



Research Article

GENETIC DIVERGENCE ANALYSIS FOR YIELD AND QUALITY TRAITS IN PIGEONPEA [*Cajanus cajan* L.]

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Abstract- Genetic divergence among 38 genotypes of pigeon pea belonging to different eco geographical regions was studied by using Mahalanobis D^2 statistics. They were grouped into 7 clusters and clustering pattern of genotypes and genetic diversity was independent of their pedigree. Hence, selection of parents for hybridization should be more based on genetic diversity rather than geographic diversity. Among the seven clusters, cluster IV having two genotypes [SKNP 0505 and Manak] registered maximum mean values for seed yield per plant, number of pods per plant, total protein content, total phenol content and methionine content. These two genotypes were thus found having genetic make-up for high productivity with desirable biochemical quality. Similarly, the cultivar GT 101 was found better for seed yield per plant, pods per plant and tannin content. The cultivar Manak, UPAS 120 and Vipula were found best source of genes for phenol content to be exploited through hybridization programme.

Keywords- Pigeon pea, Genetics divergence, D^2 statistics.

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Introduction

Success of crop improvement programme in Pigeon pea depends upon genetic diversity and the genetic variability, choice of parents and selection procedure adopted in hybridization programme and it is necessary to screen and identify suitable donors having wider genetic base in pigeon pea. Genetic diversity means variability between different genotypes of a species. Mahalanobis's [1936] is the important multivariate powerful tool to measure the genetic divergence within a set of genotypes [3]. Genetic diversity plays an important role, because hybrids between lines of diverse genetic background generally display a greater heterotic than those between closely related parents. In the present study 38 genotype of pigeon pea were chosen to study variability among the genotype for seed yield and 6 yield characters.

Materials and Methods

The experimental material comprised of 38 diverse genotypes of pigeon pea, collected from the gene pool maintained at the Centre of Excellence for Research on Pulses, Sardarkrushinagar Dantiwada Agricultural University, Banaskantha, Gujarat State. The experiment was laid out in Randomized Block Design with three replications. The plot size is 4 m x 1.2 m each plot consist of double row of four meter length. The inter-row and intra-row spacing was 60 and 20 cm, respectively. The sowing was carried out by dibbling method and date of sowing is Onset of Monsoon *kharif* 2012. Randomly among each genotype five plants are selected and observations were recorded for 12 different characters viz., days to flowering, days to maturity, number of branches per plant, pods per plant, seed yield per plant, harvest index, 100-seed weight, total protein content, total phenol content, tannin content, methionine content and water absorption capacity of seeds. Rao [1952] described the multivariate analysis of genetic divergence using Mahalanobis's D^2 statistic [4]. There are several methods available of the formation of clusters. Tocher's method was followed.

Results and Discussion

The analysis of variance revealed significant difference among 38 genotypes for twelve characters, which showed the considerable genetic variability among the genotypes. On the basis of D^2 statistics the thirty eight genotypes were grouped into seven clusters. The variation in the composition of individual cluster, large amount of diversity in the population showed by number of genotypes. The clustering pattern revealed that genetic divergence was not related to geographical diversity. Genotypes from the different geographical region had different genetic background as well as the wide divergence in the traits. Similar results have been reported by [1, 2, 6].

Table-2 Cluster composition of thirty eight pigeon pea genotypes [Tocher's method].

Cluster	Number of Genotypes	Genotypes
I	8	BRG-1, MA-6, Bahar, CoRG-9701, ICP-7119, RVSA-07-3, KPL-44, KPL-43
II	5	JKM 189, Pusa 992, Hy 3 C, ICPL 2376, TT 401
III	6	Vipula, BSMR 846, Paras, BDN 708, Banas, ICPL 87
IV	2	SKNP 0505, Manak
V	7	BRG-2, ICP 7035, BDN-2, IPA-8F, IPA-204, IPA-203, Maruthi
VII	3	GT 100, GT 101, Co-6

Cluster I was the largest with 8 genotypes followed by cluster II and III with 5 and 6, cluster IV with 2 while cluster V with 7 and VII with 3.

Table-1 Details of thirty eight genotypes of pigeon pea

Sr. No.	Genotypes	Source	Sr. No.	Genotypes	Source
1.	BRG-2	UAS, Bangalore	20.	SKNP 0505	GAU, Sardarkrushinagar
2.	BRG-1	UAS, Bangalore	21.	ICP 7119	NBPGR, New Delhi
3.	MA 6	BHU, Varanasi	22.	BSMR 846	ARS, Badnapur
4.	BSMR 736	ARS, Badnapur	23.	RVSA 07-3	C.E.R.P., Sardarkrushinagar
5.	Bahar	RAU, Dholi	24.	ICP 2376	NBPGR, New Delhi
6.	ICPL87091	ICRISAT, Hyderabad	25.	KPL 44	C.E.R.P., Sardarkrushinagar
7.	ICPL87119 (Asha)	ICRISAT, Hyderabad	26.	KPL 43	C.E.R.P., Sardarkrushinagar
8.	BSMR 853 (Vaishali)	ARS, Badnapur	27.	IPA 8F	C.E.R.P., Sardarkrushinagar
9.	JKM 189	Khargone	28.	IPA 204	C.E.R.P., Sardarkrushinagar
10.	Pusa 992	IARI, New Delhi	29.	IPA 203	C.E.R.P., Sardarkrushinagar
11.	Hy 3 C	ANGRU, Hyderabad	30.	BRG-3	UAS, Bangalore
12.	Vipula	Rahuri	31.	TT 401	BARC, Trombay
13.	CORG-9701	TNAU, Coimbatore	32.	Manak	HAU, Hisar
14.	ICP-7035	NBPGR, New Delhi	33.	Paras	HAU, Hisar
15.	GT-100	GAU, Sardarkrushinagar	34.	BDN 708	ARS, Badnapur
16.	GT-101	GAU, Sardarkrushinagar	35.	Co 6	TNAU, Coimbatore
17.	AGT 2	GAU, Sardarkrushinagar	36.	Maruti	ICRISAT, Hyderabad
18.	BDN 2	ARS, Badnapur	37.	Banas	GAU, Sardarkrushinagar
19.	UPAS 120	GBPAU&T, Pantnagar	38.	ICPL 87	ICRISAT, Hyderabad

