International Journal of Chemical Studies

P-ISSN: 2349–8528
E-ISSN: 2321–4902
IJCS 2018; 6(5): 1947-1950

Received: 01-07-2018
Accepted: 05-08-2018

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# Genetic divergence study through $D^2$ analysis in pigeonpea (*Cajanus cajan* L. Millspaugh)

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**Abstract**
A field experiment was conducted during kharif 2017 for study of genetic diversity in 45 different genotypes of pigeonpea using $D^2$ statistics method of Mahalanobis. The forty five genotypes of pigeonpea were grouped into nine clusters which indicated the presence of diversity for different traits. The maximum number of diverse genotypes (35 genotypes) appeared in cluster I followed by cluster II (3 genotypes), cluster III, IV, V, VI, VII, VIII, IX with one genotypes. The maximum intra-cluster distance was recorded within cluster I (D=8.16) and the maximum inter cluster distance was observed between II and XI (D=34.47), indicating the existence of wide genetic variability. Based on mean performances, cluster III and cluster V found superior for yield and yield contributing characters. Therefore genotypes selected for hybridization among the above said clusters would produce high heterosis and segregant for more than one economic character.

**Keywords:** genetic diversity, pigeonpea, $D^2$ Statistics, cluster analysis

## Introduction
Pigeonpea [*Cajanus cajan* (L.) Millspaugh] is often cross-pollinated crop which belong to family *Fabaceae* and sub family *papilionaceae* with chromosome number 2n=2x=22. The name "Pigeonpea" probably originated in Africa. It is widely grown in Indian subcontinent which accounts for almost 90 per cent of the world's crop. Pigeonpea main use as dhal, its tender green seeds are used as vegetables, crushed dry seeds as animal feed, green leaves as fodder, stem as fuel wood and to make husts, baskets etc. and plants are also used to culture Lac producing insects. The high protein genotypes also contain higher (about 25 %) sulphur-containing amino acids, namely methionine and cysteine (Singh *et al.* 1990) [14]. Seed contains about 57.3 to 58.7 per cent carbohydrate, 1.2 to 8.1 per cent crude fibre and 0.6 to 3.8 per cent lipids (Sinha, 1977) [15]. It is a good source of dietary minerals such as calcium, phosphorus, magnesium, iron, sulphur and potassium. It is also a good source of soluble vitamins especially thiamine, riboflavin, niacin and chlorine.
Genetic diversity is the basic requirement for a successful breeding programme. Collection and evaluation of genotype of any crop is a pre-requisite for any programme, which provides a greater scope for exploiting genetic diversity. A quantitative assessment of the genetic divergence among the collection of germplasm and their contribution of different traits towards the genetic divergence provide essential and effective information to breeder in this hybridization programme and thereby genetic improvement of yield. The necessity for finding out genetic divergence among the genotypes is more pronounced because of two reasons *i.e.* (I) the genetically diverse parent if included in the hybridization programme are likely to produce high heterotic effect, (II) a wide spectrum of variability could be expected in the segregating generation of crosses involving distantly related parents.
A method suggest by Mahalanobis (1936) [4] known as "Mahalanobis $D^2$ statistics" which is used to know genetic diversity in the available germplasm. This technique measures the force of differentiation at intra cluster and inters cluster levels and thus help in the selection of genetically divergent parents for their exploitation in hybridization programme. The $D^2$ statistics also measure the degree of diversification and determines the relative proportion of each component character to the total divergence.

## Materials and Methods
In the present investigation 45 genotypes of pigeonpea procured from the pulses research station,

Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar were evaluated in Randomized Block Design (RBD) with three replications for different quantitative characters at Agronomy Instructional Farm, C. P. College of Agriculture, SDAU, Sardarkrushinagar during kharif season of 2017. Each genotype sown in single row of 4 m length with spacing 60 cm between row and 20 cm between plants. Data were recorded for five selected competitive plants per genotype for characters Plant height (cm), Number of branches per plant, Number of pods per plant, Pod length (cm), Number of seeds per pod, Seed yield per plant (g), Test weight (g), Leaf area ($cm^2$), Harvest index (%) and Protein content (%) in each replication and averages was worked out for statistical analysis. For the characters like days to flowering and days to maturity observation were recorded on per plot basis. The experimental data was analyzed statistically by the method of analysis of variance suggested by Panse and Sukhatme (1998) [6]. Multivariate analysis was done utilizing Mahalanobis $D^2$statistic (Mahalanobis, 1936) [4] and genotypes were grouped into different clusters following Tocher's method suggested by Rao, 1952 [8].

