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Genetic Diversity Studies in Super-early Pigeonpea [*Cajanu cajan* (L.) Millsp.]

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ABSTRACT

Background: Pigeonpea is an important legume crop in India. The super early genotypes which matures within 100 days have been developed at ICRISAT. They are photo-insensitive, aids in crop intensification and escapes abiotic and biotic stresses. The super early genotypes were exploited for genetic diversity for further improvement of the genotypes.

Methods: The study was conducted at International Crop Research Institute for the Semi-Arid Tropics, Patancheru, Telangana during kharif, 2017. The thirty-super early pigeonpea genotypes developed at ICRISAT were subjected for the study of genetic diversity (Mahalanobis D^2 method) based on twelve quantitative characters.

Result: The 30 super early genotypes were grouped into five clusters. The largest number of genotypes were confined to cluster III (19 genotypes) followed by cluster IV (6 genotypes), cluster I and II (2 genotypes). Cluster V is a solitary cluster with the check MN1.The inter cluster distance was high between the clusters III and IV followed by cluster I and III. The intra cluster distance was highest for the cluster III indicating the presence of variation among the genotypes within the cluster. The highest mean for single plant yield was observed for the cluster III followed by cluster V. The clusters with more inter cluster distance can be used to select parents to be involved in hybridization programmes.

Key words: Cluster distance, D^2 statistics, Genetic diversity, Super early pigeonpea.

INTRODUCTION

Pigeonpea is the major legume crop grown in India next to chickpea. It is the richest source of protein (18 to 25%), greatly supplementing the vegetarian diet of Indian population pigeonpea is grown globally in an area of about 5.6Mha with production of 4.4 M tonnes. India is the largest producer of pigeon pea with an average yield of 768.4Kg/ha followed by Myanmar, Malawi, United Republic and Kenya. In India, pigeonpea is grown in an area of about 4.5 Mha accounting for a production of 3.3M tonnes (FAOSTAT, 2019). In India pigeonpea is majorly cultivated in states *viz.,* Maharashtra, Karnataka, Madhya Pradesh andhra Pradesh, Uttar Pradesh, Gujarat, Jharkhand, Odisha and Tamil Nadu.

The crop is well adapted to warm tropical and sub-tropical climate. However, it is susceptible to stagnant water conditions. They can withstand drought condition and fixes 30-40 kg N/ha to the soil adding to its fertility. Pigeonpea is usually grown as an annual crop, although they are perennial in nature. They are generally classified into 11 maturity groups based on number of days to 50% flowering (Saxena *et al.* 2019). The super early genotypes gain its importance due to reduced days to maturity, synchronized maturity and adapting to various agro-ecological zones (Ranjani *et al.* 2018).

Plant breeders seek for diversity in the plant genetic resources to develop new varieties with desired traits and characteristics. However, the "domestication bottleneck" due to inbreeding in cross pollinated crop is a major constraint leading to narrow gene diversity (Govindaraj *et al.* 2015.) The diversity can be assessed based on morphology, biochemical characters and genetic factors. The genotypes from diverse clusters can serve as a parent in hybrid development and to select parents with high polymorphism leading to the development of mapping populations.

MATERIALS AND METHODS

Thirty super-early pigeonpea genotypes (29 lines + 1 check) were the biological materials used in this study. The experimental materials belong to Pigeonpea Breeding, ICRISAT, Patancheru, Hyderabad. The experimental plot was RP 12B (Red precision 12B) located at ICRISAT, Patancheru, Hyderabad. The latitudinal and longitudinal location of ICRISAT is 17.51°N and 78.27°E respectively.

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The experimental plot is located at an altitude of 545 meters above MSL with an annual rainfall of 877.82 mm. The field experiment was conducted during *kharif* 2017. The experimental design involved was randomized block design (RBD) with 3 replications. The genotypes were raised in a broad bed of 4 m length and 1 m breadth each with a spacing of 30 × 10 cm. Standard cultural practices were followed as per recommendation. Morphological characterization was done with five competitive plants from the middle rows of each broad bed and are labelled excluding the border row plants. The data was recorded from the labelled plants for 12 quantitative characters. The list of quantitative characters under investigation are days to fifty per cent flowering, plant height, days to maturity, number of branches per plant, pod bearing length, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, shelling percentage, grain yield per plant. The genetic divergence among the 30 genotypes was studied. using the D^2 statistic of Mahalanobis (1928).

RESULTS AND DISCUSSION

The present study involves the analysis of 30 super early pigeonpea genotypes. The development of super early genotypes involved crosses between pigeonpea genotypes such as AL 1518-2 × ICPL 85010, AL 1621 × MN 5, AL 1518-2 × MN 8, MN 8 × AL 1518-2, MN 1 × AL 1518-2, MN 1 × AL 1621 (Srivastava *et al.,* 2012). The genetic diversity among the 30 pigeonpea genotypes under investigation was studied based on twelve quantitative characters using D^2 method. The 30 genotypes were grouped into five clusters (Table 1). The cluster III is the largest one which consisted of 19 genotypes. The cluster IV is the second largest cluster with six genotypes followed by cluster I and II each consisting of two genotypes. The cluster V was a solitary cluster with one genotype. The results were in confirmity with Singh *et al.* (2010).

