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Research Article

Genetic variability in pigeonpea (*Cajanus cajan* L. Millspaugh)

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Abstract:
One hundred germplasm lines were evaluated for variation in morphological and agronomic traits for selection of cultivar potentially suitable for growing in Bangladesh under rice-based cropping systems during the fallow period after *kharif* II season. A wide range of variation was found in twelve quantitative plant traits. The most important correlations corresponded to eight plant traits. Considering these traits, PCA could explain 76.2% of total variance. Based on cluster analysis, the genotypes were grouped into seven clusters, each cluster with greater similarities. Plant height, days to flowering and pods plant^{-1} were the discriminating variables mostly contributed in grouping the genotypes. Pods plant^{-1} played the most dominant role in explaining the maximum variance according to DFA. Genotypes grouped in 1, 4 and 7 clusters were early maturing and high yielder as compared to the other cluster members. Genotype 21 (ICP7143) representing group 1 showed promising for its short stature nature. However, genotype 32 (ICP7989) representing group 4 produced the highest yield with the shortest maturity duration. These two genotypes are particularly promising for growing in fallow period after the harvest of transplanted *aman* or *kharif* II crops.

Key words: Pigeonpea, genotypes, variation, growth, yield

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the major grain legumes grown in the tropics and subtropics. In Bangladesh, some short duration lines of pigeonpea were tested in the northern part of the country, but found promising only as intercrop (BARI, 1990). In the southern part of Bangladesh, where winter temperature remains warm enough to support the crop growth, less photosensitive and short duration pigeonpea can be introduced in transplanted aman-fallow cropping system. In the hilly areas of south-eastern part of Bangladesh also, the crop may potentially be grown during the post-rainy season. Roy *et al*. (1996) evaluated 23 genotypes of variable maturity duration to explore the potentiality of fitting pigeonpea in rice-fallow cropping pattern and found some genotypes well adapted in fallow period although the yields were not satisfactory. Therefore, the potential pigeonpea variety or cultivar selected for growing under such conditions should be of short duration with high yield potential. The present experiment was conducted to evaluate 100 genotypes of diverse growth habits obtained from the International Crops Research Institute for the Semi Arid Tropics (ICRISAT) to identify dwarf and extra-short duration genotypes.

The experiment was conducted in the Field Research Farm of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur located at $24^0 5^/$ N latitude and $90^0 16^/$ E longitude. Nearly 26% of the average annual rainfall (2270 mm) was received from the north-west monsoon during the study period and minimum and maximum temperatures recorded during period of plant growth were 18.1^0C and 34.3^0C respectively. Pigeonpea germplasm lines for the present investigation were collected from the International Crops Research Institute for the Semi - Arid Tropics (ICRISAT). A total of 100 genotypes of diverse provenance were selected from the germplasm lines collected from the ICRISAT and planted on 31st October 2002. The plot size was 2.5m×1.5m and twenty five plants of each genotype were grown in rows at 50 cm x 10 cm configuration. Appropriate cultural practices were followed to raise a healthy crop. Data were recorded on twelve traits viz. seedling emergence per cent, speed of germination, seedling vigour, seedling morphology, plant height, days to first flowering, days to 50% flowering, days to maturity, pod length, no. of pods per plant, no. of seeds per pod and seed yield per plant. Seedling emergence percentage was calculated on 12 days after seeding (DAS) as the ratio between total number of seeds sown to number of normal seedlings emerged. Speed of germination and seedling vigor were calculated according to Copeland (1988). Five plants of each genotype in the row were selected randomly to record plant height, yield attributes and seed yield. Correlation was estimated among the plant characters according to Pearson's co-efficient (Clifford and Stephenson, 1975) and derivation of variables using principal component analysis (PCA) was based on correlation matrix (Hair *et al*., 1992). Non-hierarchical K-means cluster was performed to classify the genotypes into a number of groups and discriminant function analysis (DFA) was employed for conforming the grouping of genotypes.

