

Research Note

Assessment of genetic diversity in pigeonpea germplasm collection using morphological characters

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Abstract

An investigation was undertaken to ascertain the extent of genetic diversity present among 90 pigeonpea genotypes using D^2 statistic. Cluster analysis grouped 90 germplasm into six clusters based on the degree of divergence between the genotypes. Clustering pattern revealed non parallelism between genetic diversity and geographic distribution. Inter cluster distance was least between cluster II and cluster III and cluster I and VI, indicating less divergence in these four clusters. Maximum inter cluster distance was noticed between the cluster V and cluster VI, cluster IV and cluster VI, cluster II and cluster VI and cluster I and cluster V, indicating more divergence of cluster V and this cluster had five genotypes viz., C -2291, ICP7234, ICP12225, AL1741, ICP2391. Accessions of cluster V were more divergent with maximum intra cluster distance followed by cluster I. The crossing between cluster V which is having high cluster mean value for seed yield per plant and number of pods per plant and cluster II which is having lowest mean for days to 50 percent flowering is expected to yield high yielding early pigeonpea varieties. Morphological characterization was carried out for nine traits, some of the genotypes had unique characters which helps in varietal or genotype identification.

Key words:

Pigeonpea, genetic diversity, germplasm

Pigeonpea (*Cajanus cajan* (L.) Millspaugh) ($2n = 22$) is the second most important pulse crop of India after chickpea, commonly known as arhar, redgram and tur. Pigeonpea is a grain legume belonging to the *Cajaninae* sub-tribe of the economically important leguminous tribe Phaseoleae. Based on the natural genetic variability in local germplasm and the presence of numerous wild relatives, Van der Maesen (1990) concluded that India is probably primary centre of origin. Pigeonpea is an important pulse crop that performs well in semi-arid tropics where moisture availability is unreliable or inadequate (Reddy *et al.*, 1993). India is the largest producer of pigeonpea in the world sharing approximately 70% of the production and covering 74% of the area (Bohra *et al.*, 2012). Pigeonpea occupies an area of about 4.04 million hectares in India with a production 2.65 million tonnes, with a productivity of 656 kg/ha (INDIASTAT, 2012). Although India leads the world both in area and production of pigeonpea, its productivity is lower than the world average. One of the factors responsible for the poor productivity of pigeonpea is the lack of improved cultivars. Research for genetic improvement of this crop is required to raise yield levels effectively through widening genetic base.

The experiments for the present study were conducted in the Newrea, Department of Pulses,

TNAU, Coimbatore during *Kharif* 2013. The experimental material comprised of 90 pigeonpea germplasm. The experiment was laid out in Randomised Block Design with two replications. Observations were recorded for eight quantitative traits. They are days to 50 % flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, hundred seed weight and seed yield per plant. The quantitative measurement of genetic divergence among the genotypes was carried out by Mahalanobis D^2 statistic (Rao, 1952). The observations on nine morphological characters were recorded in the form of multiscale scores. The scaling adopted as per the International Bureau for Plant Genetic Resources (IBPGR)'s descriptor (IBPGR, 1993) on pigeonpea.

The genotypes included in the present study were from the different sources and were grouped into six clusters (Table 1). Cluster I was the largest with eighty one genotypes followed by cluster V and other clusters possessing one genotype each. Clustering patterns indicated that the genotypes originating from different geographical regions grouped together into different clusters. This non parallelism may be due to genetic drift and intense natural and human selection for diverse adaptive gene complexes under different environments causing greater diversity among genotypes rather

than their geographic distances. Thombre *et al.* (2000), Rekha *et al.* (2011) also found no parallelism between genetic diversity and geographic distribution.

The grouping of the genotypes from homogenous source into different clusters, as observed in the present study, is expected because of free exchange of breeding material among different regions. Consequently, the character constellation that might be associated with particular region in nature loses their individuality under human interference.

Cluster V recorded higher intra cluster distance followed by Cluster I (Table 2). The inter cluster distance was maximum between Cluster V and cluster VI followed by Cluster IV and VI followed by cluster II and VI followed by cluster I and cluster V and cluster I and VI indicating greater divergence belonging to these clusters. The crosses which involve parents from these more divergent clusters will yield relatively good amount of heterosis in F_1 and high frequency of transgressive segregants and genetic variability in subsequent generations. The chance of getting segregants with a high yield level was quite limited, when one of the clusters had a very low yield level. So, if greater diversity was observed between two high yielding clusters, then crossing between those clusters would result in segregants with better seed yield. The minimum inter cluster distance was found between cluster II and cluster III suggesting that the genotypes of these clusters were not genetically much diverse.

The cluster mean values are presented in Table 3. Among the characters cluster V recorded the highest mean value for number of pods per plant and seed yield per plant. Cluster II had highest mean values for number of seeds per pod and hundred seed weight. Crosses between C-2291, ICP7234, ICP12225, AL1741, ICP2391 and ICPL 89 are expected to exhibit high heterosis and might result in high yielding segregants with desired traits. Cluster II had the lowest mean values for days to 50% flowering and seed yield per plant. Cluster IV had lowest mean values for days to maturity and number of seeds per pod. Cluster III had lowest mean values for plant height. Cluster VI recorded lowest mean value for number of primary branches per plant, number of pods per plant and hundred seed weight.

