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Research Paper

GERMPLASM EVALUTION IN PIGEONPEA, *Cajanus cajan* MILLSP. USING MAHALANOBIS D^2 STATISTIC

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Abstract

Genetic divergence was studied by 66 genotypes of pigeonpea, *Cajanus cajan* Millsp at Agricultural Research Station, Tandur. The mean sum of squares was significant for all the characters studied indicating the presence of variability. Characters like number of pods per plant, number of secondary branches per plant and plant height exhibited heritability coupled with high genetic advance revealing that these characters were controlled by additive gene action. The hierarchical cluster analysis indicated the presence of considerable genetic divergence among the genotypes. The genotypes were grouped into nine clusters using Ward's minimum variance method. Principal component analysis (PCA) revealed that 95.48% of the total diversity was explained on the basis of the first three principal components. The inter cluster distance was maximum between IX and VI while the least between VI and I indicated the genotypes included in these clusters will give high heterotic response and thus better segregants. The maximum cluster means were revealed by cluster IX for most of the characters. Among the nine characters studied, number of pods per plant contributed the most (59.44%) towards the divergence of genotypes.

Key words: Germplasm, Mahalanobis D^2, genetic variability, pigeonpea.

INTRODUCTION

In India pigeonpea is principal pulse crop and occupies an area of about 3.2 lakh ha and it ranks second after chickpea. The crop is grown under diverse agro production situations, across the climatic and geographic boundaries which necessitated the development of more productive varieties of diverse origin. Plant breeders are always interested in assessing genetic divergence among the varieties or advanced breeding lines available with them so as to utilize in direct breeding programme because genetically diverse parents are likely to produce high heterotic effects and the distinctly related parents within species, when utilized in cross breeding programme, are likely to produce wide spectrum of variability (Arunachalam, 1981). D2 statistic developed by Mahalanobis (1936) was used to measure genetic divergence and to classify the genetic stock into distinct groups.

MATERIAL AND METHODS

The material for the present study consisted of 66 pigeonpea germplasm accessions and the experiment was laid at Agricultural Research Station, Tandur, ANGRAU during kharif 2012. Each accession was accommodated in a single row of 4m length with a spacing of 90 x 10cm. In each accession the observations were recorded on five randomly selected plants for collection if data on seed yield and attributed traits *viz.,* days to 50% flowering, days to maturity, plant height

(cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, test weight (g), pod damage percentage and seed yield (g/plant). Data collected were subjected to analysis of variance. Principal component analysis (Rao, 1964) was carried out using WINDOSTAT statistical software (Indostat Services). Genetic divergence was computed by multivariate analysis using Mahalanobis D^2 technique and the genotypes were grouped into clusters following Euclidean method as described by Rao, (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters studied. Wide variability was observed for pod damage percent, test weight, number of primary branches per plant and seed yield per plant. The genotype ICP 15016 was found earliest in days to 50% flowering (59 days) and maturity (109 days). The range of plant height was from 46.4 cm (ICP 10912) to 165.4 (ICP 14900), number of primary branches from 3 (ICP 9045) to 15.8 (Belkatur local), number of secondary branches per plant from 0 (ICP 11627) to 10.6 (Belkatur local), number of pods per plant from 22.4 (ICP 10912) to 201.2 (ICP 6370), test weight from 5.98 (ICP 10912) to 11.7 (ICP 13191), seed yield per plant from 7 g (ICP 14929 and ICP 10912) to 113 g (Belkatur local) and pod damage percent ranged from 0 (ICP 14900) to 16.02 (Gopalpur local). The high magnitudes of phenotypic as well as genotypic coefficients of variation were observed for pod damage percent, test weight, number of primary branches per plant and seed yield per plant indicated the presence of ample amount of variation for these characters. High heritability (35-99%) combined with high genetic advance as percent of mean for pods per plant, plant height and days to maturity revealed that these characters were controlled by additive gene action, suggesting that selection for these characters would be effective for crop improvement. These results are in agreement with those reported by earlier workers Rekha. *et al* (2011).

