

Original Research Article

Assessment of Genetic Diversity using D² Statistics among the Medium Maturity Pigeonpea [*Cajanus cajan* (L.) Millspaugh] Genotypes

ABSTRACT

The experimentation was carried out for twenty-one diverse genotypes of pigeonpea for eight quantitatively inherited traits. The genotypes were grouped into six clusters following P.C. Mahalanobis D² statistical techniques. The cluster I consisted highest (16) genotypes and remaining five-clusters are solitary clusters. The maximum intra-cluster distance was observed for cluster I. The greater inter-cluster distance was recorded for cluster II and VI while the lower values were found for the cluster II and III. The maximum contribution towards the genetic diversity were found for seed yield followed by the 100-seed weight, secondary branches/plant and days to maturity. Hence, the genotypes ICPL-15072, WRG-327, AAUVT-13-20, PT-0904-1-1-2 and BAUPP-16-01 were found most genetically distant and superiority in yield and its attributing traits which may be used in hybridization programme to generate genetically divergent progenies to develop high yielding medium maturity pigeonpea genotype.

Key words: Clustering pattern, Genetic Divergence, Pigeonpea and Variability.

1. INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] is a popular *kharif* versatile leguminous crop of tropics and subtropics in India [13]. Globally, Pigeonpea is cultivated in an area ~4.4 mha with an annual production of ~3.68 mt and productivity is ~832 kg/ha [1]. Pulses are the major source of protein (19-25%) and forms an integral part of an Indian vegetarian

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diet [11]. ~~Pigeonpea~~Pigeon pea ($2n=2x=22$) with genome size of 833.07 Mbp [15] is an often-cross pollinated crop through entomophily. Diversity in the germplasm material facilitates an opportunity for the plant breeders to develop improved cultivars and even new ones with desirable traits [2]. To get the desirable improvement in ~~pigeonpea~~pigeon pea crop or any species, depends on the sufficient genetic diversity with desirable traits ~~are~~ available to breeders for desirable improvement regarding to the concerned traits in the crop improvement programme. By the exploitation of existing available varieties and germplasm for making further improvement in the crop, the genetic diversity has been declining due to artificial recurrent selection and is focussed on some targeted desirable traits. Thus, in order to overcome these, a need to broaden the genetic base of existing cultivated varieties is necessary to assess the genetic diversity in order to make an effective crop improvement programme for the mankind.

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2. MATERIALS AND METHODS

The present experimental investigation was grown during *Kharif*, 2019-20 at Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna (M.P.). The experimental materials comprised of twenty-one diverse genotypes of ~~pigeonpea~~pigeon pea obtained from the Indian Institute of Pulses Research, Kalyanpur, and Kanpur (U.P.) (Table 1). The experiment was planted in Randomized Complete Block Design (RCBD) with three replications. Treatment was grown in 4 m long and 6 rows per plot with spacing 90×25 cm². The data was recorded for five randomly selected plant for eight quantitative traits viz., days to 50% flowering, primary branches/plant, secondary branches/plant, pods/plant, plant height (cm), days to maturity, 100-seed weight (g) and seed yield (kg/ha). The experiment was performed for these yield contributing traits and was analysed by using P.C. Mahalanobis D² statistics [5]. The clusters were prepared for all genotypes by following the Toucher's method

as suggested by Rao [9]. The analysis was performed by using R software 4.1 (Agricole Package) and SPSS software Indostat 9.3 for analysis of data.

3. RESULTS AND DISCUSSION

3.1 Genetic Diversity

For the success of any crop improvement programme the ultimate goal is to create a genetic variation and exploitation of these genetic variations for further improvement in the genotype. In the present investigation, twenty-one genotypes of pigeonpea were assessed for morphological genetic diversity following P.C. Mahalanobis D^2 statistics for yield and its attributing traits. These all genotypes were grouped into six clusters by using Toucher's method based on eight quantitatively inherited characters which represent the vast genetic diversity and it could be used for further crop improvement programmes. Similar results were also reported by previous workers. Ranjani et al. [8] and Sharma et al. [12] observed seven and nine cluster were grouped from 68 genotypes, respectively; Kandarkar et al. [4] ~~were found showed~~ that the twenty-seven genotypes that they researched on were grouped into six clusters. The present investigated results revealed that among the six clusters highest number of genotypes were included in cluster I (16) whereas all the other five clusters comprised of one genotype per cluster (Table 2). The greater inter-cluster than the intra-cluster distances was recorded except for the cluster II and cluster III (Table 3), revealed that considerable genetic diversity among the lines are present and selection of genotype based on larger cluster distance can offer to get desirable combination for improvement in pigeonpea varieties used in the investigated experiment. The dendrogram depiction for twenty-one diverse genotypes of pigeonpea is elaborated in Fig 1. The maximum intra-cluster distance was observed for the cluster I (6.23) with 16 genotypes. It indicated that the genotypes present in these clusters is diverse than those in other clusters.

