HIERARCHICAL CLUSTERING AND PATH ANALYSIS IN COWPEA (*VIGNA UNGUICULATA* L. WALP.)

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ABSTRACT

Genetic variability, character association and path coefficient are pre-requisite for selection of trait specific superior genotypes in improvement of any crop and multivariate analysis helps in choosing the parents for hybridization. Studies on 43 diverse genotypes of cowpea indicated the existence of fairly high degree of variability for plant height, number of branches, peduncles and pods per plant, pod weight and pod yield per plant. Higher estimates of heritability coupled with the higher genetic advance for plant height, number of peduncles per plant, number of pods per plant and pod yield per plant indicated that heritability of these traits is mainly due to additive effects and selection may be effective. Correlation analysis pointed out the importance of number of branches, peduncles and pods per plant, pod length, pod weight and number of seeds per pod towards pod yield. Number of pods per plant exerted the maximum positive direct effect on pod yield followed by pod weight and number of branches and peduncles per plant. Selection pressure on these traits may lead to an overall increase in pod yield per plant. Forty three genotypes were mainly divided into 2 clusters with 38 and 5 genotypes at first node. The inter-cluster representatives of distant clusters would be more useful for choosing the parents in cowpea breeding programme.

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp.) as a crop has many uses like fodder, cover, green manure, which provide cheap and high quality protein in the form of vegetable and pulse to human diet. Cowpea provides 4-5% protein in immature pods and 25-305 in mature seeds (Bressani and Elias, 1980). Cowpea can fix 150 kg of nitrogen/ha (Summerfield *et al.*, 1977). The progress in breeding for the yield and its contributing characters of any crop is polygenetically controlled, environmentally influenced and determined by the magnitude and nature of their genetic variability (Wright, 1935; Fisher, 1981). Genetic variability, character association and path coefficient are pre-requisite for improvement of any crop for the selection of superior genotypes and improvement of any traits. It is very difficult to judge whether observed variability is heritable or due to environment alone. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character in future generations. Knowledge of correlation between yield and its contributing characters are basic and for most endeavor to find out guide lines for plant selection. Partitioning of total correlation into direct and indirect effect by path coefficient analysis helps in making the selection more effective. The value of multivariate analysis has been demonstrated very well for choosing the parents for hybridization (Peter and

Martinalli, 1989; Hazra *et al*., 1992). The approach is based on the assumption that the best parents may be those showing the maximum genetic divergence (Hazra, 1991; Narayanan Kutty *et al.*, 2003). Thus an attempt has been made to identify genotypes of cowpea belonging to different culti-groups through multivariate analysis which can profitably be utilized in a hybridization programme for the improvement of pod yield characters.

MATERIALS AND METHODS

The present investigation was carried out during *kharif* season, 2008 at the Research Farm of Indian Institute of Vegetable Research, Varanasi (82^{0}52$^'$ E longitude and 25^{0}10$^'$ N latitude). The experiment was laid out in randomized block design with three replications. Seeds of 43 diverse genotypes of cowpea were sown on 3.0 m ridges made at 45 cm spacing by maintaining 15 cm seed to seed distance in RBD with three replications. Each genotype was sown on one ridge in each replication. Recommended fertilizer dose and cultural practices including need-based plant protection measures were followed to raise a good crop. Observations from five randomly selected plants were recorded on nine quantitative traits viz. plant height, number of branches and peduncles per plant, days to 50% flower, number of pods per plant, pod length, pod weight, number of seeds per pod and pod yield per plant. Genotypic coefficients of variance (GCV), phenotypic coefficients of variance (PCV), heritability (broad

sense) and genetic advance was worked out as per Johnson *et al.* (1955). Correlation coefficient and path analysis was worked out as per the method suggested by Dewey and Lu (1959). Data on the characters computed and agglomerative hierarchical clustering was done using SPSS version 10.1 software employing Ward's method. The clustering was based on squared Euclidean distances and average linkage between groups was taken as average of the distance between all pairs of cases with one member of each group.

RESULTS AND DISCUSSION
Variability analysis

The variance analysis showed that genotypes differ significantly among themselves for all the characters under study (Table 1). The phenotypic coefficients of variation (PCV) were invariably higher than their corresponding genotypic coefficients of variation (GCV) due to environmental influence. The estimates of PCV and GCV indicated the existence of fairly high degree of genetic variability for plant height, number of peduncles and pods per plant, pod

weight and pod yield per plant. Plant height, number of peduncles and pods per plant, pod weight and pod yield per plant were least affected by environment. This observation draws support from the very high values of heritability recorded for these traits. Higher estimates of heritability coupled with the higher genetic advance for plant height, number of peduncles per plant, number of pods per plant and pod yield per plant indicated that heritability of these traits is mainly due to additive effects and selection may be effective. High heritability accompanied with low genetic advance for number of branches per plant, pod length, average pod weight and number of seeds per pod indicated the advancement of non-additive gene action and the high heritability is being exhibited due to favourable influence of the environment rather than genotypes. Johnson *et al.* (1955) also suggested that high GCV along with high heritability and genetic advance gave better picture for the selection of the genotypes. Similar results were also reported by Venkatesan *et al.* (2003) in cowpea.

