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Genetic Analysis of Pigeonpea [*Cajanus cajan* (L.) Millsp.] Hybrids for Yield and Yield Attributes

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ABSTRACT

An experiment was carried-out with forty-eight hybrids of pigeonpea and two checks for nine characters at Agricultural Research Station, Tandur (Professor Jayashankar Telangana State Agricultural University). Analysis of variance revealed significant differences among the hybrids for all the nine characters studied. The results of genetic parameters revealed that, high genotypic (GCV) and phenotypic coefficients of variations (PCV) were observed for seed yield and number of pods per plant. Six characters *viz.,* number of branches per plant, number of pods per plant, number of seeds per pod, pod length, test weight and seed yield exhibited high heritability estimates coupled with high genetic advance as per cent of mean which suggested that these traits were amenable for further improvement following simple selection methods. Character association revealed significant positive association of seed yield with plant height,number of branches per plant, number of pods per plant, number of seeds per pod and pod length. Based on divergence studies, the hybrids were grouped into nine clusters in Tocher's method, cluster II (14 hybrids) was the largest followed by cluster I (13), cluster VI (9), cluster IV (6), cluster IX (4) and the remaining clusters were solitary (III, V, VII and VIII). Out of the nine characters studied, seed yield, days to 50% flowering, test weight and plant height contributed 85.62 per cent of the total divergence and these traits were found to be important factors for genetic differentiation in the hybrids. The overall results of the study revealed that, hybrids under cluster IV and VIII and cluster VII and VIII had maximum and minimum inter cluster distances respectively and possessing high genetic diversity for the characters *viz*. plant height, number of branches per plant, number of seeds per pod and yield.

Key words: Analysis, Genetic, Hybrids, Pigeonpea.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.] commonly known as 'Redgram' or 'tur' or 'arhar' is a legume crop with diploid chromosome number, 2n=22, belongs to the tribe phaseoleae, sub tribe cajaninae of the sub family papilionoidae, family fabaceae. In India pigeonpea is the second most important pulse crop after chickpea and is cultivated in an area of 5.33 m ha with a production of 4.87 Mt and an average productivity of 913 kg/ha. (Indiastat, 2016-2017). It is consumed in the form of split pulse (dal) and seeds are rich sources of protein (22.3%), fat (1.7%), carbohydrate (57.6%), iron, iodine and other essential aminoacids such as lycine, cystine and arginine. A number of varieties have been released and the area also increased but the yield has remained unacceptably low because of several biotic and abiotic constraints. Hence, hybrid breeding is expected to break the yield barrier and increase the yield. Genetic variability is of greatest interest to the plant breeder as it plays a vital role in framing successful breeding programme. Heritability of a metric character is a parameter of particular significance to the breeder as it measures the degree of resemblance between the parents and the off-springs and its magnitude indicates the heritability with which a hybrid can be identified by its phenotypic expression. While genetic advance aids in exercising the necessary selection pressure. Correlation enables to identify the characters or combination of characters which might be useful as indicator of high yield by way of evaluating relative influence of various characters on yield and among themselves as well. The original concept of correlation was given by Galton (1889) and later elaborated by Fisher (1918). Genetic diversity is the basis for any crop improvement programme. Mahalanobis D^2 analysis is a useful tool to assess the genetic divergence among population.

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MATERIALS AND METHODS

The experimental material comprised of forty-eight hybrids and two checks evaluated in a randomized block design with two replications at Agricultural Research Station, Tandur, PJTSAU, Telangana, India during *Kharif* 2018. Each entry was sown in four rows of 4m length with a row to row and a plant to plant distance of 120 cm and 20 cm respectively. The recommended agronomic and plant protection measures were followed in order to raise a normal crop.

Observations on nine different quantitative characters *viz.,* days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, pod length, test weight and seed yield were recorded on five randomly selected competitive plants except for days to 50% flowering and days to maturity where data was recorded on plot basis. Mean values from the five randomly selected plants from each of the two replications were averaged and expressed as the mean of the respective character and considered for statistical analysis using Windostat version 9.2. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952). Heritability (h^2) in the broad sense was calculated according to the formula given by Allard (1960) for all characters. From the heritability estimates, the genetic advance was estimated by the following formula given by Burton (1952). Correlation coefficients were calculated at genotypic and phenotypic level using the formulae suggested by Falconer (1964). A measure of group distance based on multiple characters was given by Mahalanobis (1936) using D^2 statistic. The data collected on different characters was analyzed using Mahalanobis' D^2 analysis to determine the genetic divergence among the hybrids.