The range and mean of variation in twelve quantitative characters of the 100 genotypes is presented in Table 1. The correlation coefficient among the traits showed that out of 66 coefficients, 27 were highly significant at $P_{0.01}$, 2 were significant at $P_{0.05}$ and others were insignificant (Table 2). However, coefficients higher than 0.50 were considered as linear associations representing natural variation patterns according to Reddy (1990). In respect of seedling quality, the highest and strong positive correlation corresponded to seedling vigor and seedling emergence (r=0.90). The seedling vigor also presented strong and significant positive correlation with the speed of germination. The phenological characters were highly associated with each other and plant height showed strong positive correlations with these characters. Similar significant relationships were also observed in pigeonpea by Singh *et al*. (1995) and Bolevian *quinu* by Rojas *et al*. (2000). All the phenological characters showed negative and significant correlations with yield attributes and seed yield. This indicates that the values of yield attributes and seed yield tend to become smaller as the phenological phases became longer. The strong positive correlation between days to maturity and plant height (r=0.53) indicates that plants tended to become taller as the phenological cycle became longer. However, the negative significant correlation between plant height and other yield attributes indicates in turn that the seed yield lower in taller plants, although earlier it was reported that plant height had positive association with pods plant^{-1} (Kumar and Reddy, 1982, Patil *et al*., 1988). Among yield and yield attributes, the highest strong and positive correlation was observed between seed yield and pods plant^{-1} (r=0.85). Seed yield was also positively correlated with pod length (r=0.56). The results are in agreement with Reddy (1990) where he indicated a strong and positive correlation of seed yield with pods plant^{-1}, but weak to moderate positive correlation with pod length. Such positive correlations were also observed by many authors in their study (Balyan and Sudhakar, 1985, Dahiya *et al*., 1978, Singh *et al*., 1972). However, seeds pod^{-1} had no significant relationship with pods plant^{-1} which suggests that seed yield of pigeonpea was the product of pods plant^{-1} and pod length. Pandey and Singh (1998) also reported that pods plant^{-1} was the prime contributing character to seed yield in pigeonpea . The strong positive genotypic correlations for the above traits indicated that plant performance can be attributed mostly to genetic differences rather than environmental influences.

Principal component analysis (PCA) clearly and concisely explained the genetic variability among pigeonpea genotypes. Based on the correlation matrix (Table 2), the highly related eight plant characters i.e. seedling vigor, plant height, days to first flowering, days to 50% flowering, days to maturity, pods plant^{-1}, pod length and seed yield were analyzed for the principal components (PCs). The PCA revealed that the first four PCs had Eigen values of more than 1 and explained 28.66%, 18.36%, 15.87% and 13.31% of total variation individually and 76.20% in combination (Table 3). The plant traits that separated genotypes along the PC1 were morphological and phenological characters. The high and positive contributions of PC2 were pods plant^{-1} and seed yield and the plant traits that separated genotypes to PC2 axis were yield attribute and seed yield. The PC3 was associated mainly with seedling vigor and that of PC4 with pod length. Genotypic variation and pattern of diversity of many crop plants were evaluated through PCA by many authors (Meijer *et al*., 1996, Bisht *et at*., 1999).

The genotypes were grouped into seven clusters using k-means non-hierarchical clustering (Table 4). Each cluster contained highly similar pigeonpea genotypes. Cluster 7 contained maximum number of genotype (29) followed by cluster 2 (21), 4(20), 5(17), 3(6), 6(4), 1(3). Number of genotypes for each cluster and mean of each cluster for the 8 plant characters are presented in Table 4. The genotypes in cluster 1 were characterized with the lowest plant height, early initiation of flowering and maturity and were of moderate seedling index, pods plant^{-1}, pod length and seed yield. Cluster 2 was mainly characterized by the genotypes with the lowest seedling vigor, moderately late flowering and maturity with moderate plant height, pods plant^{-1}, pod length and seed yield. The genotypes in cluster 3 were characterized with the highest pod length; moderate maturity duration, plant height and seed yield. Cluster 4 genotypes were mainly characterized by the highest seedling vigor, pods plant^{-1} and seed yield. The genotypes were comparatively early in flowering and maturity next to cluster 1 genotypes, and had medium height and pod length. The genotypes in cluster 5 were mainly characterized by very low seed yield, lowest no. of pods plant^{-1}, minimal seedling vigor and shorter pod length. The period of flowering and maturity was similar to that of cluster 2. Genotypes in cluster 6 were tall, late in flowering and took the maximum days to mature. However, the genotypes had smallest pod length and lowest seed yield. The genotypes in cluster 7 were characterized by the high seedling vigor, short plant height and yield and yield attributes almost similar to that of cluster 1. The genotypes showed moderately high yield and, pods plant^{-1}. The duration of flowering and maturity was similar to that of cluster 3. The clustering pattern of selected genotypes revealed that genotypes of cluster 1, 4 and 7 were of short stature and early in flowering and maturity and yielded better as compared to the other clusters. Genotypes of cluster 5 and 6 were tall in height, had small pods and gave very poor yield Cluster 6 made separate group of genotypes which were late in flowering and maturity.

