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Research Article

Genetic diversity in land races of pigeonpea (*Cajanus cajan* (L.) Millsp.)

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Abstract

A study was conducted to determine the genetic diversity among sixteen pigeonpea land races for eleven characters. Highly significant differences existed among the genotypes for all the eleven characters studied. Phenotypic coefficients of variation (PCV) were found to be higher than the genotypic coefficient of variation (GCV) for all the traits. PCV and GCV values were low to moderate for the traits *viz*., plant height, the number of primary branches per plant, 100 seed weight and single plant yield. High heritability was observed for days to 50% flowering, number of pods per plant, number of seeds per pod, 100 seed weight, shelling percent, days to maturity, single plant yield and seed fibre content. High heritability coupled with high genetic advance as per cent of mean was observed for 100 seed weight and single plant yield indicating the additive gene effect, hence further improvement of these characters would be possible through direct selection. The genotypes were grouped into seven distinct clusters upon cluster analysis based on eleven traits. Cluster III was the largest and consisted of seven genotypes indicating considerable variability among the land races of pigeonpea. The genotypes with specific traits could be selected and used in the crossing programme to improve the yield and protein content in pigeonpea.

Key words
Pigeonpea, genetic variability, genetic advance as per cent of mean, heritability, quantitative traits

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp) is the second important pulse crop after chickpea in India. As it produces protein rich food with fewer inputs and can be grown in diverse cropping systems, it has a significant role in subsistence agriculture. In India, pigeonpea is cultivated in 5.34 million ha with an average productivity of 913 kg/ha (INDIASTAT, 2017). To achieve the dietary needs of the population, an increase in the production of pulses is necessary. The success of any crop improvement programme depends upon the extent of genetic variability existing among diverse germplasm, choice of parents for hybridization and selection procedure adopted. The seed yield of pigeonpea is a complex character, which is highly influenced by environmental variations. For any systematic breeding programme, knowledge on nature and magnitude of existing variability in a population due to genetic and non genetic causes is an essential prerequisite. The present study is aimed to assess the genetic diversity present in the sixteen genotypes for eleven quantitative characters.

Materials and Methods

The sixteen pigeonpea land races (Table 1) obtained from the Department of Plant Genetic Resources, TNAU, Coimbatore were raised in a randomized block design (RBD) with two replications during *Kharif* 2018 at Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. Each genotype was sown in a single row of 4 m length with a spacing of 90 × 25 cm. Observations were recorded for eleven traits *viz*., days to 50% flowering, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), shelling per cent, days to maturity, single plant yield (g), seed protein content (%) and seed fibre content (%). The observations were recorded on three randomly selected competitive plants in each accession from each replication based on descriptors for pigeonpea (PPV & FRA, 2007). The analysis of variance for yield and yield contributing characters were carried out as suggested by Panse and Sukhatme (1964). The phenotypic and genotypic variability for each character was estimated by using the method given by Burton (1952), heritability (h^2) in the broad sense according to Lush (1940) and the genetic advance as per cent of mean was worked out based on the method given by Johnson *et al*. (1955). Cluster analysis was carried out based on the Euclidean distance using standardized morphological data and dendrogram was constructed based on the UPGMA method by NTSYS pc 2.02 software.

Results and Discussion

The extent of genetic variability in base population is the fundamental stone for the success of any breeding programme. It is essential to subject a population for selection to achieve improvement in a particular trait. In the present study, the analysis of the variance showed significant difference among the genotypes for all the characters studied indicating the existence of considerable genetic variation in the pigeonpea genotypes. Mean, range, phenotypic coefficients of variations (PCV), genotypic coefficients of variations (GCV), heritability and genetic advance as per cent of mean for eleven characters are presented in Table 2. The genotype Puliampatti local-1 was found to be the earliest to flower (119 days) while, Bendrahalli local-1 was late to flower (140 days) with a mean value of 132 days for days to 50% flowering. The plant height ranged from 166.16 (BSR 1) to 258.83 cm (CRG 13-01) with a mean value of 196.67 cm. The number of pods per plant ranged from 587.28 (Vandikarankottai local) to 775.17 (Kunnathur local) with a mean value of 667.19. The single plant yield recorded the mean value of 105.79 g and it ranged from 63.44 (Singarapettai local) to 145.36 g (Kunnathur local). The hundred seed weight ranged from 6.85 (Uthangurai local) to 11.05 g (BSR-1) with a mean value of 8.41 g. The genotypes puliampatti local-2 (26.57 per cent) and Vandikarankottai local (7.91 per cent) recorded high protein and fibre content, respectively. Hulse *et al.* (1977) reported seed protein content around 22 per cent in pigeonpea genotypes. Saxena *et al.* (2000) reported the levels of protein in high-protein lines to range from 28.7 to 31.1 per cent and fibre content to range from 6.6 to 8.2 per cent.