**Results and Discussions**

The analysis of variance revealed significant differences among the genotypes for all the characters under study *viz.*, days to flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed yield per plant (g), test weight (g), harvest index (%), leaf area ($cm^2$) and protein content (%) which indicated the existence of variability in the experimental material.

Based on $D^2$ value 45 genotypes of pigeonpea were grouped into nine clusters by Tocher's method as per suggested by Rao, 1952 [8] (Table 1). The results indicate that a maximum number of diverse genotypes (35 genotypes) appeared in cluster I followed by cluster II (3 genotypes), cluster III, IV, V, VI, VII, VIII, IX with one genotypes. The pattern of grouping genotypes in different cluster proved the existence of significant amount of variability. These findings are confirmed by earlier reports of Rupika and Kannan Bapu (2014) [10], Satapathy and Panigrahi (2014) [12] and Reddy *et al.* (2015) [9].

The intra and inter cluster distances $D^2$ between all possible pairs of nine clusters were computed and presented in table 2 and depicted in figure 1. The clustering pattern showed that varieties from different source were clubbed into one group and also varieties of same source forming different cluster indicated no relationship between geographical and genetic divergence. Murthy and Arunachalam (1966) [5] stated that genetic drift and selection in different environment could cause greater diversity than geographical distance. The maximum inter cluster distance was observed between II and XI (D=34.47) followed by cluster II and VIII (D=26.96), cluster II and VI (D=24.44), cluster V and IX (D=24.41), cluster VII and cluster IX (D=23.65), cluster II and cluster III (D=23.58). The least inter cluster distance was observed between cluster IV and VII (D=7.42) followed by cluster IV and VII (D=7.42) and cluster I and IV (D=10.84). In the present study maximum intra cluster distance was observed for cluster I (D=8.16) followed by cluster II (D=4.95). In the present study more inter cluster distance was observed than the intra cluster which indicate presence of more diversity between the genotypes of inter cluster. Therefore, selection of genotypes for hybridization from between cluster possessing maximum genetic divergence is expected that more heterotic $F_1$ and most promising segregant in segregating generations. In general, more inter cluster distance than intra-cluster distance suggested homogenous and heterogeneous nature of the genotypes within and between the clusters, respectively Satapathy and Panigrahi (2014) [12]. Similar findings were reported by Singh *et al.* (2014) [13], Reddy *et al.* (2015) [9] and Satankar *et al.* (2017) [11] for the cluster analysis in pigeonpea.

The utility of $D^2$ analysis is enhanced by its application to estimates the relative contribution of various characters to genetic divergence. The contribution of each character towards total genetic diversity is presented in table 3. The present study revealed that, the characters days to flowering (26.67 %), number of pods per plant (22.63 %), plant height (20.81 %), days to maturity (19.39 %) contribute more genetic divergence. Therefore, selection for such traits may give more emphasis hybridization programme to generate large variability and will provide immense scope for the improvement of yield through selection. This type of result were also reported by Kumara *et al.* (2013) [3], Reddy *et al.* (2015) [9] and Satankar *et al.* (2017) [11].

The mean performance of cluster values for all characters is presented in table 4. Based on the mean value of days to flowering and days to maturity genotypes of cluster II and cluster VII proved to be early while, for yield and yield contributing characters like Number of pods per plant, Number of branches per plant, Seed yield per plant (g), Leaf area ($cm^2$) genotypes of cluster III and cluster V found superior. It is suggested that parent selected for hybridization among the genotypes of above said clusters would produce high heterosis and segregant for more than one economic character. The potential lines are identified from different clusters and used as parents in a hybridization programme. The choice of genotype should be based on genetic distance and depending upon the objective of the breeding programme. Similar finding reported by Patel and Acharya (2011) [7], Rupika and Kannan Bapu (2014) [10] and Chaudhary *et al.* (2016) [2].

Many workers have observed that more diverse the parents within its overall limits of fitness, the greater are the chances of heterotic expression in $F_1$'s and a broad spectrum of variability in segregating generations (Arunachalam,1981). Moreover, it will be effective to intercross genotypes belonging to more diverse clusters like cluster III and V to create wide spectrum of variability and to produce transgressive segregates for pigeonpea.