Discriminant function analysis (DFA) complemented the study, resulting in four statistically significant functions (Table 5), which separated the different groups. Moreover, it provides a graphical output illustrating the existence of groups (Singh *et al*., 1991). About 98% of the genotypes were readily classified into the seven groups identified by cluster analysis (data were not given). Table 5 summarizes the variables mostly contributed to the discriminatory functions along with their coefficient under each function. Results show that plant height, days to first flowering, days to 50% flowering and pods plant^{-1} mostly contributed in grouping of 100 genotypes. These 4 characters mostly explained 95.7% of total variance under function 1 and function 2. The coefficient of plant height (0.466) was higher in function 1 than function 2. This indicated that plant height mostly explained 72.6% of total variance observed in function 1. On the other hand, the coefficient of pods plant^{-1} (0.730) was higher in function 2 indicating that contribution of this variable to function 2 was higher in explaining 23.1% of total variance. Almost similar coefficient values of days to first flowering and days to 50% flowering in functions 1 and 2 indicates that these two variables were equally important in explaining the total variance.

Figure 1 showed the orientation of genotypes under each of seven clusters. The relative position of genotypes indicated the cumulative response of variables representing functions 1 and 2. Group centeroid of each cluster represented the optimum values of functions 1 and 2 that was resulted from the cumulative effects of all genotypes oriented under that cluster based on their response to the discriminatory variables. Therefore, the values of group centeroid represented the optimum response of that group. The deviation of the genotypes in response of discriminating variables was very close to the group centeroid and might be considered as the representative (might not the best) of that group. Accordingly, the genotype 21 (ICP 7143) in group 1, the genotype 97 (ICP 15231) in group 2, the genotype 82 (ICP 14102) in group 3, the genotype 32 (ICP 7989) in group 4, the genotype 63 (ICP 12841) in group 5, the genotype 49 (ICP 10968) in group 6 and the genotype 64 (ICP 12989) in group 7 might be considered as representative of their respective groups.

The results clearly demonstrated that a wide range of genotypic variation existed in seedling quality, phenology and seed yield. The genotypes under group 4 showed high yield potential and comparatively early maturing and genotypes of group 1 also performed better. The genotypes under these groups are particularly promising for the adaptation in transplanted *aman* cropping pattern. Further studies on morpho-physiological response of selected genotypes will help in better understanding of the genotypes for the identification and development of short duration pigeonpea. It is suggested that research directed towards molecular approach for selecting traits of interest should be carried out.

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Table 1. Range and mean of the characters of pigeonpea lines

Plant characters	Range	**Mean***	**Skewness**
Seedling quality			
Seedling emergence (%)	8-96	58.56±15.55	-0.34
Speed of germination	10.74-12.24	11.71±0.27	-0.74
Vigor index	2.32-18.07	10.73±3.22	0.07
Plant height (cm)	31.6-102.8	66.19±14.70	0.31
Phenological			
Days to first flowering	83-136	110±8.30	0.09
Days to 50% flowering	92-154	119±10.16	0.80
Days to maturity	137-172	155±4.87	0.22
Yield attributes and seed yield			
Pod length (cm)	3.36-9.52	6.90±1.61	-0.42
Pods plant^{-1}	3.80-81.40	40.66±20.38	-0.15
Seeds pod^{-1} (no.)	1.00-3.68	2.37±0.51	-0.02
Seed yield (g plant^{-1})	0.12-12.56	5.89±3.36	-0.06