The components of variance revealed that the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environmental variance in the total variance. Among the eleven characters studied, days to 50% flowering (5.31 & 5.21), number of pods per plant (8.60 & 6.84), number of seeds per pod (7.07 & 5.59), shelling per cent (3.44 & 3.23), days to maturity (3.04 & 2.75), seed protein content (2.45 & 1.87) and seed fibre content (9.59 & 8.61) were recorded low PCV and GCV (Fig. 1). Similar results were earlier reported by Verma *et al.* (2017), Anuj Kumar *et al.* (2018), Ranjani *et al.* (2018) in pigeonpea for days to 50% flowering, shelling per cent and days to maturity. The magnitude of low to moderate PCV and GCV was observed for plant height (11.79 & 8.71), number of primary branches per plant (10.19 & 7.66), 100 seed weight (16.19 & 16.05) and single plant yield (18.69 & 16.61). This was akin with earlier findings of Anuj Kumar *et al.* (2018) and Ram *et al.* (2016) for plant height. Although GCV indicates the high degree of genetic variation, heritability estimates, and genetic gain are the parameters determining the amount of heritable portion in each trait. High heritability was observed in the characters *viz.*, days to 50% flowering (96.09 per cent), number of pods per plant (63.34 per cent), number of seeds per pod (62.58 per cent), 100 seed weight (98.28 per cent), shelling per cent (88.22 per cent), days to maturity (81.57 per cent) and single plant yield (78.97 per cent) and seed fibre content (80.65 per cent). Similar results was already given by Verma *et al.*(2017), Pushpavalli *et al.* (2017), Pushpavalli *et al.* (2018). Medium heritability was recorded for plant height (54.55 per cent), number of primary branches per plant (56.44 per cent) and seed protein content (58.65 per cent).

The high genetic advance as per cent of mean was recorded for characters *viz.*,100 seed weight (32.78) and single plant yield (30.40). The traits namely days to 50% flowering (10.52), plant height (13.25), number of primary branches per plant (11.85), number of pods per plant (11.22) and seed fibre content (15.94) were shown moderate genetic advance. However, the low genetic advance as per cent of mean was recorded for characters *viz.*, number of seeds per pod (9.11), shelling per cent (6.25), days to maturity (5.11) and seed protein content (2.96). According to Johnson *et al.* (1955), heritability estimates along with the genetic gain are usually more useful. High heritability coupled with high genetic advance as per cent of mean was observed in 100 seed weight and single plant yield indicating the role of the additive gene action in expressing these traits, suggesting better scope for improvement of these traits through direct selection. Ram *et al.* (2016), Pushpavalli *et al.* (2017), Kumar *et al.* (2018) and Satyanarayana *et al.* (2018) also reported similar results for 100 seed weight and single plant yield in pigeonpea.

The sixteen pigeonpea genotypes were grouped into seven major clusters based on multivariate analysis at 15.54 dissimilarity coefficient value (Fig 2). The value of 15.54 was set only for the convenience of explanation in this case. Cluster III contained the maximum number of genotypes (7), which consisted of 43.75 per cent of all genotypes. Clusters II, cluster IV and cluster V comprised of two genotypes each and remaining were solitary clusters, indicating that the genotypes, Puliampatti local-1, CRG 13-01 and BSR 1 are distinct from other genotypes. The cluster analysis revealed that Bendrahalli local-1, and Irapputhuvarai local, were found to be 100 per cent similar. The similarity may be due to movement of seeds by the farmers.

Magnitude of phenotypic coefficient of variation in selected pigeonpea genotypes for all characters taken for the study was higher than genotypic coefficient of variation. High genetic advance as per cent of mean along with high heritability was recorded for 100 seed weight and single plant yield. The genotypes were grouped into seven distinct clusters indicating high variability among the genotypes studies. Wide variability was observed for primary yield contributing characters *viz.*, number of pods per plant, 100 seed weight and single plant yield. Apart from this high seed protein content was observed in the local land races. Hence, these genotypes could be selected and used in the crossing programme for the improvement of specific traits, yield and protein content in pigeonpea.

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Table 1. List of sixteen pigeonpea genotypes.