RESULTS AND DISCUSSION

Analysis of variance for the experiment involving a set of 50 entries for all the characters revealed highly significant differences among the hybrids for all the characters indicating the presence of sufficient variability. The results are presented in Table 1. The results pertaining to genetic parameters *viz.*, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2_{bs}) and genetic advance as percent of mean (GAM) for all the nine characters are furnished in Table 2 indicated that there is almost perfect relation between PCV and GCV of each character. This could be seen from the highest magnitude of both PCV (31.56%) and GCV (30.56%) for seed yield and number of pods per plant (23.23-20.89%) suggesting that these characters were under the influence of genetic control. So the characters can be relied upon and simple selection can be practiced for further improvement. Similar results of high PCV and GCV for seed yield were earlier reported by Pandey *et al.* (2015) and Satapathy *et al.* (2019) and for number of pods per plant by Pushpavalli *et al. (*2018). Number of branches per plant, number of seeds per pod, pod length and test weight exhibited moderate magnitudes of both PCV and GCV, respectively. The phenotypic coefficient of variation was

Table 1: Analysis of variance for nine characters in hybrids of pigeonpea [Cajanus cajan (L.) Millsp.].

Character	Mean sum of squares		
	Replications(d.f. = 1)	Treatments(d.f. =49)	Error(d.f. = 49)
Days to 50% Flowering	14.40	41.85***	1.56
Days to Maturity	15.21	41.85***	1.59
Plant Height (cm)	259.21	592.08***	66.69
Number of Branches per Plant	3.61	8.82***	1.61
Number of Pods per Plant	12.25	3134.90***	331.80
Pod Length (cm)	0.36	0.99***	0.17
Number of seeds per Pod.	0.01	0.47***	0.11
Test Weight (g)	4.00	3.70***	0.36
Yield per Hectare (kg/ha)	1713.96	491636.10***	15582.38

*Significant at p=0.05 level and ** Significant at p=0.01 level.

Table 2: Estimation of genetic parameters for nine characters in hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.].

Characters	PCV (%)	GCV (%)	ECV (%)	Heritability (h^2_{bs}) (%)	Genetic Advance as percent of Mean (1%)
Days to 50% Flowering	3.80	3.66	1.01	92.80	9.31
Days to Maturity	2.78	2.67	0.75	92.65	6.80
Plant Height (cm)	10.77	9.62	4.85	79.75	17.70
Number of Branches per Plant	12.93	10.76	7.16	69.14	24.56
Number of Pods per Plant	22.01	19.20	10.76	80.86	49.60
Number of seeds per Pod.	16.66	13.09	10.29	61.80	27.18
Pod Length (cm)	19.40	16.21	10.65	69.83	35.77
Test Weight (g)	11.11	10.05	4.72	81.95	24.03
Yield per Hectare (kg/ha)	31.56	30.56	7.87	93.86	78.58

PCV= Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation, ECV= Environmental Coefficient of Variation and GAM= Genetic Advance as percent of Mean at 1% level.

higher than genotypic coefficient of variation (GCV) for all the characters under study but the GCV was greater than the variation produced by the environment for all the characters. It signifies the role played by the environment in the expression of these characters. The results are in agreement with findings of Bhadru *et al.* (2011), Yerimani *et al.* (2013) and Satapathy *et al.* (2019). All the characters recorded high estimates of heritability. Broad sense heritability estimates ranged from 61.80 per cent (Number of seeds per pod) to 99.43 percent (Yield). All the characters recorded high estimates of heritability indicating that they were least influenced by the environmental effects, however selection for improvement of such characters may not be useful, because broad sense heritability is based on total genetic variance which includes additive, dominant and epistatic variances. Thus, the heritability values along with estimates of genetic advance would be more reliable than heritability alone (Johnson *et al*., 1967). High heritability coupled with high genetic advance was observed for number of branches per plant, number of pods per plant, number of seeds per pod, pod length, test weight and yield. Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by pedigree method of breeding. Similar results for high heritability coupled with high genetic advance for various traits have also been reported earlier for number of pods per plant, test weight and seed yield (Magar, 2003, Ram *et al*. 2016; Pushpavalli *et al.* 2017; Reddy *et al.* 2019).

Character association studies (Table 3) revealed that number of pods per plant (0.9282 G, 0.8174P) followed by number of branches per plant (0.6008 G, 0.4792 P), number of seeds per pod (0.5954 G, 0.4651 P), pod length (0.4027 G, 0.2960 P) and plant height (0.3149 G, 0.2736 P) manifested significant and positive correlation with yield at both phenotypic and genotypic levels. (G and P indicates Genotypic and Phenotypic Correlations, respectively).