***** Mean ± standard deviation

Table 2. Correlation coefficient of characters of pigeonpea lines

	Emer.	Speed	Vigor	Pht	Flow1	Flow2	Mat	PPP	Pl	Spp	Yi
Emer	1										
Speed	0.18	1									
Vigor	0.90**	0.54**	1								
Pht	-0.01	-0.06	-0.04	1							
Flow1	-0.09	-0.25*	-0.16	0.65**	1						
Flow2	-0.10	-0.21*	-0.16	0.74**	0.90**	1					
Mat	0.04	-0.15	-0.03	0.53**	0.59**	0.64**	1				
PPP	0.11	0.14	0.15	-0.44**	-0.40**	-0.44**	-0.27**	1			
Pl	0.05	-0.02	0.03	-0.52*	-0.43**	-0.57**	-0.37**	0.33**	1		
Spp	-0.09	-0.10	-0.09	0.09	0.06	0.02	0.12	0.03	0.10		
Yi	0.14	0.14	0.18	-0.58**	-0.51**	-0.59**	-0.35**	0.85**	0.56**	0.02	1

** Correlation is significant at the 0.01 level (2-tailed), * Correlation is significant at the 0.05 level (2 tailed).

Emer-Seedling emergence (%), Speed-speed of germination, Vigor-Vigor index, Pht-Plant height (cm), Flow1-Days to first flowering, Flow2-Days to 50% flowering, Mat-Days to maturity, Ppp-Pods plant^{-1}, Pl-pod length (cm), Yi-Seed yield plant^{-1}(g).

Table 3. Extracted Eigen values and latent vectors associated with the first four principal components

	Principal components			
	1st	2nd	3rd	4th
Extracted Eigen values	2.29	1.47	1.27	1.07
Percentage variance	28.7	18.4	15.9	13.3
	Eigenvectors			
Vigor index	-	-	0.75	-
Plant height (cm)	0.52	-	-	-
Days to first flowering	0.75	0.54	-	-
Days to 50% flowering	0.89	-	-	-
Days to maturity	0.63	-	-	-
Pods plant^{-1}	-	0.64	-	-
Pod length (cm)	-	-	-	0.95
Seed yield (g plant^{-1})	-	0.63	0.57	-

Table 4. Comparison profile of the seven groups of pigeonpea genotypes classified by K-means clustering

Characters	***Cluster***						
	1	2	3	4	5	6	7
No. of genotypes	*3*	*21*	*6*	*20*	*17*	*4*	*29*
Vigor index	10.7	9.6	10.0	11.7	10.0	10.2	11.5
Plant height (cm)	39.0	76.5	56.6	61.5	82.2	88.9	54.2
Days to first flowering	85.3	115.7	108.0	106.0	114.3	126.8	105.7
Days to 50% flowering	98.0	127.2	114.3	113.9	124.9	145.5	112.1
Days to maturity	146.0	157.4	154.0	152.8	156.0	163.8	153.2
Pods plant^{-1}	42.8	41.6	17.3	68.0	12.8	12.9	45.9
Pod length (cm)	7.0	6.2	8.1	7.4	5.9	4.1	7.8
Seed yield (g plant^{-1})	6.6	5.1	4.1	9.7	1.5	0.9	7.4

Table 5. Standardized canonical discriminant function coefficients of variables mostly contributed in grouping of pigeonpea genotypes

Discriminating variables	*Discriminant Functions*			
	1	2	3	4
% variance	*72.6*	*23.1*	*2.3*	*1.9*
Plant height (cm)	0.466	0.411	0.197	0.769
Days to first flowering	0.127	0.158	1.345	-0.315
Days to 50% flowering	0.409	0.441	-1.198	-0.404
Pods plant^{-1}	-0.684	0.730	-0.007	0.031

