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Research Article

Genetic divergence and stability analysis in Pigeonpea (*Cajanus cajan* L.)

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Abstract :
Thirty Pigeonpea genotypes studied for genetic divergence using Mahalanobis D^2 statistic indicated wider genetic diversity. Considerable variability was observed for days to 50% flowering, days to maturity, plant height, number of pods per plant and seed yield due to non-linear pooled deviation. The variability was low for number of primary branches per plant and test weight. Among the 7 characters studied, seed yield contributed the most (89.49%) towards the divergence of genotypes followed by number of pods per plant, days to 50% flowering and plant height. The genotypes were grouped into 8 clusters, maximum inter cluster distance being observed between the clusters III and VII (725.69). Hence, crossing of parents from these clusters would be desirable for combining earliness, short plant height, more primary branches per plant with more pod number coupled with high seed yield. The genotypes ICPL 98008, ICPHAL 4979-2 and ICP 77303 were identified as desirable and stable for days to maturity. Stability parameters along with *per se* performance across three kharif seasons revealed that ICPL 20036 and ICPL 20058 were stable genotypes for seed yield and were found to be suitable for low input cultivation while, ICPL 13198 was found suitable for input rich cultivation.

Key words:
Genetic divergence, stability, Pigeonpea

Introduction

In India, pigeonpea occupies an important place in terms of area and production among pulses for its high protein content and dietary significance. Pigeonpea has witnessed significant increase in area, production and productivity since the inception of Technology Mission on Oilseeds and Pulses in 1986. Development and adaption of high yielding varieties have been instrumental in increasing the yield and production. Success of crop improvement programme in pigeonpea depends upon genetic diversity and the extent of genetic variability, choice of parents for hybridization and selection procedure adopted. It is necessary to screen and identify phenotypically stable genotypes for yield which could be more or less uniform under different environmental conditions. D^2 statistic developed by Mahalanobis (1936) is a powerful tool to measure genetic divergence among the genotypes. In the present study 30 genotypes of pigeonpea were chosen to study variability among the genotypes for seed yield and 6 yield related traits as well as stability of these genotypes in 3 varied environmental conditions.

Material and methods

Thirty pigeonpea genotypes were grown in 6 rows of 5m length in randomized block design with three replications during three kharif seasons namely kharif 2006-07,2007-08 and 2008-09. Row to row and plant to plant spacing were maintained at 100 and 20 cm, respectively. Observations were recorded for seven traits including days to 50% flowering, days to maturity, plant height, primary branches per plant, number of pods per plant, test weight and seed yield. Plant height, number of primary branches per plant and number of pods per plant were recorded on 10 randomly selected plants from each genotype, while, days to 50% flowering, days to maturity and seed yield were recorded on the plot basis. Test weight was recorded by taking random samples from plot yield. Variability was studied on the basis of mean values pooled over three years data. Bartlett's test was applied to test the homogeneity of variance and weighted analysis was used where year x genotype interaction was absent and error variance was heterogeneous, to make comparison among varietal mean (Panse and Sukhatme, 1985).

Stability analysis was conducted using three years data following Eberhart and Russell (1966) to determine stability regression coefficients and deviations from regression. The mean square for deviations from regression was tested against the residual mean square using the appropriate test

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suggested by Eberhart and Russell (1966). Genetic diversity among the varieties was determined by using Mahalanobis (1928) D^2 statistics and varieties were grouped into different clusters.

Results and discussion

Results of the present study are being discussed in terms of variability existed in the genotypes; performance of these genotypes for different traits and strategy to combine the desirable traits through hybridization followed by selection.

Variability and genetic divergence:

Phenotypic values of the 30 genotypes (Table 1 and 5) suggested the existence of diversity among the 30 genotypes tested in this study. Considerable variability was observed for days to 50% flowering, days to maturity, plant height, number of pods per plant and seed yield but low for number of primary branches per plant and test weight. Variation in plant height, flowering and maturity duration makes these genotypes suitable for cultivation under different agro climatic zones. However, there is need of further improvement for number of primary branches per plant, number of pods per plant and test weight, which will result in higher seed yield.

