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GENETIC DIVERGENCE IN EARLY MATURING PIGEONPEA

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ABSTRACT

D^2 analysis in 42 genotypes of early pigeonpea revealed considerable diversity, on the basis of which they were grouped into 8 clusters. Branches/plant, pods/plant, harvest index and yield/plant contributed maximum to the total genetic divergence. The genotypes of clusters II and VII can be used as parents in hybridization programme to develop early maturing, high yielding pigeonpea varieties.

Key words: *Cajanus cajan*, D^2 statistic, genetic divergence.

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is an important pulse crop of Assam. Most of the varieties grown are of long duration and, therefore, winter crops cannot be cultivated as late sowing of winter crops result in poor yield. Development of early maturing varieties is inevitable for which identification of suitable parents is necessary. The selection of parents for varietal improvement programme depends on the knowledge of available diversity which is practically nonexistent for the agroclimatic conditions of Assam. Therefore, the present study has been undertaken to ascertain the nature and magnitude of genetic diversity among 42 early pigeonpea lines.

MATERIALS AND METHODS

The experimental material comprised 42 genotypes of early pigeonpea received from ICRISAT and Haryana Agricultural University, Hisar. These lines were grown in randomized block design with three replications at the Regional Agricultural Research Station, Diphu. Each plot consisted of 3 rows of 4 m length spaced at 60 cm and plants within rows at 30 cm. Observations were recorded on ten random plants for nine quantitative characters. The data were subjected to Mahalanobis D^2 statistic and genotypes were grouped into different clusters following the Tocher's method [1].

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the 42 genotypes for all the characters under study, indicating considerable variation among the genotypes. The D^2 values range from 11.5 to 2658.6 reflecting wide diversity among the genotypes. On the basis of D^2 estimates, 42 genotypes were grouped into eight clusters (Table 1). Among these, cluster I had the maximum number of 19 genotypes, followed by clusters II and III with 9 and 5 genotypes, respectively. The clusters IV, V, VI and VII had 2 genotypes each, whereas cluster VIII had a single genotype. Interestingly, the related ICPL lines and the lines of Hisar were distributed into different clusters. This results indicated that genetic divergence is not related to geographical diversity. Substantial variability among the lines evolved in the same habitat might be due diversity of their pedigree along with natural and directional selection pressure for certain agronomic traits [2]. Genetic drift and selection forces under diverse environments could cause greater diversity than geographical distance [3].

Table 1. Distribution of 42 pigeonpea genotypes into different clusters

Cluster	No. of genotypes	Cluster composition
I	19	ICPL 87111, ICPL 88032, ICPL 88039, ICPL 89004, ICPL 89008, ICPL 89011, ICPL 90030, ICPL 90031, ICPL 90032, ICPL 90035, ICPL 90036, ICPL 90038, ICPL 90039, ICPL 85010, ICPL 87095, ICPL 88009, ICPL 88015, H 88-8
II	9	ICPL 83015, ICPL 84023, ICPL 88003, ICPL 88017, ICPL 89020, ICPL 89024, ICPL 89027, ICPL 90001, ICPL 90005
III	5	ICPL 88001, ICPL 90004, ICPL 90008, ICPL 90011, ICPL 90012
IV	2	UPAS 120, Manak
V	2	ICPL 4, H 88-26
VI	2	ICPL 89012, ICPL 90033
VII	2	H 82-1, H 88-45
VIII	1	ICPL 88007

The intercluster distances were greater than intracluster distances, revealing considerable amount of genetic diversity among the genotypes studied (Table 2). Intercluster distance is the main criterion for selection of genotypes using D^2 analysis. Genotypes belonging to the clusters with maximum intercluster distance are genetically more divergent and hybridization between genotypes of divergent clusters is likely to produce wide variability with desirable segregant [4, 5]. The intracluster D^2 values ranged from 21.9 (cluster VI) to 127.4 (cluster I). The maximum intercluster D^2 values were recorded

Table 2. Intra- (in bold) and intercluster average divergence (D^2) values of 8 clusters including 42 genotypes of pigeonpea

	I	II	III	IV	V	VI	VII	VIII
I	**127.4**	377.2	338.5	213.4	276.7	663.3	829.2	271.9
II		**126.5**	557.9	599.7	368.1	1452.6	1779.2	278.7
III			**66.3**	519.2	482.8	459.1	1198.6	769.6
IV				**40.8**	157.3	526.2	439.2	379.3
V					**35.4**	1145.8	1010.1	199.9
VI						**21.9**	494.9	1484.1
VII							**105.1**	1318.8
VIII								**0.0**

between cluster II and VII (1779.2), while the divergence was minimum between cluster IV and VI (157.3).

Cluster means revealed appreciable variation for various characters (Table 3). These differences were more conspicuous for branches/plant, pods/plant, harvest index and

Table 3. Character means for different clusters of pigeonpea genotypes

Cluster	Yield per plant, g	Days to 50% flowering	Days to maturity	Plant height, cm	Pods per plant	Branches per plant	Seeds per pod	100-seed weight, g	Harvest index, %
I	20.9	72.6	132.7*	222.9	149.6	14.4	4.1	9.4	32.8
II	8.8	60.5	136.9	146.2*	80.4	10.5*	3.7	8.3	25.8
III	5.8*	71.9	146.8	191.7	72.7*	13.3	3.6*	10.7**	14.9*
IV	27.7	83.9	151.5	276.1	221.4	20.7	3.7	8.4	37.6
V	23.9	76.9	134.2	226.0	197.7	20.6	3.8	7.0*	38.9
VI	14.0	99.4	148.5	267.9	146.9	15.7	3.6	9.7	22.2
VII	44.9**	101.4**	153.0**	306.2**	301.6**	25.3**	4.0	9.3	35.7
VIII	30.6	58.0*	136.0	165.7	170.6	17.2	4.3	9.3	42.8**
Mean	18.1	73.4	138.1	210.2	139.1	14.8	3.9	9.2	29.5
CV (%)	9.8	2.9	2.9	4.5	13.4	14.2	6.4	0.1	12.5

*,**Lowest and highest means, respectively.

yield/plant, contributing substantially to total genetic divergence as reflected by their coefficient of variation. These results are in conformity with those of [4, 6]. The genotypes of cluster I were earliest in maturity and those of cluster II are shortest with early flowering and maturity. Cluster III had lowest yield/plant but highest 100-seed weight whereas, genotypes of cluster VII had highest seed yield, pods/plant and branches/plant, but were late in maturity. ICPL 88007 of cluster VIII was earliest in flowering and produced maximum number of seeds per pod with the highest harvest index.

Thus, in view of considerable genetic diversity in pigeonpea lines, there is sufficient scope for varietal improvement through hybridization between lines H 82-1 of cluster II and H 88-45 of cluster VII. Crossing among these genotypes is suggested to obtain desirable segregates giving higher yield with early maturity.

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