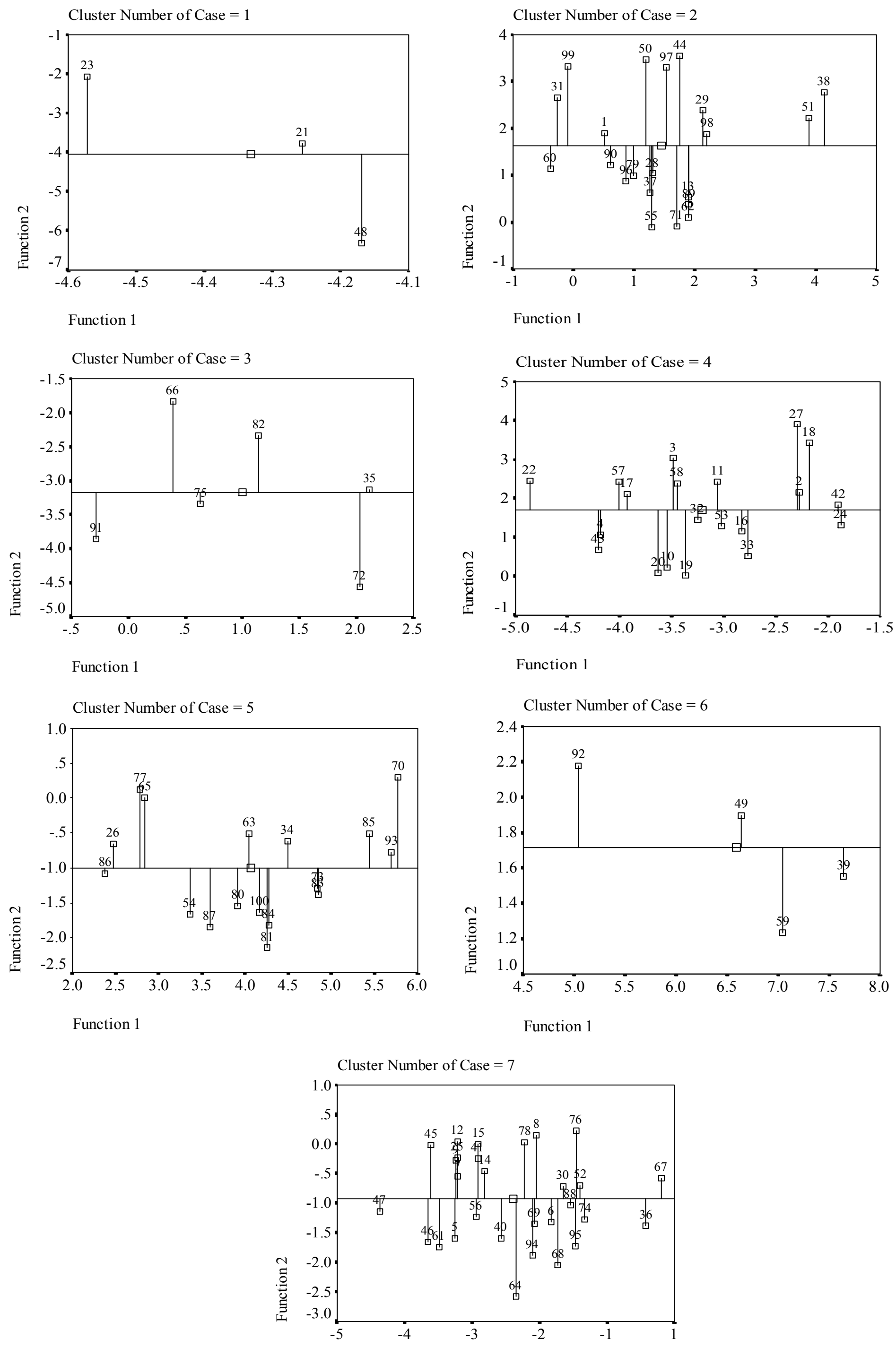

Fig. 1. Graphical illustration of genotypes under each cluster by DFA based on 8 plant characters