On the basis of D^2 values the 30 genotypes were grouped into 8 clusters (Table 2) with variable number of genotypes revealing the presence of considerable amount of genetic diversity in the material. Cluster I was the biggest cluster comprising 12 genotypes. Cluster II and IV comprised of 5 genotypes each while, cluster III had 3 genotypes. The 2 clusters I and II together included 17 genotypes reflecting a narrow genetic diversity among them (Table 3). Further cluster VII had 2 genotypes while the rest of the clusters V, VI and VIII were solitary clusters demonstrating the impact of selection pressure in increasing the genetic diversity.

The intra cluster distance ranged from 46.90 to 80.87with highest intra cluster distance for cluster VII (80.87) followed by Cluster III (74.98) and cluster IV (74.21) (Table 3). Such intra cluster genetic diversity among the genotypes could be due to heterogeneity, genetic architecture of the populations, past history of the selection in development traits and degree of general combining ability (Dikshit and Swain, 2000). The cluster II showed minimum intra cluster value of 46.90 indicating that the genotypes with in this cluster were similar. These results were in agreement with the earlier findings of Singh *et al.* (2006).

The inter cluster D^2 values ranged from 96.42 to 725.69, the maximum inter cluster distance was observed between the clusters III and VII (725.69) followed by cluster III and VIII (596.14) and cluster III and IV (507.51) which indicated that the crosses among the genotypes included in theses clusters may give high heterotic response and thus better segregants. The minimum inter cluster distance was observed between cluster I and V (96.42) indicating the close relationship among the genotypes in these clusters.

The cluster mean of each trait towards divergence are given in Table 4. The data revealed that considerable differences existed among the clusters for most of the characters studied. The cluster III recorded the highest mean value for number of primary branches per plant and seed yield. The cluster V showed the highest mean values for days to 50% flowering, days to maturity, plant height and number of pods per plant.

The data on inter cluster distances and *per se* performance of genotypes was used to select genetically diverse and agronomically superior genotypes. On the basis of the maximum inter cluster values and per se performance for seed yield, number of pods per plant and test weight, the genotypes ICP 909, ICP 20062 and ICPHAL 4985-11 were selected. The characters contributing to most of the divergence should be given more importance for the purpose of effective selection and choice of parents for hybridization. Among the 7 characters studied, seed yield contributed the most (89.49%) towards the divergence of genotypes followed by number of pods per plant, days to 50% flowering and plant height, whereas all the other characters contributed the least divergence indicating the narrow genetic divergence for those characters among the genotypes for study.

Stability analysis

Development of a stable variety is one of the major objectives of all breeding programmes. Several models were proposed for stability analysis. According to Eberhart and Russell (1966) model a stable variety is one which has above average mean yield, a regression coefficient of unity (bi=1) and non significant mean square for deviations from regression ($s^2di=0$). High value of regression (bi>1) indicates that the variety is more responsive for input rich environment, while, low value of regression (bi<1), is an indication that the variety may be adopted in poor environment.

Analysis of variance for stability of yield (Table 5) revealed the existence of substantial variability among the genotypes for seed yield. Significance of genotype x year interaction revealed that genotypes interacted significantly with environments (years). The partitioning of interaction showed that both linear and non linear (pooled deviation) components of interaction were highly significant.

The phenotypic stability of genotypes was estimated by mean performance over years (x), the regression coefficient (b) and deviation from regression. Based on stability parameters the genotype ICP 7035 was found to be stable and desirable for days to 50% flowering as indicated by non significant deviation from regression and bi>1. The genotypes ICPL 98008, ICPHAL 4979-2 and ICP 77303 with low mean, bi>1 and less deviation from regression were identified as desirable and stable for days to maturity. The genotypes ICPHAL 4978-8, ICPHAL 4989-11 and ICPX 77303 showed high mean for number of primary branches per plant, bi>1 and non significant s^2di indicating predictable performance and stable over favorable environments. The genotypes ICPL 20042, ICPL 20062, ICPL 87089 and ICPX 77303 recorded higher number of pods per plant with stable performance over average environmental conditions.

The genotypes ICPL 20036 and ICPL 20058 showed below mean performance for seed yield, unit regression coefficient and no significant s^2di values. This indicated that the performance of these genotypes can be improved by adopting suitable management practices and can also be used as one of the parents along with high mean performance to breed genotypes with high mean and wider adaptation. Therefore, it would be desirable to create variability through hybridization followed by selection to identify better genotypes for these traits. The genetic diversity has a direct relation on the creation of magnitude of variability through hybridization. The genotypes from diverse clusters should be used rather than the genotypes of clusters having low divergence to create variability for further selection in subsequent generations and to identify heterotic cross combinations for harvesting hybrid vigour. Ghosh (2002) also suggested the use of diverse parents for hybridization programme.