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Mono-genotypic cluster was observed for cluster II (ICPL 15072), cluster III (WRG 327), cluster IV (AAUVT 13-20), cluster V (PT 0904-1-1-2) and cluster VI (BAUPP 16-01) with intra-cluster distance were zero (0.00) because these clusters consisted only one genotype. Mono-genotypic cluster revealed that within these clusters the genotypes were more diverse and had entirely different genetic constitution than the remaining genotypes. These results indicated that if hybridization is attempted between the genotypes included in these cluster, lot of genetic diversity will be produced in the segregating generation and the selection for desirable genotypes can be practiced. The greater inter-cluster distance as comparison to intra-cluster distance was also reported by previous workers Bisht et al. [3], Naing et al. [6] and Pushpavalli et al. [7]. The maximum inter-cluster distance (16.54) between the cluster II and cluster VI followed by cluster IV and VI with the distance (14.34) and Cluster III and VI (13.22) indicating that genotypes from these clusters were highly divergent and hence selection of parents for hybridization from these clusters is suggested for realization of maximum heterosis. Singh et al. [13] also revealed that the greater inter-cluster distance (128.60) and intra-cluster distance (17.81) was recorded for six clusters grouped from twenty-one ~~pigeonpea~~ [pigeon pea](#) genotypes. The lower inter-cluster distance was found with inter-cluster distance values were 5.92 (Cluster II and III) followed by 7.24 (Cluster II and IV) and 7.49 (Cluster V and VI). The higher inter-cluster distance indicated that the genotypes of those clusters were distantly related, whereas the lowest inter-cluster distance indicates the closeness and similarity among the genotypes of the different clusters.

3.2 Clusters mean and percentage contribution for different traits among the six different clusters

Cluster mean for eight ~~yield attributing~~ morphological traits [associated with yield](#) for six different clusters is demonstrated in the (Table 4). The clusters with high average mean value for yield and yield contributing traits can be utilized in crop improvement to achieve higher

productivity. The cluster mean for days to 50% flowering ranged from 119 days (Cluster VI) to 135 days (Cluster IV) while days to maturity ranged from 184.67 days (Cluster V) to 212.67 days (Cluster II). The cluster mean for the primary branches/plant ranged from 22.53 to 30.27. Cluster III had the highest mean value for primary branches/plant (30.27) and secondary branches/plant (44.83) whereas the minimum cluster mean was observed 22.53 and 20.33 for primary and secondary branches/plant in the cluster IV. The genotypes included in these clusters can be used as donors for a greater number of primary and secondary branches/plant in [pigeonpeapigeon pea](#). Cluster II was found to have highest mean value for pods/plant (323.13) followed by 322.20 (Cluster V), 298.07 (Cluster IV) and 297.80 (Cluster III). Selection in these cluster group as a greater number of pods/plant is directly related to higher seed yield and hence, the genotype namely WRG 327, ICPL 15072, PT 0904-1-1-2 and AAUVT 13-20 from different cluster can be used as a donor for a greater number of secondary branches/plant and number of pods/plant. Cluster mean for the plant height ranged from 168.00 cm to 209.67 cm. The highest clusters mean for plant height (209.67 cm) was recorded in the cluster VI followed by cluster I (202.50), cluster V (190.40) and cluster III (189.60). If the breeder's objective is to get more biomass, the plant height becomes a promising trait as it results in more biomass and ultimately can be used as donors for more plant height whereas the minimum plant height (168.00 cm) was observed in the cluster IV. The cluster mean was obtained for 100-seed weight ranged from 10.93g to 12.83g. Cluster IV had the highest mean value (12.83 g) for 100-seed weight followed by cluster I (12.39), cluster II (12.37) and cluster V (12.30) and thus, the genotype comprised in these cluster can be used as a donor parent for higher 100-seed weight while the lowest 100-seed weight in cluster III (10.93 g). The cluster means for seed yield in kg/ha ranged from 1107.33 kg (Cluster II) to 1650 kg (Cluster VI). Thus, to make selection for higher seed yield the genotype viz., BAUPP 16-01 were used as a donor for yield traits.

The contribution in percentage for yield and its attributing traits towards total divergence is illustrated in (Fig 2) and ~~it~~ this indicated that seed yield kg/ha (32.38%) showed more contribution towards the genetic diversity followed by the 100-seed weight (15.71%), secondary branches/plant⁻¹ and days to maturity (15.24%). Thus, these traits were identified as a major contributing trait in relation to genetic diversity in ~~pigeonpea~~ pigeon pea genotypes. The minimum diversity was contributed by pods/plant (2.38%) followed by primary branches/plant (4.76%), days to 50% flowering (6.19%) and plant height (8.10%). This is in conformity with Naing et al. [6] when they reported that more contribution towards genetic diversity for pigeon pea are days to maturity, pods/plant, days to 50% flowering and seed yield; Ranjani et al. [8] observed that maximum contribution towards the genetic diversity for the traits ie-i.e., 100-seed weight and days to maturity; Sandeep et al. [10] reported maximum contribution for seed yield, 100-seed weight and days to 50% flowering.

