 | 3.852 | 63.475 | 11.308 | 28.086 | 24.002 | 88.333 |
| II | **139.693** | **193.840** | **199.329** | **6.059** | **17.608** | **296.597** | **4.751** | **3.913** | **63.862** | **11.359** | **26.779** | **23.617** | **77.587** |
| | 139.833 | 195.500 | 244.148 | 5.500 | 18.345 | 456.267 | 4.697 | 3.900 | 66.250 | 11.497 | 29.088 | 23.605 | 118.333 |
| III | **136.667** | **185.667** | **263.430** | **45.933** | **36.680** | **314.267** | **4.200** | **3.867** | **71.170** | **9.507** | **25.840** | **26.633** | **77.667** |
| | 162.333 | 197.333 | 190.253 | 5.4 | 15.240 | 294.95 | 5.533 | 4.833 | 64.553 | 11.697 | 24.903 | 26.100 | 77.333 |
| IV | **104.000** | **198.333** | **245.817** | **28.060** | **27.467** | **249.967** | **5.367** | **4.533** | **61.663** | **10.807** | **23.400** | **24.450** | **67.667** |
| | 136.385 | 193.821 | 202.892 | 6.079 | 17.271 | 249.564 | 4.702 | 3.877 | 63.710 | 11.347 | 25.664 | 23.161 | 63.897 |
| V | 140.981 | 193.278 | 262.197 | 27.822 | 30.550 | 256.44 | 4.579 | 4.037 | 65.689 | 11.586 | 26.276 | 23.714 | 75.000 |
| VI | 133.500 | 192.167 | 231.542 | 19.632 | 19.383 | 248.867 | 4.423 | 4.033 | 64.697 | 9.368 | 25.410 | 25.525 | 81.000 |
| VII | 142.777 | 191.111 | 281.780 | 36.633 | 33.818 | 362.200 | 4.249 | 3.944 | 65.638 | 10.889 | 24.513 | 25.832 | 83.889 |
| VIII | 104.000 | 198.333 | 245.817 | 28.060 | 27.467 | 249.967 | 5.369 | 4.533 | 61.663 | 10.807 | 23.400 | 24.450 | 67.667 |

Note : Bold figures are estimated by Tocher's method

to 50% flowering (140.667) and 100 seed weight (11.384). In Cluster II, the genotypes with low mean values for plant height (199.329), number of primary branches/plant (6.059), number of secondary branches/plant (17.608) and grain protein content (23.617), where as remaining values were high. Cluster III exhibits high mean values for plant height (263.430), number of primary branches/plant (45.933), number of secondary branches/plant (36.680), number of pods/plant (314.267), shelling percentage (71.170), grain protein content (26.633) and seed yield/plant (77.667). The High Yielding genotypes with more number of branches were included in this cluster. Cluster IV Cluster IV exhibits high mean value for days to maturity (198.33), pod length (5.367 cm) and number of seeds/pod (4.533).

The cluster mean values for 13 characters from Ward's methods are also presented in Table 5. Days to 50% flowering had a range of 104.00 for cluster VIII to 162.333 for cluster III. Days to maturity had a range of 191.111 for cluster VII to 198.333 for cluster VIII. Plant height varied from 185.232 for cluster I to 281.780 for cluster VII. Number of primary branches/plant varied from 5.400 for cluster III to 36.638 for cluster VII. Number of secondary branches/plant varied from 15.240 for cluster III to 33.818 for cluster VII. Number of pods/plant varied from 248.867 for cluster VI to 456.267 for cluster II. Pod length varied from 4.249 for cluster VII to 5.533 for cluster III. Seeds/pod ranged from 3.852 for cluster I to 4.833 for cluster III. Shelling percentage ranged from 61.663 for cluster VIII to 66.250 for cluster II 100-seed weight varied from 9.368 for cluster VI to 11.697 for cluster III. Harvest index varied from 23.40 for cluster VIII to 29.088 for cluster II. Grain protein content varied from 23.161 for cluster IV to 26.100 for cluster III. Seed yield/plant varied from 63.897 for cluster IV to 118.333 for cluster II.

Table 6. Eigen values, proportion of the variance represented by first five principal components, cumulative per cent variance and component loading of different characters in Pigeonpea.

| | 1 Vector | 2 Vector | 3 Vector | 4 Vector | 5 Vector |
|---|---|---|---|---|---|
| Eigen Value (Root) | 4.123 | 1.933 | 1.418 | 1.310 | 0.971 |
| % Var. Exp. | 31.714 | 14.867 | 10.909 | 10.079 | 7.473 |
| Cum. Var. Exp. | 31.714 | 46.581 | 57.489 | 67.568 | 75.041 |
| Days to 50% flowering | 0.002 | 0.496 | 0.452 | 0.187 | 0.048 |
| Days of maturity | -0.038 | -0.299 | -0.389 | -0.498 | 0.211 |
| Plant height (cm) | 0.450 | -0.014 | -0.064 | -0.038 | 0.058 |
| Primary branches/plant | 0.445 | -0.010 | -0.041 | 0.064 | -0.043 |
| Secondary branches/plant | 0.410 | 0.008 | -0.109 | 0.103 | 0.014 |
| Pods/ plant | 0.007 | 0.429 | -0.433 | -0.110 | -0.240 |
| Pod length (cm)) | -0.281 | 0.299 | 0.155 | -0.141 | 0.547 |
| Seeds/pod | 0.307 | 0.145 | 0.198 | -0.397 | 0.302 |
| Shelling percentage | 0.371 | -0.013 | 0.051 | 0.146 | -0.055 |
| 100 seed weight (g) | 0.020 | -0.063 | -0.359 | 0.452 | 0.676 |
| Harvest index | -0.290 | 0.229 | -0.367 | 0.091 | -0.197 |
| Grain protein content (%) | 0.090 | 0.282 | -0.028 | -0.513 | 0.025 |
| Seed yield plant (g) | 0.163 | 0.484 | -0.330 | 0.121 | 0.031 |

As given in Table 6, the first four Principal Components with eigen values more than one contributed 67.568 per cent towards the total variability. It was therefore inferred that the essential features of data set had been represented in the first four Principal Components. The first Principal Component contributed maximum towards variability (31.714%). The characters viz. plant height (0.450), number of primary branches/plant (0.445), number of secondary branches/plant (0.410) and shelling percentage (0.371) explained the maximum variance in the first Principal Component (PC1). The PC2, PC3 and PC4 contributed 14.867, 10.909 and 10.079 per cent towards the total variability.

The genotypes LRG-97, LRG-61, BRG - 2 and BDN 2010 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.

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