Table 1: Variability, heritability and expected genetic advance for cowpea genotypes

Characters	Range	Grand mean	Variability		Heritability (%)	Genetic advance	Genetic advance as % of mean
			PCV	GCV			
Plant height (cm)	31.3 - 276.4	74.4	79.81	79.67	99.60	121.86	163.83
Branches plant[-1] (No.)	2.3 - 6.4	4.3	22.47	22.26	98.10	1.96	45.47
Days to 50% flower (DAS)	48.0 - 71.7	52.7	11.21	10.65	90.40	10.99	20.86
Peduncles plant[-1] (No.)	10.7 - 33.1	19.2	30.83	30.55	98.20	11.97	62.34
Pods plant[-1] (No.)	8.3 - 31.3	16.6	33.78	33.49	98.30	11.34	68.35
Pod length (cm)	10.7 - 25.3	15.4	20.06	19.61	95.60	6.10	39.51
Pod weight (g)	2.80 - 8.27	5.44	25.19	24.70	96.20	2.72	50.00
Seeds pod[-1] (No.)	6.7 - 18.0	12.6	21.62	21.17	95.60	5.38	42.70
Pod yield (g plant[-1])	39.23 - 200.99	102.73	43.98	43.45	97.60	90.84	88.34

PCV & GCV – Phenotypic coefficient of variation and genotypic coefficient of variation, respectively

Correlation analysis

Genotypic correlation coefficients were higher than corresponding phenotypic correlation coefficients, indicating the inherent association among the traits (Table 2). The highly significant genotypic correlation coefficient was observed for number of branches per plant, number of peduncles and pods per plant, pod weight and number of seeds per pod with pod yield per plant. The number of branches per plant had positive correlation with number of peduncles per plant, number of pods per plant, pod weight and pod yield. The number of peduncles per plant showed positive correlation with number of pods per plant, pod weight and pod yield. However, the number of pods per plant exerted positive correlation with pod weight, number of seeds per pod, and pod yield per plant. Pod length had

positive correlation with pod weight, number of seeds per and pod yield per plant. The pod weight had positive correlation with the number of seeds per pod and pod yield per plant. Similarly, the number of seeds per pod exerted positive correlation with pod yield per plant. Bapna *et al.* (1972) also obtained similar results.

Direct and indirect analysis

The number of pods per plant exerted the maximum positive direct effect on pod yield followed by pod weight, number of branches and peduncles per plant (Table 3). Thus, selection pressure on these traits may lead to an over all increase in pod yield per plant. Contrarily, the number of seeds per pod showed maximum negative direct effect on pod yield followed by pod length and plant height. High positive   indirect   effect   of   pod

Table 2: Correlation coefficients at phenotypic (r_p) and genotypic (r_g) levels

Characters	Plant height (cm)	Branches plant⁻¹ (No.)	Days to 50% flower (DAS)	Peduncles plant⁻¹ (No.)	Pods plant⁻¹ (No.)	Pod length (cm)	Pod weight (g)	Seeds pod⁻¹ (No.)	Pod yield (g plant⁻¹)
Plant height (cm)	(r_p)	0.166	0.727**	0.117	0.208	0.622**	0.473**	0.411**	0.264*
	(r_g)	0.168	0.763**	0.117	0.209	0.630**	0.476**	0.414**	0.263*
Branches plant⁻¹ (No.)		(r_p)	-0.060	0.868**	0.828**	0.192	0.549**	0.132	0.817**
		(r_g)	-0.058	0.881**	0.839**	0.189	0.560**	0.129	0.830**
Days to 50% flower (DAS)			(r_p)	-0.053	-0.009	0.488**	0.259*	0.406**	0.046
			(r_g)	-0.068	-0.008	0.524**	0.277*	0.433**	0.047
Peduncles plant⁻¹ (No.)				(r_p)	0.940**	0.146	0.566**	0.188	0.891**
				(r_g)	0.955**	0.138	0.572**	0.182	0.906**
Pods plant⁻¹ (No.)					(r_p)	0.209	0.608**	0.220*	0.922**
					(r_g)	0.207	0.619**	0.219*	0.939**
Pod length (cm)						(r_p)	0.577**	0.556**	0.276*
						(r_g)	0.563**	0.538**	0.259*
Pod weight (g)							(r_p)	0.685**	0.749**
							(r_g)	0.676**	0.749**
Seeds pod⁻¹ (No.)								(r_p)	0.323**
								(r_g)	0.308**

