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D² analysis for yield and quality traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Abstract

Fifty pigeonpea genotypes were studied for genetic divergence in yield, yield components and quality traits using Mahalanobis D² statistics and grouped in to three clusters which suggested wider genetic diversity. The maximum inter-cluster distance was observed between cluster-I and cluster-II. The highest intra-cluster distance was exhibited by cluster-III. Cluster-II rendered highest cluster mean values for the characters viz., days to 50 percent flowering (89.13), days to maturity (131.00), number of branches per plant (11.10), number of pods per plant (140.40), harvest index (61.53) and grain yield per plant (55.25). Among all the traits, the contribution of harvest index (43.59%) towards divergence was maximum, followed by number of seeds per pod (16.24%), 100-seed weight (10.69%) and number of branches per plant (8.00%).

Keywords: D² analysis, yield, quality traits, pigeonpea

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is a short-lived perennial member of family Fabaceae and it is invariably cultivated as annual crop. Pigeonpea is an often cross pollinated (20-70%) crop with (2n=2x=22) diploid chromosome number. Pigeonpea is grown worldwide on 5.2 M ha land in about 50 countries and 77% of its area is in India, in India at present, pigeonpea is cultivated on 4.4 million ha area with 2.89 million tones production with a productivity of 655 kg/ha during year 2010-11. In Gujarat pigeonpea is grown on around 2.77 lakh hectares area with an annual production and productivity of 2.72 lakh tones and 986 kg/ha, respectively (FAO, 2012) [2].

In spite of their high nutritive value, most farmers were giving low priority to pigeonpea in cultivation and were assigned to rainfed and relatively less productive portions of their fields. However, recently multiple harvest potential of dual purpose pigeonpea by rendering first two pickings for green pods and remaining left over for the harvesting of dry seeds; has brought about changes in the mind set of some farmers and they are taking the cultivation more seriously than before. Therefore, breeding for dual purpose pigeonpea is being considered as a life line of subsistence agriculture. The conventional breeding procedures such as single plant selection from locally adapted cultivars and pedigree selection from inter-varietal crosses have remained main methods of improvement for higher yield with resistance to major disease, large seed size and reduced maturity (Saxena and Sultana, 2010) [10], even though the success observed in increasing yields levels as been rather small. For an outstanding breeding programme in the crop improvement, diversity analysis greatly helps the breeder in the identification and proper choice of parents for specific breeding objectives. The present study was carried out to assess the genetic diversity among different genotypes.

Materials and Methods

The present experiment comprised of 50 genotypes of pigeonpea obtained from the Pulses and Castor Research Station, Navsari Agricultural University, Navsari during the year 2014-15. The experiment was conducted in Randomized Block Design (RBD) with three replications. Each genotype consisted of three rows with plant to plant distance of 20 cm and rows were spaced 60 cm apart. The experiment sowing was made during October, 2014 at college farm NAU, Navsari. The observations were recorded on five competitive plants were randomly selected in each plot in all the three replications for the traits viz., plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, harvest index, grain yield per plant and protein content except, days to 50% flowering

and days to maturity. Multivariate analysis was done utilising Mahalanobis D^2 statistic (Mahalanobis, 1936) [3] and genotypes were grouped into different clusters following Tocher's method.

Results and Discussion

The Genetic diversity analysis among 50 genotypes was measured by employing D^2 statistics and grouped into three clusters using Tocher's method given by Rao (1952) [5]. Distribution of genotypes in each cluster is presented in Table 1. Cluster-I had maximum number of genotypes (46 genotypes), while, two genotypes each was found in cluster-II and III; which suggested presence of considerable amount of genetic diversity among the genotypes. Earlier, similar type of work on this crop was also carried out by Sreelakshmi *et al.* (2010) [12] and Satankar Navneet *et al.* (2017) [9].

The intra-cluster and inter-cluster D^2 values were estimated and presented in Table 2. The inter-cluster distance ranged from 4.66 to 8.13. The maximum inter-cluster distance (8.13) was observed between cluster-I and II, followed by those between cluster-I and III (5.63), which suggested that the crosses among the genotypes included in these clusters may give high heterotic response and thus better segregants. The minimum inter-cluster distance (4.66) was observed between cluster-II and III, which indicated the close relationship between the genotypes involved.

Intra-cluster distance ranged from 2.44 to 3.10. At intra-cluster level, cluster-III had the highest value (3.10) followed by cluster-II (2.45). 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) [1]. The minimum intra-cluster distance (2.44) was observed in cluster-I, indicating that the genotypes within this cluster were similar. These results were in agreement with the earlier findings of Pandey *et al.* (2013) [4].

The cluster mean for different traits is presented in Table 3. The cluster-II had the highest mean values for the characters days to 50 percent flowering (89.13), days to maturity (131.00), number of branches per plant (11.10), number of pods per plant (140.40), harvest index (61.53) and grain yield

per plant (55.25). Cluster-III had maximum mean value for plant height (113.70), pod length (5.14), number of seeds per pod (4.99), 100-seed weight (9.52) and protein content (23.60). While, cluster-I had minimum mean value for days to 50 percent flowering (78.31), days to maturity (120.60), plant height (87.54), number of branches per plant (8.20), number of pods per plant (100.53), pod length (4.13), number of seeds per pod (3.41), 100-seed weight (7.92), harvest index (38.22), grain yield per plant (34.72) and protein content (21.63). The similar findings were also reported by Singh *et al.* (2010) [11] and Rao *et al.* (2013) [6].

