# Hierarchical Clustering and Character Association Studies in Cowpea [*Vigna unguiculata* (L.) Walp.]

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Studies on 41 diverse genotypes of cowpea indicated the existence of fairly high degree of variability for plant height, peduncle length, number of peduncles and pods per plant, pod length, 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 days to flower and pod yield per plant indicated that heritability is mainly due to additive genetic effects. Correlation analysis pointed out the importance of number of branches per plant, number of peduncles per plant, pod length, pod weight and number of seeds per pod towards pod yield. Pod weight exerted the maximum positive direct effect on pod yield followed by number of pods per plant and pod length. Selection pressure on these traits may lead to an overall increase in pod yield per plant. The inter-cluster representatives of distant clusters would be more useful for choosing the parents in cowpea breeding programme.

**Key Words: Genetic variability, Correlation coefficient, Path analysis, Multivariate clustering, Cowpea**

## Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] has many uses like fodder, cover, green manure, and a cheap and high quality protein vegetable and pulse in the human diet. Cowpea provides 4-5 per cent protein in immature pods and 25-30 per cent in mature seeds (Bressani, 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 is basic and important endeavor to find out guidelines 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 was made to identify genotypes of cowpea belonging to different 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 of 2006 at the Research Farm of Indian Institute of Vegetable Research, Varanasi (82˚52′ E longitude and 25˚10′ N latitude). The experiment was laid out in Randomized Block Design with three replications. Seeds of 41 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 ten quantitative traits, *viz.*, plant height, number of branches and peduncles per plant, peduncle length, days to flowering, 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). The data on the characters computed and agglomerative hierarchical clustering was done using SPSS version 10.1 software

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employing Ward's method. The clustering was based on the squared Euclidean distances and the average linkage between groups was taken as the average of the distance between all pairs of cases with one member of each group (Lal *et al.*, 2007).

## 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, peduncle length, number of peduncles and pods per plant, pod weight and pod yield per plant. Plant height, number of peduncles per plant, number of days to flower, pod length, 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 days to flower 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 average pod weight, number of seeds per pod and number of branches per plant indicated 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.

### *Correlation Analysis*

Genotypic correlation coefficients were higher than corresponding phenotypic correlation coefficients, indicating the inherent association among the traits (Table 2). Highly significant genotypic correlation coefficient was observed for number of branches per plant, number of peduncles per plant, pod length, 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 days taken to flower, pod length, number of seeds per pod, pod weight and pod yield. The number of peduncles per plant showed positive correlation with number of days taken to flower, pod length, number of seeds per pod, pod weight and pod yield. However, the number of days taken to flower exerted positive correlation with number of seeds per pod, number of pods per plant and pod yield per plant. Pod length had positive correlation with number of seeds per pod, pod weight and pod yield per plant. The number of seeds per pod exerted positive correlation with pod weight and pod yield per plant. Pod weight showed positive correlation with pod yield per plant. Bapna *et al.* (1972) also obtained similar results.

### *Direct and Indirect Analysis*

The pod weight exerted the maximum positive direct effect on pod yield followed by number of pods per plant and pod length (Table 3). Thus, selection pressure on these traits may lead to an overall increase in pod yield per plant. Number of branches per plant showed the maximum negative direct effect on pod yield followed by number of seeds per pod. Considerable positive indirect effect of pod weight was recorded through pod length, and number of seeds per pod. A positive indirect effect of number of pods per plant was observed through number of peduncles per plant and peduncle length. Highest indirect

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

| Characters | Range | Grand mean | Variability PCV | Variability GCV | Heritability (%) | Genetic advance | Genetic advance as % of mean |
|---|---|---|---|---|---|---|---|
| Plant height (cm) | 42.3-351.5 | 185.56 | 39.87 | 38.30 | 92.30 | 140.64 | 75.79 |
| Branches plant$^{-1}$ (no.) | 3.3-6.0 | 4.56 | 20.16 | 12.15 | 36.30 | 0.69 | 15.13 |
| Peduncles plant$^{-1}$ (no.) | 33.1-72.3 | 51.97 | 23.07 | 18.67 | 65.50 | 16.18 | 31.13 |
| Peduncle length (cm) | 10.6-38.6 | 24.83 | 28.05 | 21.68 | 59.70 | 8.57 | 34.51 |
| Days to flower (DAF) | 40.6-68.3 | 48.74 | 15.71 | 14.86 | 89.50 | 14.12 | 28.96 |
| Pod length (cm) | 10.4-23.8 | 14.67 | 18.48 | 16.31 | 77.90 | 4.35 | 29.63 |
| Seeds pod$^{-1}$ (no.) | 9.3-15.7 | 12.93 | 14.29 | 9.22 | 41.60 | 1.58 | 12.22 |
| Pod weight (g) | 2.13-8.40 | 4.03 | 33.67 | 32.64 | 94.00 | 2.63 | 65.10 |
| Pods plant$^{-1}$ (no.) | 19.0-37.5 | 28.02 | 23.55 | 13.82 | 34.40 | 4.68 | 16.70 |
| Pod yield (g) plant$^{-1}$ | 53.4-213.4 | 110.23 | 35.78 | 31.70 | 78.50 | 63.78 | 57.86 |