The inter and intra cluster between the clusters ranged between 0-9.428 and 3.911-25.084 respectively. The maximum inter cluster distance was observed between cluster III and IV (25.084) followed by cluster I and III (24.375) and cluster II and III (22.205). (Table 2) The maximum inter cluster distance implies the fact that the genotypes from these clusters can be used in a hybrid development for exploitation of better heterosis and getting a greater number of segregants, whereas the minimum inter cluster distance represents reduced level of diversity for various traits among the genotypes of different clusters. The minimum inter cluster distance existed between cluster I and II (3.911), followed by cluster I and IV (5.768) and cluster II and IV (6.612). The intra cluster distance was maximum for cluster III (9.248) followed by cluster IV (6.891). The minimum intra cluster distance was observed in case of cluster I (2.520). (Table 2) Cluster V, which is a solitary cluster, had no intra cluster distance. The minimum intra cluster indicates that the genotypes of the particular cluster were closely related with one another. The inter cluster distance was greater than intra cluster implying the close proximity of genotypes within the cluster and the similar results were reported by Sharma *et al.* (2018), Singh *et al.* (2010), Shunyu *et al.* (2013), Singh *et al.* (2013), Singh *et al.* (2015) and Sreelakshmi *et al.* (2010).

The highest cluster mean for plant height was exhibited by the cluster III (102.915 cm) and the minimum cluster mean for plant height was observed in cluster IV (64.244 cm) (Table 3). The cluster mean for number of branches per plant was highest for cluster IV (11.122) and the lowest in cluster III (7.40). The cluster III (74.768) had maximum cluster mean for pod bearing length and the minimum was observed in case of cluster I (23.067). The maximum cluster mean for number of clusters per plant was exhibited by cluster III (40.267), whereas minimum value was possessed by cluster I (13.70). Cluster mean for number of pods per plant was highest for cluster III (68.058) and the lowest in case of cluster II (31.633). The cluster means for the traits pod length (5.107), number of seeds per pod (3.880), days to fifty percent flowering (62.33), days to maturity (95.00) were the highest in Cluster V. In case of hundred seed weight, shelling percentage and single plant yield the highest cluster mean was observed for clusters II (7.083), IV (70.970) and III (13.258) respectively. Minimum cluster mean was observed in case of cluster I for pod length (4.368), number of seeds per pod (3.373), days to fifty per cent flowering (49.833) and days to maturity (83.500), cluster V for hundred seed weight (5.833) and shelling percentage (62.337), cluster II for single plant yield (6.567).

The performance of the genotypes for yield and its attributes are readily available from the cluster means for various traits. The cluster mean for single plant was the

Table 1: Cluster distribution of the 30 super-early pigeonpea genotypes.

Clusters	No of genotypes	Membership %	Members
I	2	6.66	ICPL 11249, ICPL 20338
II	2	6.66	ICPL 11273, ICPL 11253
III	19	63.33	ICPL 20328, ICPL 11244, ICPL 11296, ICPL 11276, ICPL 11279, ICPL 11301, ICPL 11300, ICPL 20329, ICPL 20327, ICPL 20325, ICPL 20333, ICPL 11245, ICPL 11326, ICPL 11242, ICPL 11285, ICPL 20326, ICPL 11292, ICPL 11303, ICPL 11298
IV	6	20	ICPL 11255, ICPL 20340, ICPL 20341, ICPL 20336, ICPL 11252, ICPL 11256
V	1	3.33	MN I

highest in case of cluster III, whereas cluster II recorded the lowest cluster mean for single plant yield. The cluster distance between the cluster III and II was 22.205 indicating that the selection of parents for development of high yielding genotypes from these clusters will lead to a successful breeding program. Likewise, for yield attributing traits like number of pods per plant, hundred seed weight and number of seeds per pod the cluster mean was highest in case of clusters III, II and V respectively. The lowest cluster mean was recorded in case of clusters II, V and I for number of pods per plant, hundred seed weight and number of seeds per pod respectively. The diversity for the trait number of pods per plant was the highest and can be subjected to development of high yielding hybrids. Therefore, the beneficial crosses can involve cluster III and II: cluster III and IV for development of promising genotypes with high yield and reduced days to maturity. The results were on par with the research findings of Manyasa *et al*. (2009), Satapathy and Panigrahi (2014).

Contribution of each quantitative trait to the total divergence was estimated by ranking of the individual character. The maximum contribution to diversity was from plant height (50.57%) followed by single plant yield (21.38%), days to maturity (15.63), whereas the minimum contribution was exhibited by traits like number of clusters per plant (0.00), followed by number of pods per plant (0.23%), number of branches per plant (0.69%), shelling percentage (0.69%) and days to fifty percent flowering (0.69%)(Fig 1). The results were in accordance with (Chaudhary *et al*. 2016), for traits projecting minimum per cent for total diversity. Patel *et al*. (2018) reported minimum contribution (zero per cent) of traits like test weight and leaf area towards divergence.