Thus, it can be inferred that selection based on any one of these traits either alone or in combination, will result in identifying high yielding strains. Highly significant and positive correlation between grain yield and other traits as obtained in the present investigation have also reported for number of branches per plant and number of pods per plant (Kumar *et al.* 2014); for plant height , pod length, number of seeds per pod, number of branches per plant and number of pods per plant (Baldaniya *et al.* 2018); Significant positive correlation of number of pods per plant and test weight with seed yield were reported by Devi *et al.* (2012), Mittal *et al.*

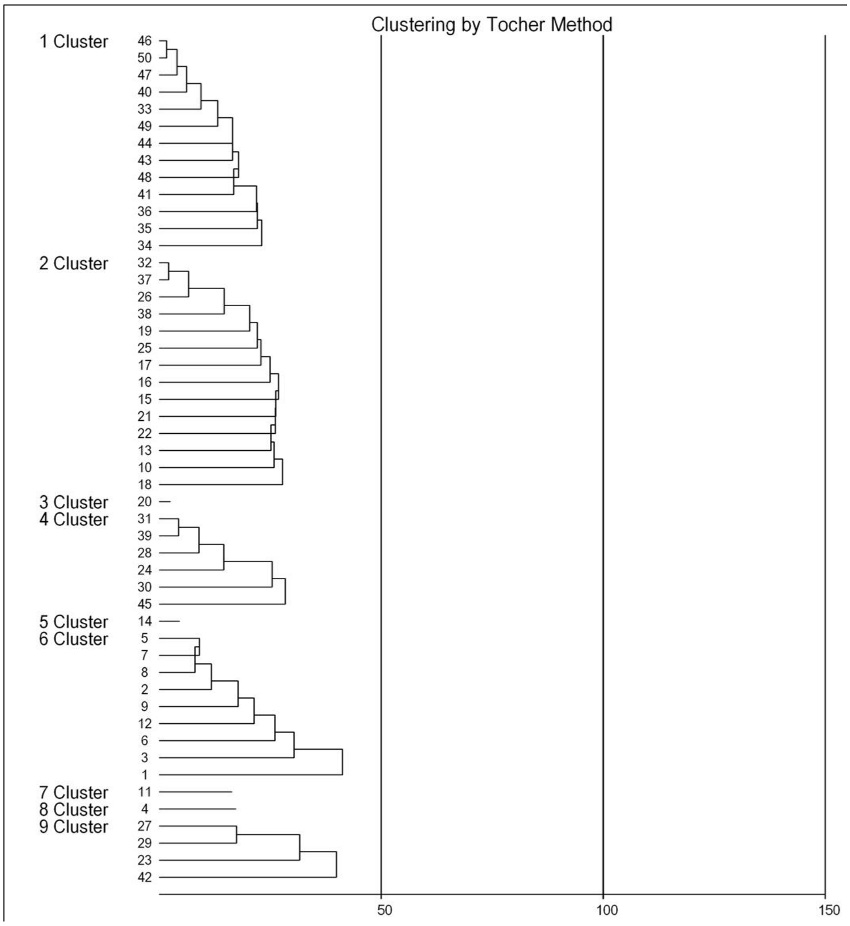

Fig 1: Dendrogram for divergence in fifty hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.] employing Tocher's method.

Table 3: Estimates of Phenotypic (r_p) and genotypic (r_g) correlation coefficients among yield and its attributes in hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.].

Characters		Days to 50% Flowering	Days to Maturity	Plant Height	Number of Branches per Plant	Number of Pods per Plant	Number of seeds per Pod	Pod Length (cm)	Test Weight (g)	Yield per Hectare (kg/ha)
Days to 50% Flowering	r_g	1.0000	0.9999***	0.1328	-0.0167	0.0469	-0.0501	-0.1534	-0.0581	0.0376
	r_p	1.0000	0.9998***	0.0884	-0.0177	0.0126	-0.0510	-0.1194	-0.0350	0.0346
Days to Maturity	r_g		1.0000	0.1322	-0.0189	0.0433	-0.0542	-0.1571	-0.0588	0.0351
	r_p		1.0000	0.0895	-0.0207	0.0098	-0.0540	-0.1197	-0.0349	0.0314
Plant Height	r_g			1.0000	0.3526***	0.3944***	0.0468	-0.0710	-0.0263	0.3149***
	r_p			1.0000	0.2313*	0.3186**	0.0362	-0.0348	-0.0250	0.2736**
Number of Branches per Plant	r_g				1.0000	0.6729***	0.5624***	0.1006	-0.1801	0.6008***
	r_p				1.0000	0.4927***	0.2800***	0.1092	-0.1337	0.4792***
Number of Pods per Plant	r_g					1.0000	0.6236***	0.3392***	-0.1669	0.9282***
	r_p					1.0000	0.3637***	0.1977*	-0.1369	0.8174***
Number of seeds per Pod.	r_g						1.0000	0.9545***	0.0223	0.5954***
	r_p						1.0000	0.6546***	-0.0026	0.4651***
Pod Length (cm)	r_g							1.0000	0.3320***	0.4027***
	r_p							1.0000	0.2361*	0.2960***
Test Weight (g)	r_g								1.0000	-0.2156
	r_g								1.0000	-0.1934