The results of the present study indicated that none of the genotypes studied was found superior for all the characters in all the environments. The stable genotypes identified could be used as parents in future breeding programme for developing suitable genotypes with wider adaptability. The results showed that crossing parents from clusters III and VII will result in considerable variability and genotypes with combined traits for early maturity, short plant stature, more primary branches and pod yield may be developed.

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Table: 1 Mean values for yield and its component traits in 30 genotypes of Pigeonpea

Entry	Days to 50% flowering			Days to maturity			Plant height (cm)			Number of primary branches per plant			Number of pods per plant			Test weight (g)			Seed yield (kg/ha)		
	Mean	**bi**	**s^2di**	**Mean**	**bi**	**s^2di**	**Mean**	**bi**	**s^2di**	**Mean**	**bi**	**s^2di**	**Mean**	**bi**	**s^2di**	**Mean**	**bi**	**s^2di**	**Mean**	**bi**	**s^2di**
ICP L 20036	110.78	2.05	-3.64	172.0	1.27	-10.10	173.11	1.24	380.32	6.22	1.08	0.55	175.67	0.01	489.14	8.54	2.98	0.29	907.11	0.82	-926.06
ICPL 20042	118.33	-0.46	-5.53	179.78	-1.60	68.09	186.11	1.42	-37.93	6.56	0.82	1.80	211.78	1.02	858.02	8.48	1.14	0.06	986.78	1.14	7400.34
ICPL 20058	118.00	2.30	-5.92	182.12	-0.51	-10.07	177.22	1.28	23.77	5.34	0.13	-0.38	187.45	0.62	322.39	8.35	-2.25	0.27	912.00	0.97	4143.76
ICPL 20062	118.67	-2.07	-8.35	177.45	-0.83	-7.27	171.78	1.36	107.39	6.78	0.88	0.15	228.56	1.52	336.64	8.08	2.34	-0.06	843.78	1.20	645.24
ICPL 332	115.56	0.19	-8.11	175.46	-0.03	-10.23	175.11	0.80	23.24	5.78	0.43	-0.50	199.00	3.36	959.26	8.97	1.67	-0.03	860.56	1.76	2595.34
ICPL 84060	119.33	1.03	-5.13	178.78	-1.71	-6.43	180.56	1.03	-30.88	5.00	0.56	0.49	156.45	2.16	248.65	7.49	12.37	2.38	893.22	1.32	2192.32
ICP L 85063	125.89	0.35	43.22	181.89	1.53	-7.61	163.89	0.98	947.91	6.48	0.93	2.12	162.78	1.06	955.71	8.36	5.41	0.55	952.45	1.25	7514.87
ICPL 87089	124.55	-0.56	-5.72	178.54	2.90	-9.28	161.33	0.00	284.62	4.78	1.04	-0.51	206.33	0.49	771.74	8.56	-3.29	0.74	913.33	1.18	4542.19
ICPL 909	112.89	1.35	12.06	174.11	1.59	10.47	178.22	1.26	-39.51	5.66	0.18	3.98	146.11	2.47	109.36	8.28	5.13	0.20	979.67	-0.11	1526.58
ICPL 97253	122.00	-0.58	28.13	174.76	-0.46	-5.62	162.22	0.45	530.85	6.44	0.68	0.26	136.67	0.58	-106.36	8.79	-2.97	0.16	918.22	0.67	-289.92
ICPL 98008	107.78	1.83	43.10	166.89	3.85	-1.10	149.67	0.75	766.72	5.11	1.07	1.18	113.67	-0.89	-34.81	8.42	-7.57	1.18	1026.89	0.82	-1679.0