4. CONCLUSION

Based on the observation on the present study of greater inter-cluster distance between the cluster II, IV& VI and III & V; the hybridization between the genotype consisted within these cluster namely ICPL 15072, WRG 327, AAUVT 13-20, PT 0904-1-1-2 and BAUPP 16-01 will produced wide range of genetic variation in segregating generations and desirable segregants may be obtained. The character seed yield kg/ha, 100-seed weight, secondary branches/plant and days to maturity showed more contribution towards the genetic diversity. Thus, these characters were identified as major contributing characters towards the genetic divergence.

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Table 1. Genotypes investigated during experimentation

| S. No. | Genotypes | S. No. | Genotypes |
|--------|--------------|--------|----------------|
| 1. | ICPL 87119 | 11. | PT 0904-1-1-2 |
| 2. | BDN 716 | 12. | AAUVT 13-20 |
| 3. | JKM 189 | 13. | ICPL 15072 |
| 4. | BAUPP 16-01 | 14. | ICPL 15062 |
| 5. | CRG 16-11 | 15. | GJP 1820 |
| 6. | WRG 327 | 16. | GJP 1801 |
| 7. | WRG 369 | 17. | IBTDRG 8 |
| 8. | SKNP 1614 | 18. | IBTDGR 10 |
| 9. | BDN 2013-5 | 19. | RPS 2007-106-1 |
| 10. | PT 10-36-1-2 | 20. | AKTM 1637 |
| | | 21. | AKTM 1644 |

Table 2. Clustering Patterns of genetic diversity

| Cluster No. | Genotypes in number | Genotypes |
|-------------|---------------------|---|
| I | 16 | PT 10-36-1-2, RPS 2007-106-1, IBTDRG 8, ICPL 15062, IBTDGR 10, AKTM 1644, GJP 1820, BDN 716, GJP 1801, ICPL 87119, WRG 369, CRG 16-11, SKNP 1614, BDN 2013-5, JKM 189, AKTM 1637. |
| II | 1 | ICPL 15072 |
| III | 1 | WRG 327 |
| IV | 1 | AAUVT 13-20 |
| V | 1 | PT 0904-1-1-2 |
| VI | 1 | BAUPP 16-01 |

Table 3. Intra (Diagonal) and Inter-cluster distance based on D² Values

| | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI |
|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| Cluster I | 6.23 | 8.50 | 8.80 | 8.51 | 9.76 | 11.86 |
| Cluster II | | 0.00 | 5.92 | 7.24 | 11.48 | 16.54 |
| Cluster III | | | 0.00 | 9.23 | 8.50 | 13.22 |
| Cluster IV | | | | 0.00 | 11.21 | 14.34 |
| Cluster V | | | | | 0.00 | 7.49 |
| Cluster VI | | | | | | 0.00 |

