

Genetic diversity in germplasm of pigeonpea

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The genetic divergence among fifty-five genotypes of pigeonpea (*Cajanus cajan*) were evaluated for nine different characters and was estimated by Mahalanobis D^2 statistic. The genotypes were grouped into seven clusters. The clustering pattern of the genotypes showed high degree of genetic diversity. The highest intra cluster distance was noticed for the cluster IV ($D^2 = 2.069$) and the lowest for the cluster VII ($D^2 = 1.619$). The highest intra-cluster distance was observed between clusters VI and III ($D^2 = 4.598$) where as the lowest inter-cluster D^2 value was observed between cluster I and II ($D^2 = 2.308$). The cluster mean estimated for nine characters revealed that cluster IV had highest mean values for days to 50 per cent flowering, days to maturity and plant height. For seed yield per plant, highest mean was recorded for cluster VII and lowest for cluster II with over all mean of 69.05. Therefore, the result of the present study suggest that while selecting parents, inter-cluster distance must be taken into consideration so as to initiate a crossing programme to produce new recombinants with desired characters in pigeonpea.

Key words : Divergence, Pigeonpea, Cluster

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INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp] is a multipurpose legume crop and is well adapted even in marginal lands. Pigeonpea serves as important food and excellent protein source. Additionally, the seeds and sometimes the pods are eaten as vegetable and also used as flour additive in soups and rice. A species of bacteria, Rhizobia is capable of fixing 41 to 280 kg/ha of nitrogen due to their intrinsic capacity to symbiotically associate with the root nodules of pigeonpeas. Parrota (2001) reported the use of their leaf preparations for the treatment of jaundice, inflammation and sores of the mouth.

Information on genetic divergence among the plant materials is vital to a plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute desirable segregants and or to produce high heterotic crosses. Murty and Arunachalam (1966) stated that more diverse the parents greater are the chances of obtaining high heterotic F_1 s and broad spectrum of variability in segregating generations. Improvement in yield and quality is normally achieved by selecting genotypes with desired character combinations existing in the nature or by hybridization. The parents identified on the basis of divergence analysis would be more promising. According to Griffing and Lindstrom (1954); Murty and

Arunachalam (1966) and Gaur *et al.* (1978) in both cross and self pollinated crops genetic diversity is one of the most important tools to quantify genetic variability. Rao (1952) and Jain *et al.* (1975) stated that the qualification of genetic diversity through biometrical procedures has made it possible to choose genetically diverse parents for a successful hybridization program. D^2 statistic developed by Mahalanobis (1936) is a powerful tool to measure genetic divergence among the genotypes.

RESEARCH METHODOLOGY

The experiment was conducted on fifty five genotypes of pigeonpea at the Regional Research Station, Saini, Kausambi of C.S. Azad University of Agriculture and Technology, Kanpur during three *Kharif* seasons namely *Kharif* 2008-09, 2009-10 and 2010-11. The experiment was laid out in a Randomized Block Design with three replications. Row to row and plant to plant spacing were maintained at 90 and 20 cm, respectively. Each genotype was grown in a single row plot of 5.0 m length. Observations were recorded for nine traits including days to 50 per cent flowering, days to pod emergence, days to maturity, plant height (cm), primary branches per plant, pod per plant, seed per pod, 100-seed weight (g) and seed yield per plant (g). the recommended package of practices was followed to raise a good crop.

Genetic diversity was estimated following Mahalanobis's D^2 -statistic by Mahalanobis (1936) extended by Rao (1952). Tocher's method was followed for determining the group constellations. Based on D^2 values, the fifty-five genotypes were grouped into different clusters.

RESEARCH FINDINGS AND ANALYSIS

The analysis of variance revealed highly significant variation among the genotypes for all the traits studied. These differences could be used in distinguishing genotypes based on their morphology. Mahalanobis D^2 statistic was computed for all the nine characters in order to assess the genetic diversity present among the genotypes under study. In all, seven clusters were formed (Table 1). Cluster I was the biggest cluster having 12 genotypes which was followed by

cluster IV with 11 genotypes, cluster III with 9 genotypes, cluster II and V with 7 genotypes, respectively, cluster VI with 5 and cluster VII with 4 genotypes. This may be attributed to the fact that these fifty-five genotypes of pigeonpea grouped into seven clusters were revealing the presence of considerable amount of genetic diversity in the material.