Sl.No.	Genotypes
1	Puliampatti local-1
2	Jambukuttaipattilocal
3	Bendrahalli local-1
4	Puliampatti local-2
5	Bendrahalli local-2
6	Singarapettai local
7	Pillayakothur local
8	Vandikarankottai local
9	Kunnathur local
10	Uthangarai local
11	Irapputhuvarai local
12	Soolagiri local-1
13	Soolagiri local-2
14	Gengusettipatti local
15	CRG 13-01
16	BSR 1

Table 2. Genetic parameters for 11 characters in pigeonpea land races

Characters	Mean	Range	PCV (%)	GCV (%)	h^2 (%)	GAM
Days to 50% flowering	132.00	119.00 -140.00	5.31	5.21	96.09	10.52
Plant height (cm)	196.67	166.16-258.83	11.79	8.71	54.55	13.25
Number of primary branches per plant	20.44	17.66-23.17	10.19	7.66	56.44	11.85
Days to maturity	178.00	166.00 -183.00	3.04	2.75	81.57	5.11
Number of pods per plant	667.19	587.28-775.17	8.60	6.84	63.34	11.22
Number of seeds per pod	3.90	3.67-4.50	7.07	5.59	62.58	9.11
Shelling per cent	64.50	61.51-68.03	3.44	3.23	88.22	6.25
100 seed weight (g)	8.41	6.85-11.05	16.19	16.05	98.28	32.78
Single plant yield (g)	105.79	63.44-145.36	18.69	16.61	78.97	30.40
Protein per cent	25.52	24.63-26.57	2.45	1.87	58.65	2.96
Fibre per cent	7.16	6.17-7.91	9.59	8.61	80.65	15.94

*PCV- Phenotypic coefficient of variation: GCV-Genotypic coefficient of variation: h^2 -heritability: GAM- genetic advance as per cent of mean

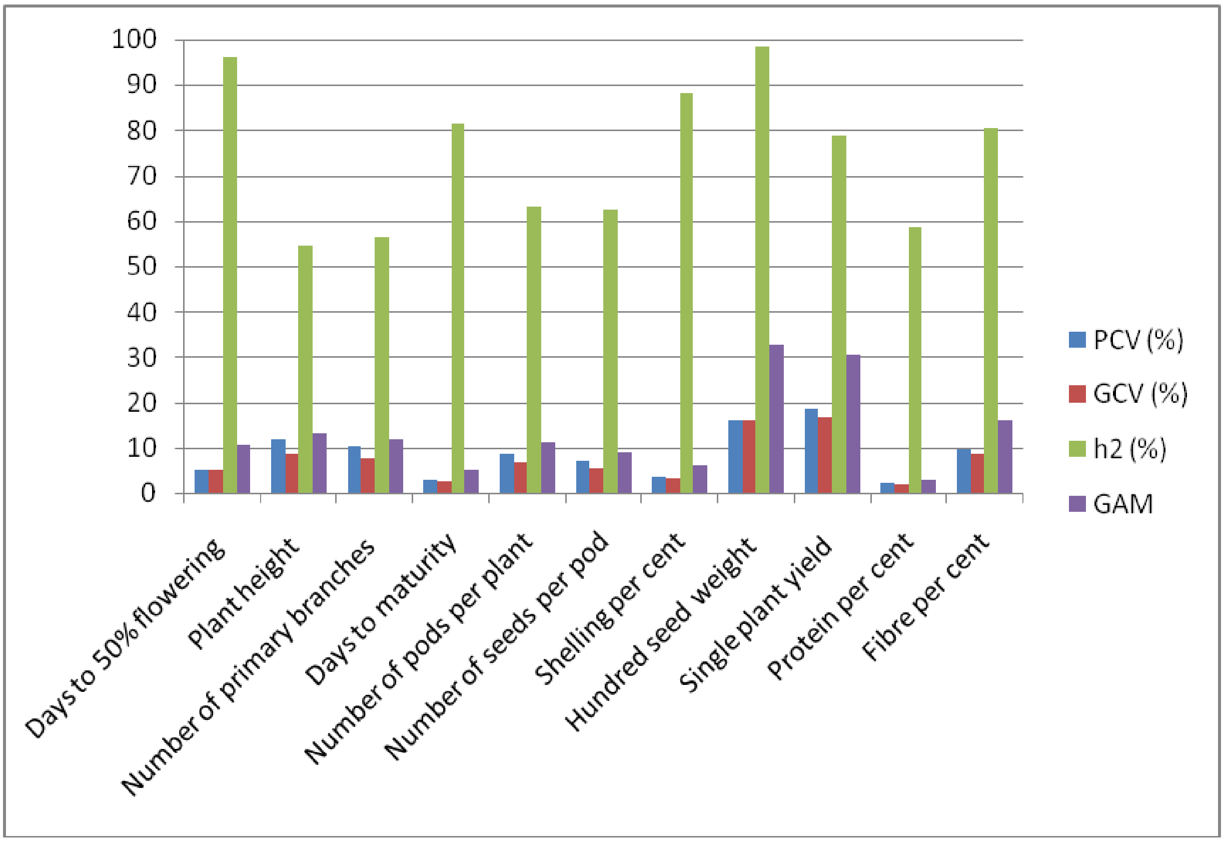

Fig. 1. **Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), Heritability (h^2) and Genetic advance as per cent of mean (GAM) for 11 characters in pigeonpea**