Considering the mean performance for different characters of genotypes belonging to diverse clusters, the promising genotypes for exploitation as parents in hybridization programme were C-2291, ICP7234, ICP12225, AL1741, ICP2391 of cluster V, ICPL 89 for cluster II and ICPR525585 for cluster IV. Among the traits, number of pods

per plant exhibited maximum percentage towards genetic divergence followed by days to maturity (Table 4).

Morphological traits are important for varietal description. The percentage of variation for each morphological trait is presented in Table 5. The good level of variability was observed for growth habit, base flower color, pattern of streaks, pod color, pod form and seed color pattern. Considering the individual trait a majority of genotypes showed, 96.66 per cent showed yellow color, 94.44 per cent showed semi-spreading growth habit, 94.44 per cent showed mixed pod color, 66.66 per cent showed cylindrical pod shape, 66.66 per cent showed light brown color seeds and 52.22 per cent showed sparse streaks. Similar results were being reported by Upadhyaya *et al.* (2007) and Manyasa *et al.* (2008) for growth habit, base flower color, pattern of streaks, pod color, pod form and seed color pattern. These traits can be used for identifying individual germplasm.

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Table 1. Cluster composition of ninety pigeonpea germplasm

Cluster Number	No. of accessions	Accession number
1	81	ICP245335,ICP245375,ICP245474,ICP245517,ICP245527, ICP245532,ICP245534,ICP245541,AF284/2,VBN3,AS46/1,AL601,AL61 1/2,CRG9060,AS36,IC525466,IC525473,IC525489,IC525490,IC525505,IC525519,PUSA992,ICPL86020,CRG5/6,ICPR2431, ICPR2438,ICPR2363,ICPR2447,IC525514,IC525468,ICP1, ICP2387,IC73999,DPP-2-89,DPP-2-183,DPP-3-2,DPP-3-244, ICPL81-3,ICPL149,CO(Rg)7,ICPL88034,ICPL90047,ICPL92047, UPAS120,ICP10697,IC73895,IC332084,IC342747,IC339057,IC123325,AL1692,AL1727,AL1733,AL1734,AL1736,AL1739,ICPL88039,ICP24550 7,ICP245520,ICP245531, ICP245534, AF284/1,IC73353,C2542,DPP-2-52, DPP-2-177,ICP13271,ICP7919,ICP12912, ICP3-81,IC339116,IC73799,IC74016,AL1685,AL1727, ICPL88039-1,ICPL161,ICPL86022, AL1730,AL1740,DPP-2-188
2	1	ICPL89
3	1	CO5
4	1	ICPR 525585
5	5	C-2291,ICP7234,ICP12225,AL1741,ICP 2391
6	1	C-11

Table 2. Average intra (in bold) and inter cluster D² distances

Cluster No	I	II	III	IV	V	VI
I	41.28	68.73	71.33	73.54	105.65	89.26
II	68.73	0.00	15.93	22.93	50.30	125.14
III	71.33	15.93	0.00	21.87	48.74	121.69
IV	73.54	22.93	21.87	0.00	49.22	126.47
V	105.65	50.30	48.74	49.22	55.92	157.27
VI	89.26	125.14	121.69	126.47	157.27	0.00

Table 3. Cluster mean values for biometric characters in pigeonpea

S. NO	Characters	I	II	III	IV	V	VI
1	Days to 50% flowering	74.07	69.00	81.00	79.00	72.00	119.00
2	Days to maturity	112.68	113.00	119.00	108.00	108.70	176.00
3	Plant height	106.83	111.95	105.63	131.8	114.94	109.90
4	Number of primary branches per plant	8.02	7.50	7.76	9.15	8.36	5.39
5	Number of pods per plant	108.28	213.40	219.5	215.7	267.98	65.20
6	Number of seeds per pod	4.09	4.50	4.00	3.80	3.98	4.00
7	Hundred seed weight	8.51	9.56	8.14	8.65	9.26	7.95
8	Seed yield per plant	27.8	21.12	31.68	36.14	37.77	30.26



Table 4. Relative contribution of different characters towards divergence

S. No.	Characters	Number of times Ranked First	Contribution Percentage
1.	Days to 50 % flowering	31	0.77%
2.	Days to maturity	515	12.86%
3.	Plant height	313	7.82%
4.	Number of primary branches per plant	17	0.42%
5.	Number of pods per plant	2754	68.76%
6.	Number of seeds per pod	19	0.47%
7.	100 seed weight	89	2.22%
8.	Seed yield per plant	267	6.67%

Table 5. Morphological characterization of nine characters in pigeonpea

S.NO	Trait	Phenotype	Percentage
1	Growth habit	Erect and compact	4.44
		Semi-spreading	94.44
		Spreading	1.11
2	Base flower color	Yellow	96.66
		Orange-yellow	3.33
3	Second flower color	Red	98.88
		Purple	1.11
4	Pattern of streaks	Sparse streaks	52.22
		Medium amount of streaks	37.77
		Dense streaks	8.88
		Uniform coverage of second color	1.11
5	Flowering Pattern	Determinate	96.66
		Indeterminate	3.33
6	Pod color	Green	1.11
		Mixed	94.44
		Dark Purple	4.44
7	Pod form	Flat	33.33
		Cylindrical	66.66
8	Seed color pattern	Plain	100
9	Base seed color	Cream	8.88
		Light brown	66.66
		Reddish –brown	23.33
		Purple	1.11

