

Genetic Diversity in Pigeon Pea [*Cajanus Cajan* (L) Millsp.] Genotypes of Nagaland

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Abstract – The nature and magnitude of genetic divergence were assessed in 30 local pigeon pea genotypes of Nagaland. Based on the relative magnitude of D^2 values, 30 genotypes were grouped into seven clusters. The coefficient of variation for different characters indicated that number of pods per plant, number of cluster per plant and seed yield per plant contributed maximum towards divergence. The genotypes belonging to cluster VII could be utilized as diverse parent in hybridization program with the genotypes of cluster I and cluster IV respectively, to achieve greater variability in the segregation generations.

Keywords – Clusters, D^2 Values, Genetic Diversity, Pigeon Pea.

I. INTRODUCTION

In any crop, germplasm is a valuable source of base population and provides the scope for wider adaptability. However, to understand the useable variability, grouping or classification of genetic stocks based on minimum divergence or resemblance between them is quite imperative. The nature and magnitude of genetic divergence helps the plant breeder in choosing the right type of parents for higher amount of heterotic expression in F_1 and broad spectrum of variability in subsequent segregation generations (Maurya and Singh, 1977). Since information available on genetic diversity in pigeon pea [*Cajanus cajan* (L.) Millsp.] genotypes of Nagaland is limited, therefore, the present study was carried out to analyze the genetic diversity in pigeon pea genotypes in order to select the potential parents for breeding program.

II. MATERIALS AND METHODS

The present investigation was carried out in the year 2006-2007 at the experimental farm of genetics and plant breeding, NU. SASRD, Medziphema. The 30 genotypes NU4, NU5, NU6, Tenyiphe1, Tenyiphe2, Medziphe1, Medziphe2, Medziphe3, ICPL96058, ICPL85010, ICPL96053, ICPL88039, ICPL332, ICPL84031, ICPL99004, ICPL98015, ICPL88034, ICPL98010, ICPL13092, ICPL161, ICPL366, ICPL8863, ICPL84023, ICPL87051, ICPL85063, ICPL89056, ICPL87, UPAS120, C. cajanifolius and PA134 were grown in randomized block design replicated thrice in plot size of 1.8 X 3 m consisted of three rows with a planting distance of 15cm and row to row distance of 60cm. All the recommended agronomical practices were followed for raising a good crop. Observations were recorded on 5 sampled plants selected randomly in each replication for different quantitative characters viz., days to 50% flowering, days to maturity, number of primary branches, plant height at maturity, number of pods per plant, number of cluster per

plant, pod length, number of seeds per pod, 100 seed weight, number of pods per cluster and seed yield per plant.

The genetic divergence among genotypes was computed by means of Mahalanobis D^2 technique (Rao, 1952) and genotypes were grouped into different clusters following Tocher's method of cluster formation. The relative contribution of characters towards divergence was estimated according to Sharma (Sharma, 1998).

III. RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters indicating high genetic variability present in the population. Based on the relative magnitude of D^2 values, 30 genotypes were grouped into seven clusters (Table 1). Cluster I had maximum number of 13 genotypes followed by cluster III with 8 genotypes, while cluster V, VI and VII had minimum of 1 genotype each. The pattern of distribution of genotypes in different clusters indicated that genetic diversity was not related to ecosystem differentiation. This was in agreement with the findings of Jag (1989). Many genotypes of close geographic proximity fell in different cluster and vice-versa. Clustering of genotypes from different eco-geographic locations into one cluster could be attributed to the possibility of free exchange of breeding materials.

The estimates of intra and inter cluster distances has been presented in table 2. The intra-cluster distance ranged from 0.00 (cluster V, VI and VII) to 17 (cluster IV). The inter cluster distance was observed to be highest between cluster IV and VII (53.74) followed by cluster I and VII (45.19) indicating diversity between these clusters. Hence the genotype of cluster VII could be utilized as diverse parent in hybridization program with the genotypes of cluster I and cluster IV respectively, to achieve greater variability in the segregation generations. Inter cluster distance was minimum between cluster I and cluster VI (23.02) indicating genotypes belonging to these clusters are relatively closer. Such analysis was meant to avoid selection of parents from genetically closer clusters which may in turn result narrow genetic base and inbreeding depression.

