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Genetic divergence studies in early maturing pigeon pea (*Cajanus cajan* (L.) Millsp.) genotypes

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Abstract
Genetic diversity of the twenty-one genotypes of pigeon pea was accessed for fourteen characters in a randomized block design (RBD) with three replications at ICR farm, Assam Agricultural University during Kharif 2017-18. Among the twenty-one genotypes in the sample, two were from BNCA, AAU (Biswanath Chariali College of Agriculture, Assam Agricultural University, Jorhat), while the other nineteen were from ICRISAT, Hyderabad. The analysis of divergence was carried out by the D^2 statistic of Mahalanobis (1936) and Tocher's method followed for cluster formation as described by Rao (1952). Twenty-one genotypes were grouped into 4 clusters. The highest number of genotypes were found in Cluster I (13) followed by Cluster II (6) and Cluster III (1) and Cluster IV (1). The average intra-cluster distance was maximum in Cluster II (45.02) followed by Cluster I (36.96). The maximum inter-cluster distance was found between Cluster I and Cluster IV (151.74) followed by Cluster II and IV (75.19). The highest intra-cluster distance was observed for cluster II. Hence, genotypes belonging to this cluster viz. Local 1, ICP 14930, ICP 11613, ICP 11639, ICP 10920, and ICP 15312 may be utilized as parents in future breeding programmes.

Keywords: Pigeon pea, genetic diversity, early maturity, D^2 statistics

Introduction
The pigeon pea (*Cajanus cajan* L. Millsp.) is an important pulse crop grown in tropical and subtropical regions (Sarkar *et al*., 2020) [4]. India is the largest producer of pigeon pea contributing 75-80 percent of world production. It is grown on a 4.43 MHA area in India, with a total production of 4.25 MT and a 960 kg/ ha productivity. In Assam, the area is 6 thousand ha, with a production of 4.9 thousand tonnes and productivity of 833 kg/ha (Agricultural Statistics, 2018).

Pigeon pea, also known as 'arhar, tur, or red gram', is a food crop (dried peas, flour, or green vegetable peas) and a forage or cover crop. It has the ability to fix atmospheric nitrogen. It offers multiple benefits-protein rich seeds (21- 25% protein), fuel, fodder, and erosion control. It is cultivated mainly as a Kharif crop, sole crop, and mixed crop. In Assam intercropping is done with green gram/black gram and sesame. Traditional varieties of pigeon pea are long-duration types taking more than ten months to mature and cannot be fitted into multiple crop systems (Borah *et al*,2020) [5]. Winter crops cannot be grown in Assam since the majority of the varieties grown are of long duration which gives poor yields when sown late. Development of early maturing varieties is inevitable for which identification of suitable parents is necessary. The selection of parents for varietal improvement programs depends on the knowledge of available diversity. Early-duration pigeon pea is photo-insensitive with compact plant stature suitable for intercropping (Ranjani *et al*. 2021) [6]. The lack of diversity and photosensitivity is causing stagnant productivity of pigeon pea leading to a gap between demand and supply over the years (Sameerkumar *et al*., 2016) [8].

Classification and identification of diverse heterotic groups in germplasm with possible breeding values in the manifestation of the breeding potential of genotypes can be possible through the assessment of genetic diversity. Genetic diversity can provide ample scope for the identification of genetic parents for various heterosis breeding programmes and progenies derived from diverse crosses are expected to show a broad spectrum of variability, helping for isolating transgressive segregates in advanced generations. (Mahalanobis, 1936) [2] D^2 analysis is useful to measure genetic diversity among different genotypes. It is the most popularly used method for assessing genetic diversity in various crops (Shridevi *et al*. 2019) [7].

Pigeon peas must be bred into high-yielding, early maturing, and reasonably statured varieties that are consistent with the agro-climatic conditions of Assam to become a more lucrative crop. Hence in the present study, an effort has been made to identify diverse parents for a future breeding programme.

Materials and Method

The research experiment was conducted at ICR Farm, Assam Agricultural University, Jorhat, during Kharif 2017–18. Twenty-one genotypes constituted the material for the current research, of which two genotypes were obtained from BNCA, AAU, and nineteen genotypes were received from ICRISAT, Hyderabad. Three replications of the experiment were undertaken using the Randomized Block Design (RBD) method. The plot measured 16 m 11 m with a 60 cm x 15 cm spacing. Fourteen quantitative characters were considered for this experiment. To make thorough observations, five plants from each genotype from each of the three replications were randomly chosen. The analysis of divergence was carried out by the D^2 statistic of (Mahalanobis, 1936) [2] and Tocher's method followed for cluster formation as described by (Rao, 1952) [3]. The criterion for clustering is that the genotypes belonging to a single cluster have smaller D2 values and those belonging to different clusters have larger D^2 values. All statistical analysis was carried out with help of INDOSTAT Statistical software.

Results and Discussion

The most appropriate method to estimate the diversity within any crop species is the D^2 statistics (Priyanka *et al.*, 2021) [11]. 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, 21 genotypes were grouped into four clusters (Table 1). Cluster I was the largest comprising 13 genotypes followed by Cluster II (6 genotypes) whereas clusters III and IV were mono-genotypic with a single genotype. Cluster III (ICP 14927) and IV (ICP 11610) with mono-genotype. Mono-genotypic clusters revealed that they were more diverse genotypes from the rest of the genotypes, thus these two genotypes have entirely different genetic make-up.