The relative importance of the different characters in relation to their contribution to total divergence is known by their respective rank totals. Lesser the rank total of a character, higher is its contribution to divergence and vice

Table 2: Inter and Intra (Diagonal) cluster distance for 5 clusters of 30 super early pigeonpea lines.

Clusters	I	II	III	IV	V
I	2.520	3.911	24.375	5.768	17.895
II		2.760	22.205	6.162	15.818
III			9.248	25.084	15.520
IV				6.891	17.201
V					0.000

Table 3: Cluster Means for 12 quantitative characters of 29 super early pigeonpea lines with one check.

Clusters	Plant height	Number of branches per plant	Pod bearing length	Number of clusters per plant	Pods per cluster	Pod length	Number of seeds per plant	100 seed weight	Shelling per cent	Days to 50% flowering	Days to maturity	Single plant yield
I	65.900	11.100	23.067	13.700	36.067	4.368	3.373	6.917	69.837	49.833	83.500	7.117
II	68.983	9.300	23.600	14.100	31.633	4.553	3.587	7.083	69.310	51.000	84.167	6.567
III	102.915	7.400	74.768	40.267	68.058	4.780	3.788	6.123	66.929	58.596	92.491	13.258
IV	64.244	11.122	24.011	14.144	38.989	4.623	3.544	6.611	70.970	52.596	84.833	7.450
V	87.000	11.000	32.067	25.867	48.200	5.107	3.880	5.833	62.337	62.333	95.000	9.200

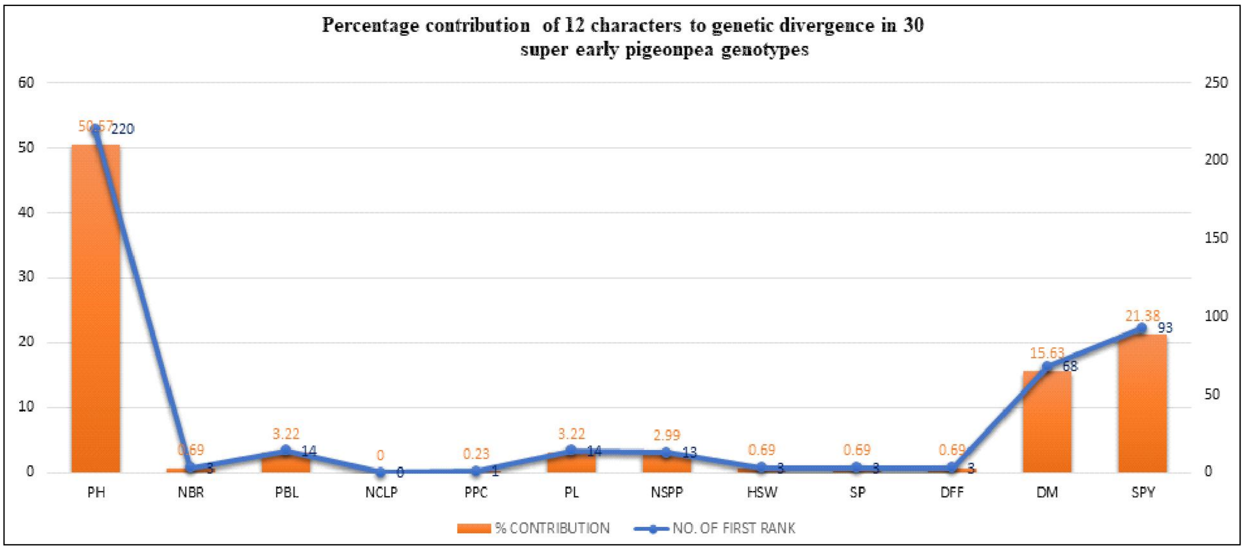

Fig 1: Percentage contribution of 12 characters to genetic divergence in 30 super early pigeonpea genotypes. PH-Plant height in cm; NBR-Number of branches per plant; PBL-Pod bearing length in cm; NCPL-Number of clusters per plant; PPC-Number of pods per plant; PL- Pod length in cm; NSPP-Number of seeds per pod; HSW- Hundred seed weight in g; SP- Shelling percentage; DFF- Days to 50% flowering; DM- Days to maturity; SPY- Single plant yield in g.

versa. The percentage contribution of a character towards genetic divergence was calculated as the percentage of mean. The result indicated that the plant height contributed more to divergence followed by single plant yield and days to maturity. The lowest contribution to divergence was offered by number of clusters per plant. Similar research findings were reported by Pandey *et al*. (2013) for contribution of days to maturity to divergence by Kumar *et al*. (2013), Satapathy and Panigrahi (2014), Singh (2015) and Pushpavalli *et al*. (2017) for contribution of single plant yield to divergence.

CONCLUSION

The overall outlook of the clusters revealed the fact that the advance lines obtained from the crosses of similar parents occupied the same clusters indicating the nature of narrow genetic base for the parents utilized in the hybrid development programme. It was a fact that the hybrid development program was majorly for the development of super-early lines hence genotypes which mature earlier were chosen as parents adding up to the bottleneck. However, the diverse genotypes identified can be used in developing mapping populations to study the genes involved in earliness.

Conflict of interest: None.

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