The intra cluster distance ranged from 1.619 to 2.069 (Table 2) with highest intra cluster distance for cluster IV ($D^2 = 2.069$) with eleven genotypes. This cluster was the most divergent group and genotypes falling in this cluster could be utilized as parents for hybridization. Cluster I ($D^2 = 2.000$) with twelve genotypes and cluster III ($D^2 = 1.852$) with nine genotypes were next most divergent groups. Such intra cluster genetic diversity among the genotypes could be due to heterogeneity, genetic architecture of the populations, past

Table 1: Distribution of 55 genotypes of pigeonpea on the basis of D^2 statistic

Cluster	Number of genotypes	Genotypes
I	12	ICPL 3585, KWR 97-1, V 77, V 78, KPBR 80-2-2, BWR 37, ICPL 353, ICPL 14670, ICPL 16195, ICPL 22494, ICPL 56064, ICPL 56068
II	7	K 3623, K 3640, K 3646, K 3652, K 3992, K 3740, DPPA 85-15
III	9	ICPL 189, B 110, Selda 3-1, ICPL 15707, ICPL 25059, T 7, ICPL 28207, ICPL 28213, ICPL 33715
IV	11	ICPL 25065, ICPL 26113, ICPL 28199, ICPL 28201, ICPL 28220, ICPL 33022, ICPL 33755, ICPL 33835, ICPL 47233, ICPL 49539, ICPL 52935
V	7	MA 71-1, ICPL 14987, ICPL 14997, ICPL 28204, ICPL 52973, ICPL 56062, ICPL 56063
VI	5	ICPL 14991, ICPL 22554, ICPL 26191, ICPL 28206, ICPL 3415
VII	4	Bahar, Azad, ICPL 8372, ICPL 56061

Table 2: Intra-cluster (in-bold) and inter cluster distances in pigeonpea

Cluster	I	II	III	IV	V	VI	VII
I	2.000	2.308	2.554	3.328	3.146	3.838	3.325
II		1.795	4.420	3.194	3.585	3.022	4.452
III			1.852	3.928	3.205	4.598	2.547
IV				2.069	3.590	2.961	4.137
V					1.796	3.271	3.465
VI						1.755	3.445
VII							1.619

Table 3: Cluster means for various characters in 55 genotypes of pigeonpea

Characters	Clusters							Overall mean
	I	II	III	IV	V	VI	VII	
Days to 50% flowering	118.83	130.71	118.89	134.82	125.86	134.60	119.75	125.95
Days to pod emergence	144.50	155.57	140.22	159.27	151.71	160.60	146.50	150.69
Days to maturity	235.67	241.86	228.78	247.09	243.71	246.90	227.00	239.03
Plant height	148.17	121.57	163.11	193.73	129.71	128.20	153.00	152.53
Primary branches/ plant	4.33	3.14	6.50	4.91	3.86	4.60	5.50	4.70
Pods per plant	228.58	178.57	329.89	250.45	398.00	234.20	308.25	271.04
Seeds per pod	3.00	3.14	3.00	3.18	3.14	4.00	4.01	3.24
100Seed weight	9.87	9.99	9.64	11.23	8.04	9.39	9.46	9.81
Seed yield per plant	52.59	41.81	83.31	74.42	80.83	77.24	88.40	69.05

history of the selection in development traits and degree of general combining ability by Dikshit and Swain (2000). The cluster VII showed minimum intra cluster value of 1.619 indicating that the genotypes with in this cluster were similar. These results are in agreement with the earlier findings of Singh *et al.* (2006) and Sreelakshmi *et al.* (2010).

As far as inter-cluster divergence is concerned, the inter-cluster distance values ranged from 2.308 to 4.598. the member of cluster VI and III exhibited maximum divergence ($D^2 = 4.598$) followed by cluster VIII and II ($D^2 = 4.452$), cluster III and II ($D^2 = 4.42$), cluster VII and IV ($D^2 = 4.137$), cluster IV and III ($D^2 = 3.928$) indicating that genotypes belonging to these cluster were genetically more divergent that order. Crosses among these genotypes included in these clusters may give high heterotic response and thus better segregants. Natarajan *et al.* (1988) have also opined that selection of parents for hybridization should be done based on the inter-cluster distance to get maximum variability. On the other hand, lowest inter-cluster D^2 value was observed between cluster I and II ($D^2 = 2.308$) indicating that genotypes of these clusters are closer. Murthy and Arunachalam (1966) and Sreelakshmi *et al.* (2010) also observed similar results.

The cluster mean estimated for nine characters (Table 3) revealed that cluster means for days to 50 per cent flowering varied from 118.83 days in cluster I to 134.82 days in cluster IV with overall mean of 125.95 days. cluster IV had highest mean values for days to 50 per cent flowering, days to maturity and plant height. Cluster VII had highest mean values for seeds per pod and seed yield per plant. cluster II exhibited highest mean for 100 seed weight, cluster III for number of primary branches per plant, cluster V for pods per plant and cluster VI for days to pod emergence, respectively. For seed yield per plant, highest mean was recorded for cluster VII and lowest for cluster II with overall mean of 69.05.

This indicated that none of the clusters contained genotypes with all the desirable characters which could be directly selected and utilized. Therefore, the result of the present study suggest that while selecting parents for hybridization inter-cluster distance must be taken into consideration to select genetically diverse and agronomical superior that may provide wide spectrum of variation in the segregating generations.

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