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

**Table 2. Correlation coefficients at phenotypic ($r_p$) and genotypic ($r_g$) levels**

| Characters | Plant height (cm) | Branches plant$^{-1}$ (no.) | Peduncles plant$^{-1}$ (no.) | Peduncle length (cm) | Days to flower (DAF) | Pod length (cm) | Seeds pod$^{-1}$ (no.) | Pod weight (g) | Pods plant$^{-1}$ (no.) | Pod yield plant$^{-1}$ (g) |
|---|---|---|---|---|---|---|---|---|---|---|
| Plant height (cm) | ($r_p$) | 0.259 | 0.162 | 0.044 | 0.205 | -0.021 | 0.162 | 0.129 | 0.068 | 0.119 |
| | ($r_g$) | 0.410* | 0.180 | 0.036 | 0.211 | -0.021 | 0.223 | 0.134 | 0.076 | 0.124 |
| Branches plant$^{-1}$ (no.) | | ($r_p$) | 0.684** | 0.071 | 0.232 | 0.396* | 0.389* | 0.597** | 0.489** | 0.742** |
| | | ($r_g$) | 0.684** | 0.039 | 0.453** | 0.812** | 0.335* | 0.851** | -0.103 | 0.806** |
| Peduncles plant$^{-1}$ (no.) | | | ($r_p$) | 0.012 | 0.347* | 0.587** | 0.436** | 0.701** | 0.486** | 0.913** |
| | | | ($r_g$) | 0.047 | 0.468** | 0.846** | 0.448** | 0.794** | 0.253 | 0.934** |
| Peduncle length (cm) | | | | ($r_p$) | 0.244 | -0.066 | -0.073 | -0.105 | 0.121 | -0.020 |
| | | | | ($r_g$) | 0.282 | -0.052 | -0.156 | -0.133 | 0.189 | -0.042 |
| Days to flower (DAF) | | | | | ($r_p$) | 0.231 | 0.271 | 0.229 | 0.182 | 0.325* |
| | | | | | ($r_g$) | 0.256 | 0.420* | 0.257 | 0.384* | 0.411* |
| Pod length (cm) | | | | | | ($r_p$) | 0.398* | 0.771** | 0.065 | 0.737** |
| | | | | | | ($r_g$) | 0.615** | 0.898** | 0.109 | 0.957** |
| Seeds pod$^{-1}$ (no.) | | | | | | | ($r_p$) | 0.485** | 0.114 | 0.460** |
| | | | | | | | ($r_g$) | 0.590** | -0.245 | 0.554** |
| Pod weight (g) | | | | | | | | ($r_p$) | -0.080 | 0.828** |
| | | | | | | | | ($r_g$) | -0.278 | 0.895** |
| Pods plant$^{-1}$ (no.) | | | | | | | | | ($r_p$) | 0.442** |
| | | | | | | | | | ($r_g$) | 0.177 |

