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GENETIC DIVERGENCE IN PIGEONPEA (*CAJANUS CAJAN* (L.) MILLSP.)

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ABSTRACT

Forty early maturing genotypes of pigeonpea (*Cajanus cajan*) from different geographic regions were selected for D^2 analysis and canonical analyses. All genotypes of pigeonpea were grouped into three clusters. Genetic diversity was independent of geographic origin. High variability could be obtained for earliness, seed yield and protein content in crossing programme involving genotypes from widely related clusters.

Key words: Variability, diversity, clusters, pigeonpea.

The D^2 statistic has found favour as a tool for estimating genetic divergence. In a breeding programme, progenies derived from diverse crosses are expected to show a broad spectrum of genetic variability, providing a greater scope for isolating high yielding segregates in the advanced generations. Genetic diversity has been analysed in many crops but such studies in pigeonpea are very limited.

MATERIALS AND METHODS

Forty early maturing genotypes of pigeonpea from different geographic regions were grown in randomized block design with four replications. Each entry had one 4 m long row with 45 cm and 20 cm spacing between rows and plants, respectively. Five competitive plants per replication in the middle of the row were taken in each genotype and observations recorded on individual plants for 15 morphological and developmental traits.

The analysis of variance was carried out for all characters individually. The data were subjected to the statistical analysis as per standard method [1]. The clustering of genotypes was done by the Tocher's method [2], and canonical analysis was done following the usual procedure.

RESULTS AND DISCUSSION

Analysis of variance for each individual character showed highly significant differences among the genotypes for all the 15 characters studied. The divergence for characters within the lines, tested by the Wilks' criterion, was significant ($\chi^2 = 1700$ for 585 d.f.). Thus, the analysis of genetic divergence among the genotypes used in the study was considered to be relevant.

The D^2 values ranged from 4.3 to 348.7. By the application of clustering technique, the 40 genotypes were grouped into three clusters. The constituents of different clusters with their source are presented in Table 1. Among the three clusters, cluster I was the largest having 38 genotypes from different geographic regions. The remaining two genotypes, DA9 and WB 20/105, represented clusters II and III, respectively. The clustering pattern of genotypes from different geographic regions was of random nature. Genotypes belonging to different states of India constituted a single cluster (cluster I). Clusters II and III had one genotype each from Bihar and West Bengal, respectively.

Table 1. Composition of D^2 clusters in pigeonpea

Cluster	No. of strains	Strains/varieties	Source/origin
I	38	CO5, CORG 5, 6, RG 8401, 8402, 8403, 8404 and 8405	Tamil Nadu
		DA 6	Bihar
		ICPL Nos. 1, 6, 14, 81, 85, 87, 107, 111, 112, 142, 146, 154, 161, 186, 189, 269 and 8330	ICRISAT
		EC 117712/3	CIAT (Columbia)
		HY 2	Andhra Pradesh
		H 77/216 and 80/110	Haryana
		H 77/208	Punjab
		Prabhat, T 21, UPAS 120 and VL 23	Uttar Pradesh
		Pusa 33 and Pusa 78	IARI, New Delhi
		TT 5	BARC, Bombay
II	1	DA 9	Bihar
III	1	WB 20/105	West Bengal

The clustering pattern revealed that the tendency of genotypes from diverse geographic regions to group together in one cluster may be due to similarity in requirements and selection approaches followed under domestic cultivation [3, 4]. It was also observed that eight genotypes from Tamil Nadu were grouped in a single cluster, which may be due to commonness in genetic structure and selection history.

Table 2. Cluster means for fifteen characters in pigeonpea

Character	Mean values of different clusters			Pooled mean
	I	II	III	
Plant height (cm)	73.9	44.2	83.0	73.4
Days to flowering	77.9	61.0	97.3	78.0
Days to maturity	116.7	100.3	142.5	116.9
No. of branches	4.6	3.9	6.4	4.7
No. of clusters	15.3	11.6	20.4	15.4
Pods per cluster	2.5	2.1	2.2	2.5
Pods per plant	36.8	22.4	41.6	36.6
Seeds per pod	3.7	3.7	3.9	3.7
Pod length (cm)	5.7	5.3	5.8	5.7
100-seed weight (g)	7.7	3.7	10.9	7.7
Protein content (%)	24.8	26.9	21.8	24.8
Leaf area index	1.3	0.7	2.2	1.3
Harvest index (%)	30.4	20.7	32.6	30.2
Dry matter production (g)	22.7	8.3	30.8	22.6
Seed yield (g)	6.9	1.7	10.1	6.9

Another feature that came to light was that two varieties from Bihar were placed in separate clusters, indicating wide genentic diversity among genotypes originating from the same geographic region. The clustering pattern, thus, failed to indicate any relationship between genetic divergence and geographic distribution. This is in agreement with the earlier findings in pigeonpea [5, 6].

The only intracluster distance obtained for cluster I was low (6.18), indicating closeness of genotypes within this cluster (Table 3). Among the three clusters, intercluster distance was relatively higher between clusters II and III (19.61). These clusters also had maximum mean values for most of the characters (Table 2). Genotypes from these two clusters may be selected for more effective crossing programme and should result in a wide spectrum of variability. Selection could be made for earliness combined with high seed yield and high protein content in the subsequent generations.

Table 3. Average intracluster (in bold) and intercluster distances (d) in pigeonpea

Clusters	I	II	III
I	**6.18**	11.71	12.34
II			19.61
III			

The canonical analysis confirmed the clustering pattern arrived at by D^2 statistic. The distribution of genotypes reflected a general parallelism between the grouping pattern obtained by the two methods (D^2 and canonical) of analysis.

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