Comparison of cluster means (Table 3) revealed that cluster II and cluster VII gave exceptionally high values of four characters each namely number of primary branches per plant, number of pods per plant, number of cluster per plant and seed yield per plant for cluster II and Days to 50% flowering, days to maturity, plant height at maturity and number of seeds per pod for cluster VII, cluster mean for pod length was highest for cluster V, number of pods per cluster for cluster III and 100-seed weight for cluster

VI. The coefficient of variation for different characters indicated that number of pods per plant, number of cluster per plant and seed yield per plant contributed maximum towards divergence. Similar results were reported by Firoz *et al.* (2006), Samal *et al.* (2001), Viramgama and Goyal (1994), Sarma & Roy (1994) for number of pods per plant & seed yield per plant and Singh *et al.* (2010) for seed yield per plant.

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Table 1: Clustering Pattern of 30 Genotypes of Pigeon Pea on the Basis of Genetic Divergence

| Cluster No. | No. of genotypes | Genotypes included |
|-------------|------------------|--|
| I | 13 | ICPL 13092, ICPL 87, ICPL 96053, ICPL 85063, ICPL 89056, ICPL 96058, Medziphema 3, Tenyiphe 1, Tenyiphe 2, ICPL 87051, Tenyiphe 1, ICPL 161, Medziphe 1. |
| II | 2 | UPAS 120, PA 134. |
| III | 8 | NU 5, ICPL 8863, ICPL 366, NU 4, ICPL 88034, ICPL 84031, ICPL 99004, ICPL 98015. |
| IV | 4 | ICPL 88039, ICPL 9810, ICPL 84023, Bahar. |
| V | 1 | ICPL 85010. |
| VI | 1 | ICPL 332. |
| VII | 1 | NU 6. |

Table 2: Average Intra and Inter Cluster Distance

| Cluster No. | I | II | III | IV | V | VI | VII |
|-------------|--------------|-------------|--------------|--------------|-------------|-------------|-------------|
| I | 14.08 | 66.72 | 27.56 | 23.02 | 35.48 | 23.02 | 45.19 |
| II | | 5.97 | 45.12 | 69.19 | 51.21 | 62.23 | 34.09 |
| III | | | 16.88 | 32.13 | 25.99 | 25.97 | 28.41 |
| IV | | | | 17.00 | 29.47 | 28.42 | 53.74 |
| V | | | | | 0.00 | 24.62 | 44.17 |
| VI | | | | | | 0.00 | 42.03 |
| VII | | | | | | | 0.00 |

Table 3: Cluster Wise Mean Value o 11 Characters Of In Pigeon Pea

| Cluster No. | No. of cluster | Days to 50% Flowering | Days to maturity | No. of primary branches /plant | Plant height at maturity (cm) | No. of pods/ plant | No. of cluster/ plant | Pod length (cm) | No. of seeds/pod | 100 seed weight (gm) | No. of pods/ cluster | Seed yield/plant (gm) |
|-------------|----------------|-----------------------|------------------|--------------------------------|-------------------------------|--------------------|-----------------------|-----------------|------------------|----------------------|----------------------|-----------------------|
| I | 13 | 160.17 | 202.0 | 17.33 | 194.82 | 116.0 | 29.65 | 4.91 | 4.10 | 9.87 | 3.83 | 33.48 |
| II | 2 | 118.00 | 166.58 | 25.40 | 260.23 | 508.13 | 101.10 | 4.53 | 3.93 | 8.90 | 5.02 | 148.22 |
| III | 8 | 138.66 | 192.78 | 16.80 | 217.14 | 204.32 | 39.72 | 5.63 | 4.23 | 11.20 | 5.19 | 76.25 |
| IV | 4 | 100.05 | 149.17 | 14.17 | 178.53 | 54.73 | 19.97 | 5 | 3.82 | 10.18 | 2.99 | 17.54 |
| V | 1 | 86.00 | 130.60 | 18.53 | 129.47 | 115.27 | 28.20 | 6.40 | 4.47 | 16.20 | 4.09 | 67.16 |
| VI | 1 | 159.40 | 202.73 | 10.73 | 132.87 | 78.13 | 18.60 | 6.33 | 4.47 | 19.47 | 4.20 | 60.99 |
| VII | 1 | 175.33 | 208.13 | 18.67 | 277.07 | 197.80 | 43.07 | 6.07 | 5.27 | 15.60 | 4.60 | 126.55 |
| CV | | 25.07 | 16.95 | 25.96 | 28.93 | 84.77 | 70.98 | 13.47 | 11.18 | 30.72 | 17.57 | 62.15 |