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

**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.) | Peduncles plant$^{-1}$ (no.) | Peduncle length (cm) | Days to flower (DAF) | Pod length (cm) | Seeds pod$^{-1}$ (no.) | Pod weight (g) | Pods plant$^{-1}$ (no.) | Pod yield plant$^{-1}$ (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Plant height (cm) | G | **0.052** | -0.072 | 0.009 | 0.001 | 0.014 | -0.006 | -0.009 | 0.113 | 0.023 | 0.124 |
| | P | **-0.028** | 0.010 | 0.053 | 0.001 | 0.004 | -0.002 | -0.005 | 0.068 | 0.019 | 0.119 |
| Branches plant$^{-1}$ (no.) | G | 0.021 | **-0.175** | 0.034 | 0.001 | 0.030 | 0.229 | -0.014 | 0.712 | -0.032 | 0.806** |
| | P | -0.007 | **0.037** | 0.224 | 0.001 | 0.005 | 0.045 | -0.011 | 0.313 | 0.137 | 0.742** |
| Peduncles plant$^{-1}$ (no.) | G | 0.009 | -0.120 | **0.049** | 0.001 | 0.031 | 0.239 | -0.018 | 0.665 | 0.078 | 0.934** |
| | P | -0.005 | 0.025 | **0.328** | 0.001 | 0.007 | 0.066 | -0.013 | 0.368 | 0.137 | 0.913** |
| Peduncle length (cm) | G | 0.002 | -0.007 | 0.002 | **0.004** | 0.019 | -0.015 | 0.006 | -0.112 | 0.058 | -0.042 |
| | P | -0.001 | 0.003 | 0.004 | **-0.005** | 0.005 | -0.007 | 0.002 | -0.055 | 0.034 | -0.020 |
| Days to flower (DAF) | G | 0.011 | -0.079 | 0.023 | 0.001 | **0.067** | 0.072 | -0.017 | 0.216 | 0.118 | 0.411* |
| | P | -0.006 | 0.009 | 0.114 | -0.001 | **0.021** | 0.026 | -0.008 | 0.120 | 0.054 | 0.325* |
| Pod length (cm) | G | -0.001 | -0.143 | 0.042 | 0.001 | 0.017 | **0.282** | -0.025 | 0.752 | 0.033 | 0.957** |
| | P | 0.001 | 0.015 | 0.192 | 0.001 | 0.005 | **0.113** | -0.012 | 0.404 | 0.018 | 0.737** |
| Seeds pod$^{-1}$ (no.) | G | 0.012 | -0.059 | 0.022 | -0.001 | 0.028 | 0.174 | **-0.040** | 0.494 | -0.074 | 0.554** |
| | P | -0.005 | 0.014 | 0.143 | 0.001 | 0.006 | 0.045 | **-0.029** | 0.254 | 0.032 | 0.460** |
| Pod weight (g) | G | 0.007 | -0.149 | 0.039 | -0.001 | 0.017 | 0.253 | -0.024 | **0.838** | -0.085 | 0.895** |
| | P | -0.004 | 0.022 | 0.230 | 0.001 | 0.005 | 0.087 | -0.014 | **0.525** | -0.022 | 0.828** |
| Pods plant$^{-1}$ (no.) | G | 0.004 | 0.018 | 0.012 | 0.001 | 0.026 | 0.031 | 0.010 | -0.232 | **0.308** | 0.177 |
| | P | -0.002 | 0.018 | 0.159 | -0.001 | 0.004 | 0.007 | -0.003 | -0.042 | **0.281** | 0.442** |

effect of pod length was exhibited via pod weight. Path coefficient analysis revealed the importance of characters such as number of 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.

### *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 dendrogram, it can be

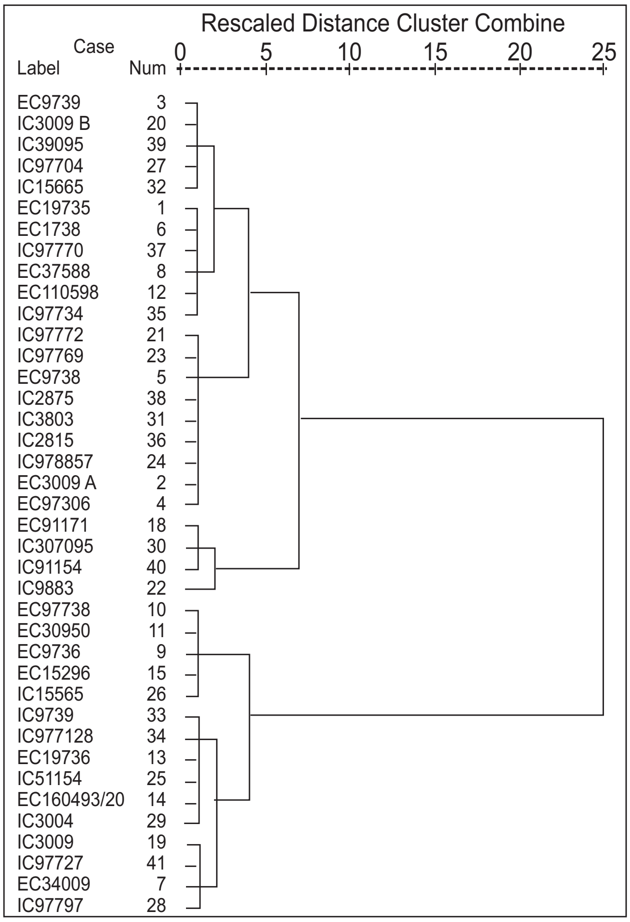

**Fig. 1: Multivariate cluster analysis of 41 cowpea genotypes using Ward's Method**

concluded that 41 genotypes were mainly divided at first node into 2 clusters with 24 and 17 genotypes in different groups. Cluster with 24 genotypes was again divided into 2 groups at second node with 20 and 4 genotypes. Similarly, 20 genotypes further divided into 2 groups at third node with 11 and 9 genotypes and 11 genotypes again divided into 2 groups at the fourth node with 6 and 5 genotypes, respectively. However, cluster of 17 genotypes further divided into 2 groups at second node with 12 and 5 genotypes and 12 genotypes again equally divided into 2 groups at third node with 6 genotypes in each group, 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 Hazra *et al.* (1992) and Lal *et al.* (2007).

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