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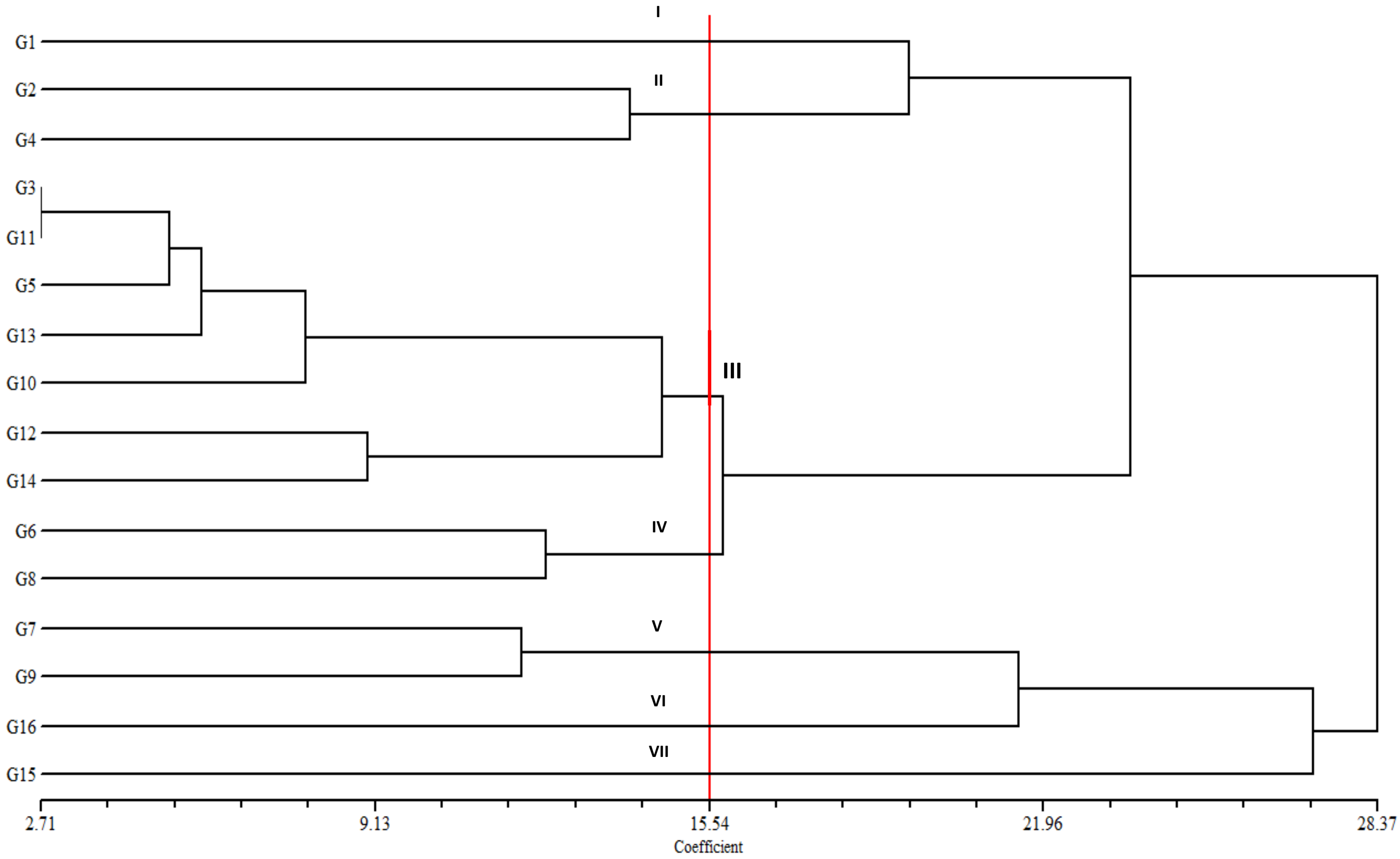

Fig. 2. **Cluster analysis of 16 pigeonpea genotypes based on 11 characters.**

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