The utility of D^2 statistics is enhanced by its applicability to estimate relative contribution of various traits towards genetic divergence which is given in Table 4 and depicted in Figure 1. Harvest index (43.59%) contributed maximum towards total divergence, followed by number of seeds per pod (16.24%), 100-seed weight (10.69%) and number of branches per plant (8.00%). While, other characters such as days to maturity (6.45%), plant height (5.39%), days to 50 percent flowering (4.57%), grain yield per plant (2.61%) and protein content (1.96%) contributed less towards genetic divergence in the present material. Pod length (0.41%), number of pods per plant (0.08%) had very low contribution to the genetic divergence. These results were in line with Rekha *et al.* (2011) [8] and Reddy *et al.* (2015) [7].

Conclusion

Mahalanobis (1936) [3] D^2 analysis offers a reliable technique to estimate the divergence present in the population. In the present investigation, the traits harvest index, number of seeds per pod, 100-seed weight and number of branches per plant contributed maximum towards total divergence and should be given more importance for the purpose of selection and choice of parents for hybridization. The cluster-I and cluster-II were more divergent clusters. The genotypes of cluster-II exhibited highest cluster mean values for most of the yield contributing traits and the genotypes of cluster-I showed superior performance as early flowering and early maturity. Therefore, genotypes from cluster-I and cluster-II can be utilized as potential parents in hybridization program for improving most of the yield and yield contributing traits in pigeonpea.

Table 1: Grouping of 50 genotypes of pigeonpea into different clusters

Cluster	No of genotypes	Genotypes
1	46	GT-1, GT-100, GT-101, GT-103, AGT-2, BDN-2, BDN-711, ICPL-87119, ICPL-87, ICP-886, C-11, GNP-552, GNP-554, GNP-555, GNP-556, GNP-557, GNP-558, GNP-561, GNP-562, T-BULK-1, T-BULK-2, T-BULK-4, T-BULK-5, T-BULK-6, T-BULK-7, T-1, T-8, T-10, T-11, T-16, T-17, T-18, T-20, T-22, T-26, T-28, T-29, T-34, GNP-359, GNP-360, GNP-367, GNP-370, GNP-371, NPMK-14-6, NPMK-14-9, NPMK-14-11
2	2	GNP-551, T-9
3	2	Vaishali, GT-102

Table 2: Estimates of average Intra and Inter – cluster (D^2) values for 3 clusters constructed from 50 genotypes of pigeonpea

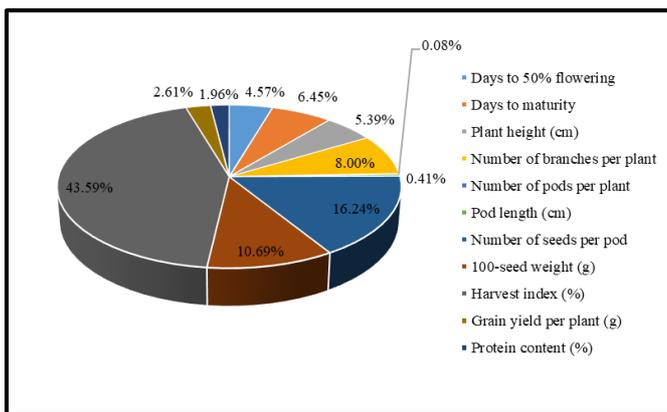
Cluster	1	2	3
1	2.44	8.13	5.63
2		2.45	4.66
3			3.10

Table 3: Cluster mean values of 11 traits in 50 genotypes of pigeonpea

Cluster Number	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-Seed weight (g)	Harvest index (%)	Grain yield per plant (g)	Protein content (%)
1	78.31	120.60	87.54	8.20	100.53	4.13	3.41	7.92	38.22	34.72	21.63
2	89.13	131.00	112.62	11.10	140.40	5.00	4.45	8.85	61.53	55.25	23.22
3	88.87	130.83	113.70	9.93	108.08	5.14	4.99	9.52	49.02	43.27	23.60

Table 4: Contribution of 11 characters under study towards total divergence in 50 pigeonpea genotypes

Sr. No	Character	% contribution towards divergence
1	Days to 50% flowering	4.57%
2	Days to maturity	6.45%
3	Plant height (cm)	5.39%
4	Number of branches per plant	8.00%
5	Number of pods per plant	0.08%
6	Pod length (cm)	0.41%
7	Number of seeds per pod	16.24%
8	100-seed weight (g)	10.69%
9	Harvest index (%)	43.59%
10	Grain yield per plant (g)	2.61%
11	Protein content (%)	1.96%
	Total	100%

**Fig 1:** Percent contribution of 11 characters under study towards total divergence in 50 pigeonpea genotypes

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