* Significant at 5% level   ** Significant at 1% level   G =Genotypic level;   P=Phenotypic level.

(2010), Pandey *et al.* (2015), Sharma *et al*. (2012) and Pushpavalli *et al.* (2018).

Mahalanobis's Euclidean squared distances grouped the material into nine clusters. The cluster composition is given in the Table 4. The clustering pattern was depicted by ward's minimum variance dendrogram (Fig 1) Among the clusters, cluster II was the largest comprising of 14 hybrids followed by cluster I with 13 hybrids, cluster VI with 9hybrids, cluster IV with 6 hybrids, cluster IX with 4 hybrids and the remaining clusters are solitary (III, V, VII and VIII). The average intra and inter cluster D^2 values are presented in Table 5. Most of the intra clusters were closely related and clustervalues ranged from 0.00 (cluster III, V, VII and VIII) to 6.73 (cluster IX). From the inter cluster D^2 values, it could be observed that the highest divergence was between cluster IV and cluster VIII (12.67) whereas the lowest

Table 4: Clustering pattern among fifty hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.] by Tocher's Method.

Cluster	Number of Hybrids	Entries
I	13	2047A X ICPL 15070, 2098A X ICPL 15078,2211A X ICPL 15084, 2098A X AGL 1640,2047A X AGL 1640, 2098A X PRIL B 31,2098A X ICPL 15081, 2043 X ICPL 15083, 2211A X ICPL 15072, 2211A X PRIL B 26, 2211A X AGL1636, 2211A X ICPL 15070, 2047A X ICPL 15072.
II	14	2098A X ASHA, 2043 X PRIL B 31, 2211A X ICPL 15081, 2211A X TDRG 58, 2047A X AGL 1636, 2047A X PRIL B 26, ASHA, 2047A X ASHA, 2043 X ASHA, 2047A X ICPL 15081, 2098A X ICPL 15072, 2047A X ICPL 15048, 2047A X TDRG 4, 2043 X ICPL 15078.
III	1	2047A X ICPL 15078
IV	6	2211A X PRIL B 100, 2043 X TDRG 4, 2047A X TDRG 58, 2043 X TDRG 58, 2211A X ICPL 15083, 2211A X ASHA.
V	1	2098A X ICPL 15083
VI	9	2047A X PRIL B 31, 2043 X ICPL 15070, 2098A X TDRG 4, 2043 X ICPL 15072, 2211A X PRIL B 31, 2043 X PRIL B 100, 2047A X PRIL B 100,2098A X PRIL B 26, 2043 X AGL 1636.
VII	1	ICPH 2740
VIII	1	2047A X ICPL 15083
IX	4	2211A X AGL 1640, 2098A X TDRG58, 2098A X ICPL 15048, 2098A X ICPL 15070.

Table 5: Average intra (bold) and inter cluster D^2 and D values for fifteen clusters in fifty hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.].

Cluster	ClusterI	ClusterII	ClusterIII	ClusterIV	ClusterV	ClusterVI	ClusterVII	ClusterVIII	ClusterIX
ClusterI	(4.45)19.80	(6.30)39.69	(6.83)46.64	(6.66)44.35	(7.10)50.41	(10.89)118.59	(8.65)74.82	(11.29)127.46	(7.25)52.56
ClusterII		(5.23)27.35	(5.91)34.92	(6.80)46.24	(6.07)36.84	(8.80)77.44	(7.04)49.56	(9.65)93.12	(7.90)62.41
ClusterIII			(0.00)0.00	(4.38)19.18	(8.55)73.10	(7.72)59.59	(8.75)76.56	(11.99)143.76	(10.10)102.01
ClusterIV				(5.08)25.80	(9.23)85.19	(9.10)82.81	(9.71)94.28	(12.67)160.52	(9.90)98.01
ClusterV					(0.00)0.00	(8.84)78.14	(5.21)27.14	(6.03)36.36	(5.90)34.81
ClusterVI						(5.51)30.36	(7.13)50.83	(8.93)79.74	(11.77)138.53
ClusterVII							(0.00)0.00	(4.16)17.30	(9.04)81.72
ClusterVIII								(0.00)0.00	(9.93)98.60
ClusterIX									(6.73)45.29

Figs in parenthesis indicate D values.