PPE 45-2	111.45	4.00	-7.44	173.00	2.05	-10.24	176.44	0.90	26.30	6.22	0.96	1.46	153.11	2.64	38.18	9.35	0.02	-0.03	1036.22	1.03	1569.0
ICP 10531	112.11	1.87	10.25	177.42	-1.05	5.73	175.00	0.90	-7.03	6.55	0.85	-0.44	135.56	-0.07	77.58	8.51	-1.49	-0.05	1048.00	0.39	4945.0
ICP 11321	120.11	-4.27	-6.66	174.00	0.37	41.45	182.22	0.22	-5.95	5.66	0.92	1.32	144.22	1.20	729.63	8.42	-1.21	-0.04	1018.77	0.27	-1509.0
ICP 3615	113.33	1.96	16.15	175.86	1.09	-7.23	182.89	0.58	141.29	6.88	1.62	0.11	126.67	0.05	922.65	7.81	-0.66	-0.04	1027.33	0.04	5684
ICPHAL 4978-4	112.22	-2.17	-5.37	173.56	-3.00	-4.08	177.00	1.04	33.29	6.00	1.02	-0.41	135.33	0.53	-60.90	8.01	2.98	0.08	1081.67	0.64	-1117
ICP HAL4978-5	114.78	3.25	-6.81	175.54	1.87	-10.65	179.67	1.33	149.43	5.89	0.90	0.66	187.67	0.07	-81.14	8.67	-2.54	0.08	1017.78	1.43	1744
ICPHAL 4978-8	117.33	1.73	-5.55	175.78	3.43	20.40	180.00	0.64	-35.63	7.11	1.73	-0.04	182.11	2.09	525.23	9.17	-8.40	0.42	1093.89	1.09	2684
ICPHAL 4979-2	118.89	0.65	-7.35	177.00	1.34	-2.04	188.33	1.53	-11.48	6.89	1.41	0.01	154.12	0.42	743.68	7.92	-3.36	-0.06	984.00	1.36	1236.65
ICPHAL 4985-1	110.22	5.77	2.22	171.89	4.35	-9.98	183.11	0.89	13.99	5.23	0.54	3.58	134.33	0.43	945.01	8.70	-2.63	0.22	991.11	1.43	1447.83
ICPHAL 4985-10	118.45	-1.69	1.96	176.89	-1.16	-8.14	185.81	1.39	-39.51	5.23	1.64	1.07	128.89	-0.42	550.23	9.85	1.82	-0.03	945.88	1.26	2996.31
ICP HAL4985-11	116.22	2.77	7.14	174.45	2.50	-8.94	178.45	1.04	-18.76	6.78	1.37	-0.46	163.22	2.15	134.74	8.64	2.26	0.37	946.67	1.97	548.20
ICPHAL 4985-4	115.22	3.18	-8.41	179.67	-0.34	-8.47	180.67	0.69	52.86	5.23	0.65	-0.40	157.67	2.56	-131.14	9.35	0.34	0.24	1141.56	0.65	-1313
ICP HAL4986-1	120.33	-3.51	-8.51	174.44	1.59	48.48	173.78	1.12	-35.07	5.34	1.51	0.28	195.22	0.00	511.32	8.77	3.34	0.00	1102.89	1.27	6465
ICPHAL 4989-7	121.45	-1.29	-5.73	177.89	0.63	-8.23	189.11	1.54	15.92	5.66	1.07	-0.29	176.89	0.84	34.11	8.14	6.50	1.10	1049.67	1.29	10786
ICP L7035	105.78	1.19	-8.42	166.67	0.47	-10.61	168.00	1.61	28.01	6.66	1.99	1.63	84.22	0.28	571.72	10.51	20.23	2.61	1076.00	0.70	2210
ICP X 77303	113.00	2.07	-2.37	173.56	1.70	-6.38	186.78	1.12	-28.63	6.77	1.86	-0.41	217.89	1.80	383.88	8.11	3.77	0.00	1021.33	0.86	3241
ICPL 8094	112.22	0.48	-6.39	172.33	-0.14	-7.25	179.78	0.97	-8.59	5.78	0.47	0.38	158.56	2.16	-65.32	8.52	-1.39	-0.02	1031.78	0.85	-1706
ICP 13198	113.56	-1.42	-8.23	173.45	-0.90	-9.89	173.33	0.65	75.24	6.45	0.58	0.02	170.56	0.60	-128.15	8.87	-1.99	0.20	1055.67	1.54	-1725
ICPL 87119	101.89	9.97	15.87	161.44	9.11	15.33	165.67	0.28	536.59	5.12	1.12	-0.27	117.22	0.29	3.33	8.09	-2.54	-0.04	842.89	0.87	-106.92