* and ** - Significant at 5% and 1 % level, respectively

weight, number of branches and peduncles per plant through number of pods per plant was the main cause of positive and significant association with net pod yield per plant. Despite negative direct effect of number of seeds per pod and pod length on pod yield, the correlation of these two traits with pod yield was significantly positive due to positive indirect effect via pod weight and number of pods per plant. Path coefficient analysis revealed the importance of characters such as number of branches, peduncles and pods per plant, pod weight and pod length in selection of superior genotypes for pod yield. Similar results were also obtained by Lal *et al.* (2007) in cowpea.

Table 3: Direct (diagonal) and indirect effect of yield contributing traits at phenotypic (P) and genotypic (G) levels

Characters		Plant height (cm)	Branches plant⁻¹ (No.)	Days to 50% flower (DAS)	Peduncles plant⁻¹ (No.)	Pods plant⁻¹ (No.)	Pod length (cm)	Pod weight (g)	Seeds pod⁻¹ (No.)	Pod yield (g plant⁻¹)
Plant height (cm)	G	**-0.022**	0.012	0.033	0.007	0.131	-0.047	0.182	-0.032	0.263*
	P	**-0.013**	0.011	0.020	0.016	0.109	-0.038	0.187	-0.029	0.264*
Branches plant⁻¹ (No.)	G	-0.004	**0.070**	-0.002	0.049	0.527	-0.014	0.214	-0.010	0.830**
	P	-0.002	**0.067**	-0.002	0.122	0.436	-0.012	0.218	-0.009	0.817**
Days to 50% flower (DAS)	G	-0.017	-0.004	**0.043**	-0.004	-0.005	-0.039	0.106	-0.033	0.047
	P	-0.010	-0.004	**0.028**	-0.007	-0.004	-0.030	0.103	-0.029	0.046
Peduncles plant⁻¹ (No.)	G	-0.003	0.061	-0.003	**0.056**	0.600	-0.010	0.218	-0.014	0.906**
	P	-0.002	0.058	-0.001	**0.140**	0.494	-0.009	0.224	-0.013	0.891**
Pods plant⁻¹ (No.)	G	-0.005	0.058	0.001	0.053	**0.629**	-0.015	0.236	-0.017	0.939**
	P	-0.003	0.055	0.001	0.132	**0.526**	-0.013	0.241	-0.016	0.922**
Pod length (cm)	G	-0.014	0.013	0.022	0.008	0.130	**-0.074**	0.215	-0.041	0.259*
	P	-0.008	0.013	0.013	0.020	0.110	**-0.061**	0.229	-0.039	0.276**
Pod weight (g)	G	-0.011	0.039	0.012	0.032	0.389	-0.042	**0.381**	-0.052	0.749**
	P	-0.006	0.037	0.007	0.079	0.320	-0.035	**0.396**	-0.049	0.749**
Seeds pod⁻¹ (No.)	G	-0.009	0.009	0.019	0.010	0.138	-0.040	0.258	**-0.077**	0.308**
	P	-0.006	0.009	0.011	0.026	0.116	-0.034	0.271	**-0.071**	0.323**