Table 6: Cluster mean values (Tocher's Method) for nine characters in fifty hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.].

	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Number of Branches per Plant	Number of Pods per Plant	Number of seeds per Pod	Pod Length (cm)	Test Weight (g)	Yield per Hectare (kg/ha)
ClusterI	121.42	166.42	166.69	16.69	148.04	3.04	3.65	13.62	1079.19
ClusterII	122.18	167.18	158.71	16.39	181.64	3.00	3.61	11.93	1666.39
ClusterIII	129.50	174.50	160.50	17.50	161.50	3.00	3.00	13.00	1667.00
ClusterIV	128.33	173.33	173.00	15.83	156.33	3.08	3.83	12.67	1295.42
ClusterV	117.00	162.00	163.50	17.00	200.00	3.00	4.50	14.00	1916.50
ClusterVI	125.22	170.17	186.00	19.22	234.44	3.78	4.33	12.67	2308.44
ClusterVII	116.00	161.00	187.50	21.50	233.00	3.50	4.00	12.00	2062.00
ClusterVIII	112.00	157.00	199.50	20.00	229.00	4.00	5.00	12.50	2425.50
ClusterIX	117.38	162.38	151.88	14.50	154.63	3.75	5.13	14.13	1352.38

Table 7: Contribution (%) of different characters towards divergence in fifty hybrids for nine characters of pigeonpea [*Cajanus cajan* (L.) Millsp.].

Characters	Times ranked first	Contribution (%)
Days to 50% Flowering	374	30.53
Days to Maturity	8	0.65
Plant Height (cm)	113	9.22
Number of Branches per Plant	19	1.55
Number of Pods per Plant	32	2.61
Number of seeds per Pod.	54	4.41
Pod Length (cm)	63	5.14
Test Weight (g)	149	12.16
Yield per Hectare (kg/ha)	413	33.71

divergence was noticed between cluster VII and cluster VIII (4.16). Greater the distance between the two clusters, wider the genetic diversity among the entries of these clusters. Cluster mean values (Table 6) for yield contributing characters indicated that considerable differences existed for all the traits. Highest cluster mean values were noticed for Days to 50% flowering in cluster III (129.50), Days to Maturity in cluster III (174.50), Plant Height in cluster VIII (199.50), Number of Branches per Plant in cluster VII (21.50), Number of Pods per Plant in clusterVI (234.44), Number of seeds per pod in cluster VIII (4.00), Pod Length in cluster IX (5.13), Test Weight in cluster IX (14.13) and Seed yield in cluster VIII (2425.50). The data on inter cluster distances and *per se* performance of hybrids were used to select genetically diverse and agronomically superior entries.

The characters contributing to greater divergence should be given more importance for effective selection. The contribution of different characters towards the genetic diversity is presented in Table 7.Seed Yield (ranked first 413 times out of 1225 total numbers of combinations) contributed 33.71 percent to the divergence of hybrids. This was followed by days to 50% flowering (30.53%) by 374 times, test weight (12.16%) by 149 times, plant height (9.22%) by 113 times, pod length (5.14%) by 63 times, number of seeds per pod (1.55%) by 19times and days to maturity (0.65%) by 8 times contributed less towards divergence.The characters contributing maximum to the divergence were given greater emphasis for further selection in pigeonpea improvement. The results revealed that seed yield and days to 50% flowering have contributed more towards divergence, so the direct selection for these traits would be helpful as evident from the number of times these traits appeared or ranked first during contribution to diversity.

CONCLUSION

The characters *viz.,* number of branches per plant, number of pods per plant, number of seeds per pod, pod length, test weight and seed yield exhibited high heritability estimates coupled with high genetic advance which suggested that these traits were amenable for further improvement by following simple selection methods. Character association revealed significant positive association of single plant yield with plant height number of branches per plant, number of pods per plant, number of seeds per pod and pod length. Based on cluster mean values the hybrids of cluster VIII exhibited highest *per se* performance for seed yield hence these are identified as potential parents for developing high yielding hybrids.

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