The principal component analysis (PCA) performed to analyze the structure of the genetic diversity in the germplasm set revealed that 95.48% of the total diversity was explained on the basis of the first three principal components (Table 3) based on the Eugine value – one criterion. The first principal component (PC1) had an Eugine value of 483.37 and explained 72.23% of the total variation. Number of pods per plant, plant height and test weight had the highest positive Eugine vector. The second principal component PC2 was responsible for 16.23% of the total variation and was positively related with days to 50% flowering, days to maturity, plant height and number of secondary branches per plant whereas number of pods per plant, number of primary branches per plant and test weight had the negative Eugine vector. The third principal component accounted for only 7.01% of the variation with higher positive contribution of number of pods per plant, days to 50% flowering, days to maturity and number of secondary branches per plant and negative from plant height, test weight, number of primary branches per plant and seed yield per plant. These results are in agreement with the earlier findings of Akande (2007).

The hierarchical cluster analysis of Ward's minimum variance method produced a dendrogram showing successive fission of individuals which clearly partitioned into the genotypes into eight clusters. The genotypes within each cluster were closer to each other than the genotypes grouped into different clusters. The maximum intra cluster distance was observed in cluster III (48.47) followed by cluster IV (40.23) and cluster I (39.32) indicating wide genetic variability within the genotypes of these three clusters (Table 2).The highest inter cluster distance was observed between IX and VI (371.86) followed by IX and I (317.51) and IX and II (300.20) suggesting wide diversity between genotypes of these clusters. Therefore genotypes belonging to theses clusters may be used in hybridization programmes for improvement of pigeonpea and may giver better segregants. The least inter cluster distance was observed between the clusters VI and I (63.13), II and I (67.9) indicating close relationship between the genotypes of these two clusters. Thombre *et al,* (2000) reported similar results in pigeonpea.

The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 3). The highest cluster mean revealed by cluster IX for

seed yield per plant, number of pods per plant, number of primary branches per plant, number of secondary branches per plant and plant height, while cluster VI showed minimum cluster means for days to 50% flowering and days to maturity. These results showed that the genotypes in these clusters were superior for different characters and genotypes much in use of these characters would offer a good scope of improvement of pigeonpea through rational selection. Vange and Moses. (2009) also reported similar results in pigeonpea.

Amongst the characters, number of pods per plant contributed the maximum towards genetic divergence (59.44%) followed by days to maturity (21.03%), plant height (13.47%), while characters *viz.,* number of secondary branches per plant (2.94%) and days to 50% flowering (1.77%) contributed least to genetic divergence (Table 5). These results are in conformity with those reported by Thombre *et al* , (2000).

Since varieties with narrow genetic base are more vulnerable to diseases and adverse climatic conditions, therefore the availability of the genetic diverse genotypes for hybridization programme becomes more important. In the present study the maximum inter cluster distance observed between cluster IX and VI, cluster IX and I and cluster IX and II and crosses among the genotypes *viz*., Belkatur local, ICP 13191, Gopalpur local and ICP 10912 would be resulted in transgressive segregants. Since number of pods per plant, plant height and days to maturity contributed maximum towards the divergence, direct selection of these traits help in crop improvement.

Table 1: Average intra and inter cluster distances (D^2 values) for nine clusters of in pigeonpea germplasm lines

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**39.32**	67.9	124.15	80.31	106.45	63.13	163.78	133.54	317.51
II		**38.78**	97.36	89.75	79.79	93.53	142.47	108.80	300.20
III			**48.47**	81.75	104.40	168.30	79.49	118.23	220.92
IV				**40.23**	102.57	128.66	106.98	129.32	250.33
V					**21.57**	146.08	116.41	127.94	266.53
VI						**0.00**	215.10	156.97	371.86
VII							**0.00**	148.35	162.52
VIII								**0.00**	287.66
IX									**0.00**

Table 2: Eigene values, proportion of the total variance represented by first three principal components, cumulative percent variance and component loading of different characters in pigeonpea germplasm lines