Table-3 Average intra cluster [diagonal] and inter cluster distances [D^2] for six clusters in pigeon pea

Cluster	I	II	III	IV	V	VI	VII
I	385.90	550.12	1067.21	2113.16	623.45	1413.30	1511.58
II		494.96	849.05	2003.70	796.53	957.47	1397.85
III			413.57	874.89	370.37	841.91	703.41
IV				599.59	1071.59	1295.80	524.14
V					394.54	1178.26	784.48
VI						639.56	958.53
VII							477.60

On the basis of D^2 estimate the genotype were grouped seven clusters, the maximum intra cluster distance was VI [639.56]. The maximum inter cluster distance was observed between cluster I and IV [2113.16] followed by cluster II [2003.70] while the least being between cluster III and V [370.37] [Table-3] indicating that accessions belonging to clusters I, II and IV could have greater genetic diversity and hence selection of parents from such clusters for hybridization programmes would help to achieve more transgressive segregants in advanced generations. These results are in accordance with the findings [7]. The additional advantage of D^2 analysis is the various character contributed the expression of the genetic diversity. This analysis indicated that the phenol content [41.11], 100-seed weight [4.84] and number of pods per plant [1.56] contributed more than 90 per cent towards total divergence in the material. These results were supported by [5].

Table-4 Contribution of different characters to genetic diversity in the population of 38 genotypes of pigeon pea

Characters	Number of first rank	Contribution [percentage]
Days to flowering	4	0.56
Days to maturity	15	2.13
Number of branches per plant	1	0.14
Pods per plant	11	1.56
Seed yield per plant (g)	0	0
Harvest index (%)	5	0.71
100-Seed weight (g)	34	4.84
Total protein content (%)	0	0
Total phenol content (mg/g)	289	41.11
Tannin content (mg/g)	37	5.26
Methionine content (mg/g)	159	22.62
Water absorption (ml/g)	148	21.05

The cluster means for various characters [Table-5] indicated that cluster IV recorded high mean values for phenol content [2.928] similarly pods per plant [127.500], seed yield per plant [95.422], protein content [19.33] and methionine [3.083] Followed by cluster I for phenol content [1.185], cluster VII for days to flowering, days to maturity, harvest index and tannin content. Cluster II for number of branches per plant, the genotypes from cluster IV, VII and II can be utilized as potential parent in the crossing programme for obtaining superior segregants [5].

Table-5 Cluster means for twelve characters in Pigeonpea

Cluster	Days to flowering	Days to maturity	No. of branches per plant	Pods per plant	Seed yield per plant (g)	Harvest index (%)	100-Seed weight (g)	Total protein content (%)	Total phenol content (mg/g)	Tannin content (mg/g)	Methionine content (mg/g)	Water absorption (ml/g)
I	113.333	207.583	11.375	93.338	83.372	27.375	9.725	18.416	1.185	2.134	1.983	1.274
II	113.400	206.333	13.133	76.800	83.629	31.400	10.187	18.468	1.691	2.449	1.607	1.523
III	115.778	210.889	12.833	84.722	83.491	34.000	9.861	18.331	2.622	2.839	2.100	1.301
IV	112.667	186.333	13.000	127.500	95.422	30.167	9.867	19.335	2.928	3.197	3.083	1.250
V	114.714	194.667	12.810	87.905	83.214	29.000	9.105	18.624	1.809	2.453	2.433	1.137
VI	113.810	184.524	12.619	106.429	86.285	26.476	10.886	18.080	2.453	2.869	2.014	1.810
VII	118.000	180.778	12.667	122.444	89.229	36.333	8.978	18.323	2.489	3.580	2.656	1.341

Conclusion

From the present investigation, it was concluded that Among the seven clusters, cluster IV having two genotypes [SKNP 0505 and Manak] registered maximum values for seed yield per plant, number of pods per plant, total protein content, total phenol content and methionine content. These two genotypes were thus most appropriate for improving productivity with quality and inbuilt resistance towards biotic stresses on basis of the biochemical content. So cluster IV could be selected for hybridization programme, as it showed superior performance and recorded the highest cluster mean values for most of the character. Similarly, the

accession GT 100, GT 101 and Co-6 from the cluster VII for days to flowering, days to maturity, harvest index and tannin content and cluster II include JKM 189, Pusa 992, Hy 3 C, ICPL 2376, TT 401 for number of branches per plant may be considered for inclusion in the breeding programme. It is suggested that crosses should be made among the genotype for improving more than one economic character to develop potential segregant for further selection and to developed high yielding lines in pigeon pea.

Conflict of Interest: None declared

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