**Table 1:** Distribution of 45 genotypes of pigeonpea into different clusters.

| Cluster No. | No. of genotypes | Genotypes included |
|---|---|---|
| I | 35 | AAUVT 13-35, AAUVT 15-08, SKNP 1521, KDPV 1935, BSMR 853, JKM 189, TJT 501, NTL 740, SKNP 1621, AGT 2, BDN 711, BP 12-24, ICPL 2039, GJP 1508, WRGE 96, TDRG 179, LRG 133, GJP 1502, GT 103, NPEK 15-14, WRG 223, NPEK 15-25, GJP 1, ICPL 15058, ICPL 11023, ICPL 161, SKNP 1601, SKNP 1412, PA 426, PT 0012, ICPL 15068, BRG 14-1, ICPL 15052, ICPL 11084, ICP 14282 |
| II | 03 | ICPL 20336, ICPL 20340, ICPL 11263 |
| III | 01 | WRG 97 |
| IV | 01 | NTL 669 |

| | | |
|---|---|---|
| V | 01 | ICPL 15050 |
| VI | 01 | ICPL 15042 |
| VII | 01 | ICPL 87091 |
| VIII | 01 | ICP 14304 |
| IX | 01 | ICP 13092 |

**Table 2:** Intra (diagonal) and inter cluster D value of 45 genotypes of pigeonpea

| Cluster | I | II | III | IV | V | VI | VII | VIII | IX |
|---|---|---|---|---|---|---|---|---|---|
| I | 8.16 | 19.55 | 10.63 | 10.84 | 11.95 | 11.96 | 13.04 | 13.61 | 19.30 |
| II | | 4.95 | 23.58 | 21.47 | 22.98 | 24.44 | 19.97 | 26.96 | 34.47 |
| III | | | 0.00 | 15.38 | 7.20 | 14.27 | 16.17 | 18.81 | 22.45 |
| IV | | | | 0.00 | 18.55 | 15.76 | 7.42 | 12.34 | 18.18 |
| V | | | | | 0.00 | 11.85 | 19.52 | 19.87 | 24.41 |
| VI | | | | | | 0.00 | 18.87 | 12.06 | 17.97 |
| VII | | | | | | | 0.00 | 17.26 | 23.65 |
| VIII | | | | | | | | 0.00 | 10.49 |
| IX | | | | | | | | | 0.00 |