Table: 2 Number and name of genotypes in different clusters

Cluster	No. of genotypes	Genotype
I	12	ICPL 85063, ICPL 87089, ICPL 84060, ICPL 332, ICPL 97253, PPE-45-2, ICP 10531, ICPL 98008, ICPHAL 4989-7, ICPL 7035, ICPX 77303, ICPL 8094
II	5	ICP11321, ICP 3615, ICPHAL 4978-4, ICPHAL 4978-5, ICP 13198
III	3	ICPL 20042, ICPL 20058, ICPL 20036
IV	5	ICPHAL 4985-1, ICPHAL 4985-10, ICPHAL 4979-2, ICPHAL 4978-8, ICPL 87119
V	1	ICPL 909
VI	1	ICPL 20062
VII	2	ICPHAL 4985-4, ICPHAL 4986-1
VIII	1	ICPHAL 4985-11

Table: 3 Intra (Diagonal) and Inter cluster distance (D^2 values) of the cluster

Cluster	I	II	III	IV	V	VI	VII	VIII
I	73.87	114.14	272.54	248.78	96.42	130.43	467.03	341.44
II		46.90	367.28	151.96	125.40	214.02	370.88	249.31
III			74.98	507.51	287.09	180.12	725.69	596.14
IV				74.21	259.20	346.12	234.52	125.90
V					0.00	182.76	482.58	366.92
VI						0.00	557.26	425.27
VII							80.87	138.27
VIII								0.00

Table: 4 Cluster means of 8 clusters for 7 quantitative traits in Pigeonpea

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Test weight (g)	Seed yield (kg/ha)
I	117.75	177.75	155.88	5.88	186.00	8.55	715.13
II	119.75	179.75	153.50	6.75	191.00	9.48	616.25
III	117.00	177.00	155.00	7.33	180.67	9.68	979.67
IV	116.50	176.50	152.00	5.25	167.00	9.08	476.25
V	123.00	183.00	166.00	5.00	268.00	7.93	710.00
VI	122.00	184.00	150.00	7.00	120.00	8.29	816.00
VII	103.00	163.00	136.00	5.00	99.50	10.85	261.50
VIII	104.00	164.00	141.00	5.00	87.00	13.82	393.00

Table: 5 ANOVA for variance and stability of yield and its component traits in pigeonpea

Source of variation	Df	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Test weight (g)	Seed yield (kg/ha)
Rep within Envi	6	15.132	25.062	44.214	1.485	367.424	0.037	3205.404
Genotypes	29	86.491***	57.498***	241.210	1.407	3412.030*	1.132	18752.530
E +(G x E)	60	16.459	16.496	609.246***	3.723***	1847.399	0.896*	34842.890***
Environments	2	39.831*	51.393*	13743.360***	78.312***	15695.570***	0.677	714495.6000***
Gen x Envi	58	15.653	15.293	156.345	1.151	1369.876	0.903*	11406.580
Envi (Lin)	1	79.663**	102.786**	27486.720***	156.625***	31391.140***	1.353	1428991.000***
Gen x Env(Lin)	29	20.747*	18.434	139.373	1.183	1163.287	1.377***	10611.190***
Pooled deviation	30	10.208	11.747	167.540***	1.083***	1523.915***	0.416***	11795.250***
Pooled error	174	8.298	10.249	39.422	0.484	123.286	0.059	1699.705
Total	89	39.279	29.856	489.324	2.969	2357.222	0.973	29599.960

Table :3 Number and names of genotypes in different clusters

Cluster	No. of genotypes	Genotype
I	15	Kumbhari local, Chincholi jute, PVR 656, Suratgaon 2, Tamalwadi local, Barshi jute, PVR 661, PVR 655, RSV 1112, PVR 654, RSV 1077, EP 72, RSV 1094, Wadgaon siddeswar, Tangrolingal maldandi
II	5	RSV 1126, Hadaspar dagdi, RSV 821, PVR 657, RSV 1080
III	4	Yermala loacal, Phule chitra, RSV 744, Chungi maldandi
IV	9	RSV 1046, Barshi maldandi, Phule maule, PVR 660, Arni local, PVR 658, PVR 659,RSV 1044, Sholapur dagdi
V	10	Jangoan maldandi, EP 90, M35-1, EP 84, EP 92, EP 83, Siddeswar local, CSV 22R, EP 94, PVR 624
VI	5	PVR 617, EP 95, Mahad 3, EP 87, EP 86
VII	5	Musti local, Sherol dagdi, Wasadmani, Dahithane local, EP 85
VIII	1	RSV 1037