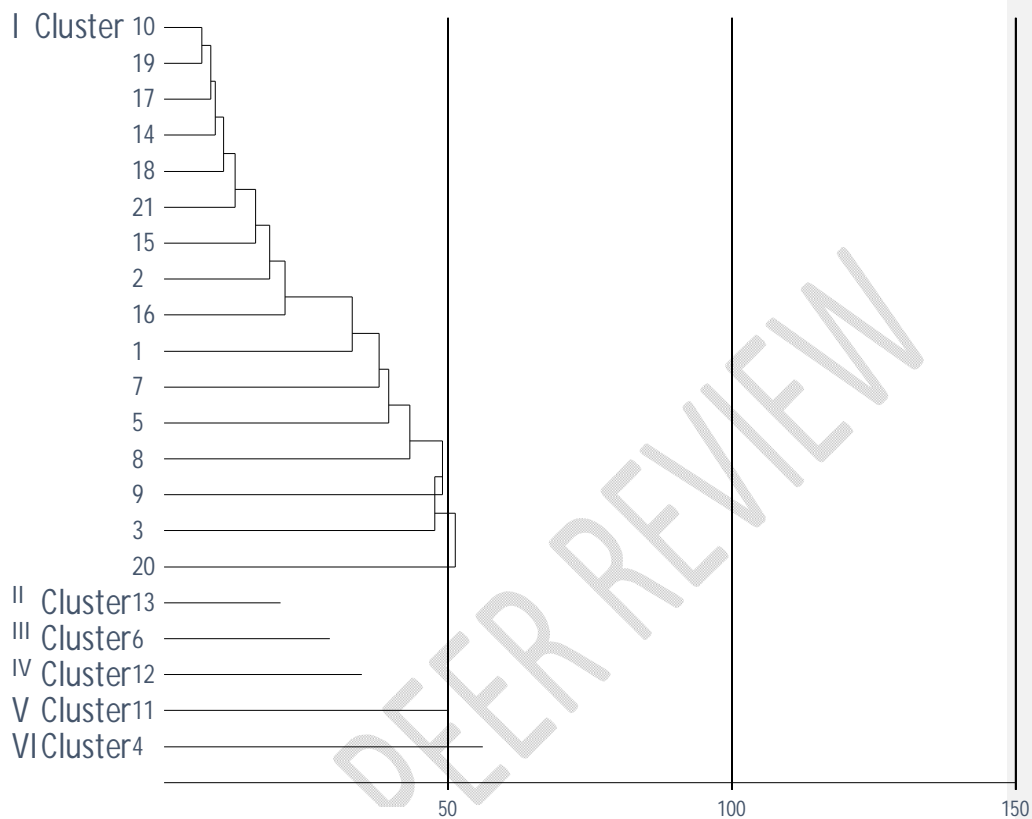


Fig 1. Dendrogram for 21 Genotypes among the different clusters in Pigeonpea by Toucher's Method

Table 4. Average cluster mean for eight quantitative traits among the six different cluster

| Cluster No. | Days to 50% flowering | Primary branches plant ⁻¹ | Secondary branches plant ⁻¹ | Pods plant ⁻¹ | Plant height in cm | Days to maturity | 100-seed weight in g | Seed yield in kg ha ⁻¹ |
|-------------|-----------------------|--------------------------------------|--|--------------------------|--------------------|------------------|----------------------|-----------------------------------|
| I | 133.33 | 24.03 | 34.38 | 264.85 | 202.50 | 209.90 | 12.39 | 1334.98 |
| II | 134.67 | 26.80 | 43.73 | 323.13 | 169.27 | 212.67 | 12.37 | 1107.33 |
| III | 132.33 | 30.27 | 44.83 | 297.80 | 189.60 | 203.00 | 10.93 | 1190.67 |
| IV | 135.00 | 22.53 | 20.33 | 298.07 | 168.00 | 206.00 | 12.83 | 1180.00 |
| V | 119.67 | 24.13 | 42.20 | 322.20 | 190.40 | 184.67 | 12.30 | 1329.67 |
| VI | 119.00 | 23.13 | 28.00 | 277.67 | 209.67 | 186.00 | 11.30 | 1650.00 |

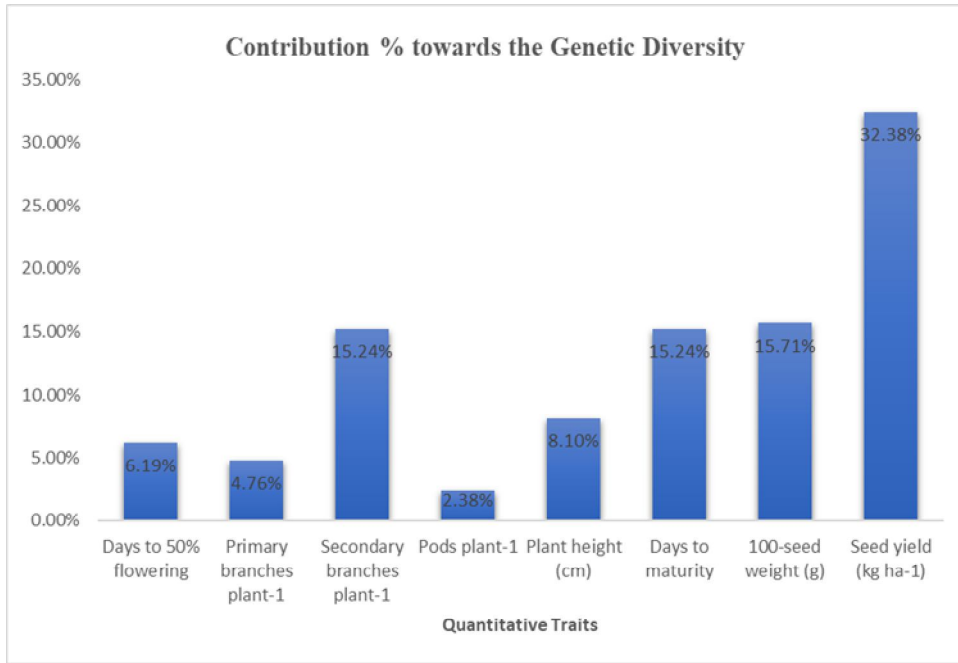


Fig 2. Contribution % towards the genetic diversity for 21 diverse genotypes for eight quantitative traits

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