	PC1	**PC2**	**PC3**
Eigene value (root)	**233649**	**52504.61**	**22696.08**
Percent Var. Exp	**72.23891**	**16.23322**	**7.01711**
Cumulative variance explained	**72.23891**	**88.47214**	**95.48925**
Days to 50% flowering	0.14492	0.57015	0.14115
Days to maturity	0.17626	0.75377	0.11089
Plant height (cm)	0.37217	0.10418	-0.88496
Number of primary branches per plant	0.02264	-0.00988	-0.04203
Number of secondary branches per plant	0.03598	0.09950	0.04414
Number of pods per plant	0.86563	-0.26067	0.38397
Seed yield (kg/ha)	0.00436	-0.00196	-0.01634
Test weight (g)	0.24126	-0.13305	-0.17963
Pod damage %	0.00825	0.01617	-0.03086

Table 3: Cluster means of 66 accessions for seven quantitative traits in pigeonpea germplasm lines

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of pods per plant	Test weight (g)	Seed yield (kg/ha)	Pod damage %
Cluster I	62.41	111.59	80.59	5.12	0.85	65.71	8.13	19.06	3.25
Cluster II	94.53	155.05	94.39	5.24	2.81	73.16	8.06	19.53	3.85
Cluster III	101.87	161.87	109.20	6.13	4.75	157.27	8.10	36.00	3.77
Cluster IV	62.11	111.44	101.67	6.27	3.33	131.11	8.60	35.56	2.67
Cluster V	89.50	154.5	168.00	8.00	3.20	80.50	9.12	25.00	4.87
Cluster VI	62.00	112.00	46.00	4.40	1.20	22.0	5.98	7.00	2.68
Cluster VII	94.00	154.00	158.00	12.60	9.80	181.00	8.90	80.00	16.02
Cluster VIII	108.00	168.00	94.00	5.60	10.20	102.00	11.70	29.00	5.09
Cluster IX	95.00	155.00	225.00	15.80	10.60	325.00	10.20	113.00	6.77

Table 4: Percent contribution of different characters towards genetic divergence in pigeonpea germplasm lines

Source	Times ranked I st	Contribution %
Days to 50% flowering	38	1.77
Days to maturity	451	21.03
Plant height (cm)	289	13.47
Number of primary branches per plant	0	0.00
Number of secondary branches per plant	63	2.94
Number of pods per plant	1275	59.44
Seed yield (kg/ha)	0	0.00
Test weight (g)	28	1.31
Pod damage %	1	0.05

Table 5: Genetic parameters for agro morphological traits in pigeonpea germplasm lines

Character	PCV	GCV	Heritability (%)	GA	GA as % of mean
Days to 50% flowering	37.60	22.48	0.357	22.99	27.68
Days to maturity	17.47	17.31	0.981	49.09	35.32
Plant height (cm)	28.53	28.11	0.971	56.83	57.04
Number of primary branches per plant	95.11	33.48	0.124	1.43	24.27
Number of secondary branches per plant	275.11	274.50	0.996	25.56	564.20
Number of pods per plant	51.21	51.10	0.996	108.80	105.03
Seed yield (kg/ha)	89.28	15.44	0.030	0.45	5.50
Test weight (g)	61.52	61.49	0.999	35.19	126.64
Pod damage %	136.83	82.24	0.361	3.84	101.78

Table 6: Clustering pattern of pigeonpea germplasm lines accessions:

Cluster	Genotype
I	ICP 14999, ICP 14930, ICP 16303, ICP 11639, ICP 16307, ICP 15013, ICP 15016, ICP10926, ICP 14929, ICP 15014, ICP 14992, ICP14929, ICP 15021, ICP 14394, ICP 15011, ICP 14407, ICP 15017
II	ICP 2746, ICP 7, ICP 11059, ICP 15068, ICP 11477, ICP 7223, ICP 14900, ICP 7366, ICP 7148, ICP 12596, ICP 939, ICP 14903, ICP 11627, ICP1126, ICP 772, ICP 13011, ICP 3046, ICP16309, ICP12596
III	ICP 12410, ICP6370, ICP6929, ICP655, ICP6128, ICP 9414, ICP 1156, ICP 995, ICP 11543, ICP10503, ICP 2377, ICP 2698, ICP 12419, ICP 6992, ICP 9045
IV	ICP14933, ICP 16335, ICP14471, ICP 11717, ICP14397, ICP14732, ICP15015, ICP 15012, ICP 11633
V	ICP 14900, ICP 16308,
VI	ICP 10912
VII	Gopalpur local
VIII	ICP 13191
IX	Belkatur local

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