Table 1: Cluster distribution of 21 pigeon pea genotypes based on D^2 statistics

Clusters	Genotypes	Name of genotypes
Cluster I	13	ICP 14665, ICP 7645, ICP 8025, ICP 7632, ICP 11612, ICP 11495, ICP 11595, ICP 11599, ICP 12931, ICP 14664, ICP 15011, ICP 6973, Bahar
Cluster II	6	Local 1, ICP 14930, ICP 11613, ICP 11639, ICP 10920, ICP 15312
Cluster III	1	ICP 14927
Cluster IV	1	ICP 11610

The maximum intra-cluster distance was observed in Cluster II (45.02) followed by Cluster I (36.96). The minimum intra-cluster distance was found in mono-genotypic clusters III and IV (0.00). The inter-cluster distance was found maximum between clusters I and IV (151.74) followed by Cluster II and IV (75.19), while the minimum distance was exhibited by clusters II and III (48.01) (Table 2). The higher inter-cluster distance indicates the genotypes of those clusters were distantly related, whereas the lowest inter-cluster distance indicates the likeliness among the genotypes of the different clusters (Ranjani *et al.* 2021) [6]. (Reddy *et al*, 2015) [9], (Shridevi *et al.* 2019) [7], (Kandarkar *et al*, 2020) [10], and (Ranjani *et al.* 2021) [6] all found high inter-cluster and intra-cluster distances for genotypes of pigeon pea. Hybridization based on the selection of genotypes having diverse intra-cluster and inter-cluster distances can provide useful combinations which can be utilized in the improvement of pigeon pea varieties.

Table 2: Average Intra (diagonal) and inter-cluster distance

Cluster	I	II	III	IV
I	36.96	54.62	68.41	151.74
II		45.02	48.01	75.19
III			0.00	72.76
IV				0.00

The cluster mean values of twelve characters (Table 3) revealed that Cluster III was found to be better for early flowering (79.40), early maturity (89.47), and short plant height (81.40). Therefore, genotypes belonging to Cluster III can be utilized in the breeding of early maturing pigeon pea genotypes. Cluster IV showed good characters for the maximum number of pods per plant (13.00), high yield (5.67), and Harvest index (84.10). More number of seeds per pod was found in cluster II (3.32). Similarly, long pods (4.12) and bold seeds (4.15). were observed in cluster I while Cluster II (5.24) had the lowest yield. The clusters with a high average mean values for yield and yield-contributing traits can be utilized in crop improvement to obtain high productivity.

Table 3: Mean performance of genotypes in the individual cluster for fourteen traits

Cluster	PH	BPP	CPP	DTF	DTHF	DTFF	DTIPS	DTM	PPP	PL	SPP	SW	HI	SYP
I	94.29	2.18	2.61	104.99	116.16	126.13	114.90	119.36	6.29	4.12	2.87	15.26	38.98	5.64
II	90.51	2.61	3.01	100.20	110.38	118.58	106.95	111.97	7.73	4.15	3.32	15.44	54.91	5.24
III	81.40	1.67	4.00	79.40	89.73	98.53	84.80	89.47	12.47	3.63	2.67	13.03	44.87	5.33
IV	89.73	3.00	4.77	93.93	106.00	113.40	100.53	104.73	13.00	3.57	3.13	13.67	84.10	5.67

Abbreviations: PH: Plant height, DTF: Days to first flowering, DTHF: Days to 50% flowering, DTFF: Days to 90% flowering, DTM: Days to maturity, BPP: Branches per plant, CPP: Clusters per plant, PPP: Pods per plant, PL: Pod length, SPP: Seeds per pod, SW: 100 Seed weight, HI: Harvest index, SYP: Seed yield per plant

Further, the efficacy of D^2 -statistics is improved by its applicability to estimate the relative contribution of the various characters towards genetic divergence. The inter-cluster and intra-cluster variances along with ratio R^2 (inter-cluster variance to the total variance) were estimated for all the fourteen characters and represented in Table 4. The maximum extent of R2 value was found for the character's harvest index (34.29), seed yield per plant (19.05), pod length (11.43), 100 seed weight (8.57), and days to first flowering (4.76). (Ranjani *et al*. 2021) [6] reported days to 50 percent flowering (21.12%) contributed more to genetic diversity followed by 100 seed weight (13.92%), pod length (13.92%), plant height (13.21%) and single plant yield (13.13%). (Shridevi *et al*. 2019) [7] also concluded that based on the R^2 value, the characters, viz., days to maturity, the number of pods per plant, and the number of pod clusters per plant contributed much to the total genetic divergence.

Table 4: Character contribution

Character	Contribution (%)
PH	4.29
BPP	4.29
CPP	1.43
DTF	4.76
DTHF	2.86
DTFF	2.38
DTIPS	0.95
DTM	1.9
PPP	1.9
PL	11.43
SPP	1.9
SW	8.57
HI	34.29
SYP	19.05

Abbreviations: PH: Plant height, DTF: Days to first flowering, DTHF: Days to 50% flowering, DTFF: Days to 90% flowering, DTM: Days to maturity, BPP: Branches per plant, CPP: Clusters per plant, PPP: Pods per plant, PL: Pod length, SPP: Seeds per pod, SW: 100 Seed weight, HI: Harvest index, SYP: Seed yield per plant.

Conclusion

The classification of 21 pigeon pea genotypes into four different clusters based on D^2 statistics helps in the selection of desirable parents for different breeding aspects. The pattern of distribution of pigeon pea genotypes in various clusters revealed the existence of considerable diversity present in the material. The highest intra-cluster distance was observed for cluster II. Hence, genotypes belonging to this cluster viz. Local 1, ICP 14930, ICP 11613, ICP 11639, ICP 10920, and ICP 15312 may be utilized as parents in future breeding programmes.

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