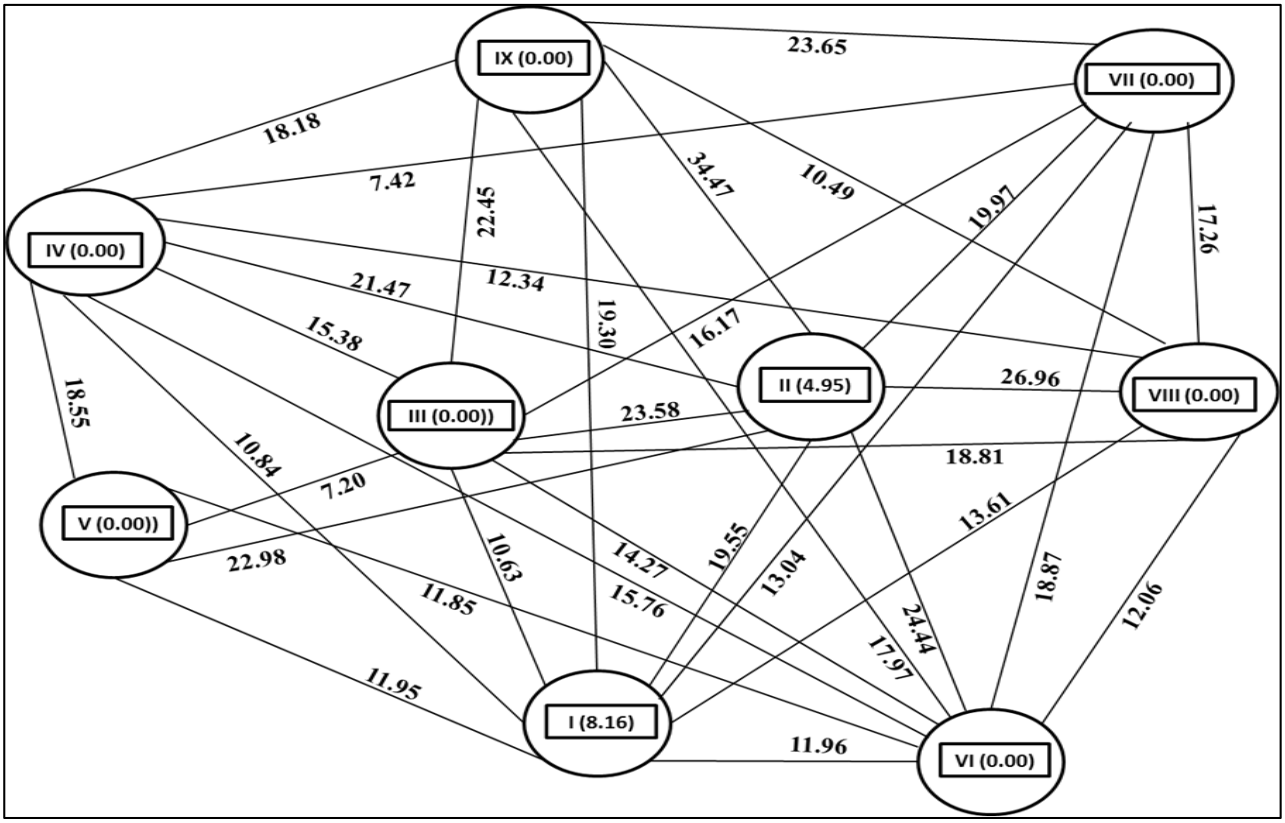


**Fig 1:** Cluster diagrame

**Table 3:** The percent contribution of different quantitative characters to total genetic divergence in pigeonpea.

| Sr. No. | Characters | Contribution % |
|---|---|---|
| 1. | Days to flowering | 26.67 |
| 2. | Days to maturity | 19.39 |
| 3. | Number of seeds per pod | 0 |
| 4. | Pod length (cm) | 0 |
| 5. | Number of pods per plant | 22.63 |
| 6. | Number of branches per plant | 3.03 |
| 7. | Plant height (cm) | 20.81 |
| 8. | Seed yield per plant (g) | 2.42 |
| 9. | Harvest index (%) | 2.63 |
| 10. | Test weight (g) | 0 |
| 11. | Leaf area ($cm^2$) | 0 |
| 12. | Protein content (%) | 2.42 |

**Table 4:** Cluster mean for seed yield and its component in pigeonpea

| Cluster | DF | DM | NS/P | LP | NP/P | NB/P | PH | SY/P | HI | TW | LA | PC |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 140.91 | 182.90 | 3.82 | 5.45 | 97.45 | 18.84 | 133.23 | 21.41 | 21.02 | 10.05 | 5084.80 | 19.37 |
| II | 76.00 | 141.00 | 3.63 | 4.69 | 30.29 | 14.71 | 65.10 | 8.93 | 31.51 | 7.93 | 2471.78 | 19.48 |
| III | 147.67 | 177.00 | 4.13 | 5.25 | 210.53 | 27.20 | 168.36 | 36.47 | 17.12 | 11.07 | 7664.21 | 19.37 |
| IV | 142.67 | 183.67 | 4.35 | 6.85 | 71.93 | 13.47 | 132.02 | 16.33 | 14.27 | 10.98 | 3981.95 | 18.57 |
| V | 144.67 | 188.33 | 3.53 | 4.98 | 161.13 | 33.07 | 122.65 | 31.73 | 25.25 | 8.14 | 6848.33 | 19.73 |
| VI | 160.00 | 205.33 | 3.78 | 5.35 | 57.93 | 32.40 | 130.35 | 14.33 | 11.60 | 10.27 | 6813.49 | 20.44 |
| VII | 131.33 | 170.67 | 5.58 | 6.94 | 109.27 | 14.13 | 129.05 | 26.13 | 25.28 | 12.54 | 4498.22 | 20.30 |
| VIII | 165.67 | 214.00 | 4.64 | 5.65 | 20.00 | 12.27 | 158.16 | 7.80 | 9.87 | 10.99 | 3921.39 | 18.51 |
| IX | 172.33 | 218.00 | 3.94 | 5.42 | 17.60 | 8.27 | 151.46 | 7.40 | 9.93 | 11.44 | 5081.91 | 19.50 |

DF: Days to 50% flowering, DM: Days to maturity, NS/P: Number of seeds per pod, PL: Pod length (cm), P/P: Number of pods per plant, NB/P: Number of branches per plant, PH: Plant height (cm), SY/P: Seed yield per plant (g), HI: Harvest index (%), TW: Test weight (g), LA: Leaf area ($cm^2$), PC: Protein content (%)

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