Hierarchical cluster analysis

Multivariate hierarchical clustering was carried for ten different quantitative characters (Fig. 1). Distance between all pairs of genotypes was calculated using squared Euclidean distance method and genotypes were clustered based on Ward's method. From the dendogram, it can be concluded that 43 genotypes were mainly divided at first node into 2 clusters with 38 and 5 genotypes in different groups. Cluster with 38 genotypes was again divided into 2 groups at second node with 31 and 7 genotypes. Similarly, 31 genotypes further divided into 2 groups at third node with 30 and 1genotypes and 30 genotypes again equally divided into 2 groups at the fourth node with 15 genotypes in each group, respectively.
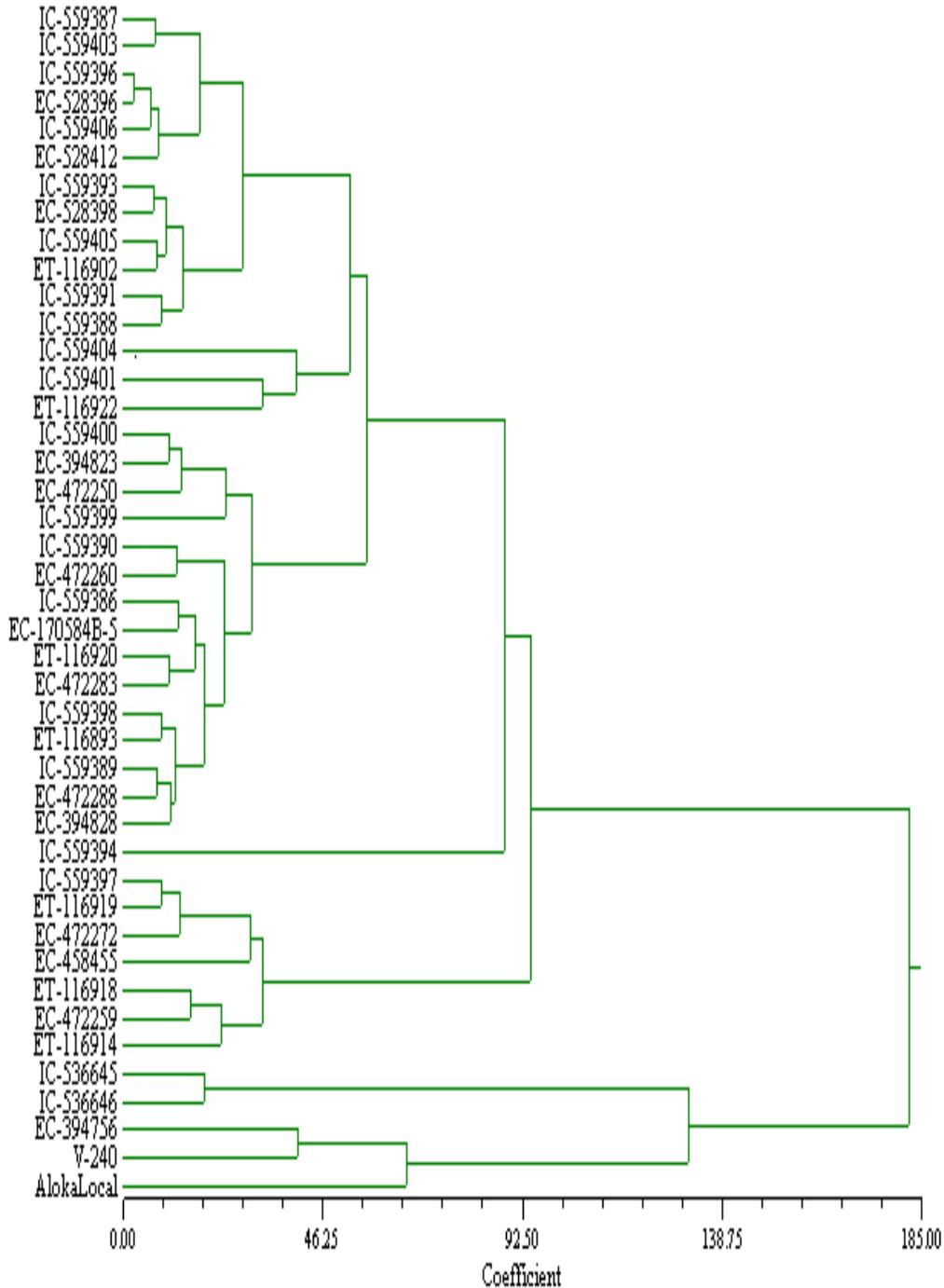

Figure 1: Multivariate cluster analysis of 43 cowpea genotypes using Ward's Method.

However, cluster of 15 genotypes further divided into 2 groups at fifth node with 12 and 3 genotypes and cluster of 12 genotypes again equally divided into 2 groups at sixth node with 6 genotypes in each group, respectively. Likewise, cluster with another 15 genotypes at node fourth again divided into 2 groups at the fifth node with 11 and 4 genotypes, and group of 11 genotypes further divided into 2 groups at sixth node with 9 and 2 genotypes, respectively. Since these clusters are group of individuals possessing similar characters mathematically gathered into the same cluster, these individuals are supposed to exhibit higher external heterogeneity. Genotypes included in the same

clusters with a high order of divergence will be expected to provide the best breeding material for achieving the maximum genetic advance for yield *per se,* provided other factors do not operate to limit the realization of this potential. It is rather encouraging that the divergence revealed in the present genotypes due to these characters will offer a good scope of improving pod yield through rational selection. A crossing programme involving parents selected on the basis of genetic divergences of yield components may likely to produce transgress segregates for yield potential. These results were in close conformity with the findings of those Hazra *et al.* (1992) and Lal *et al.* (2007).

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