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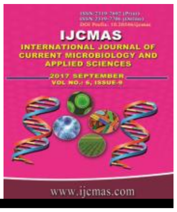

**Original Research Article**

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# Variability and Genetic Diversity in Yard Long Bean (*Vigna unguiculata* subsp. *sesquipedalis*.)

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## ABSTRACT

**Keywords**

Yard long bean, Variability, Genetic Divergence, Clustering of genotypes

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Yard long bean is an important vegetable crop that supplies the dietery protein through the edible tender pods. The twelve genotypes of yard long bean from different locations of the country were collected and analysed for studying their variability and diveregence. Mean performance and the estimates of GCV and PCV of the yield contributing traits were worked out to analyse the variability. The highest yielder was Acc 18 (Puthuppady local). On the basis of Mahalanobis $D^2$ statistics, the genotypes were grouped into five clusters. Study of the genetic divergence in the genotypes revealed the genetic distance between the genotypes. Genotypes from divergent clusters can be selected for hybridisation programme to get desirable recombinants.

## Introduction

Cowpea, *Vigna unguiculata*, belonging to leguminosae family, serves as rich source of protein and has the unique ability to fix atmospheric nitrogen even in poor soils, Hence it is a component of sustainable agriculture in marginal lands. *Vigna unguiculata* subsp. *sesquipedalis*, commonly called as the yard long bean is considered to be one of the most important vegetable crop in parts of Indonesia, Thailand, Philippines, Taiwan, China and India. Extensive cultivation of yard long bean is seen in Kerala and hence affected by many pest and diseases. Intensive studies were being carried out to assess its full potential as a protein supplier and to impart pest and disease resistance. One of the most important techniques for crop improvement is hybridisation programme, success of which mainly depends on the genetic diversity of the parents chosen for the trait. To produce higher heterotic effects genetically diverse parents have to be crossed. However, maximum heterosis is obtained at an intermediate level of genetic diversity.

To measure the genetic diversity the widely adopted method is Mahalanobis $D^2$ statistic (Mahalanobis, 1936) and the same has been used in the current study.

## Materials and Methods

The present study was conducted in the Department of Plant Breeding and Genetics, College of Agriculture, KAU, during 2016. The twelve genotypes studied were planted in RBD with three replications and it is listed in Table 1. The entire field was divided into 3 blocks of twelve plots each and the treatments were allotted at random. The following characters were studied *viz*., days to 50 per cent flowering, days to first harvest, pod yield plant $^{-1}$ (g), pods plant$^{-1}$, length of pod (cm), weight of pod (g), seeds pod$^{-1}$, 100 seed weight (g), length of harvest period (days) and crop duration (days) from observations recorded on five randomly selected plants from each plot and their mean was calculated. The cluster analysis was carried out using Mahalanobis D$^2$ statistic tool to determine genetic diversity of cowpea genotypes.

## Results and Discussion

The variability and genetic divergence estimated in twelve yard long bean genotypes has been discussed below.

### Mean performance of accessions

Analysis of variance revealed significant differences among the 12 genotypes of yard long bean for all the characters studied *viz*., days to 50 per cent flowering, days to first harvest, pod yield plant $^{-1}$ (g), pods plant$^{-1}$, length of pod (cm), weight of pod (g), seeds pod$^{-1}$, 100 seed weight (g), crop duration (days). The character length of harvesting period did not record significance. Similar results in vegetable cowpea was reported by Manju (2006), Lovely () Sivakumar *et al.*, (2014) and Litty and Celine (2015).

The mean values of each of the 12 genotypes for the 10 characters are presented in Table 2. Among the genotypes, days to 50 per cent flowering ranged from 40.67 to 50.67. Acc 20 was the earliest to flower and Acc 1 and Acc 26 were the latest to flower. Regarding days to first harvest Acc 2 (50 days) was the earliest and Acc 26 (58 days) was the latest. The genotypes Acc 27, Acc 23, Acc 25, Acc 18, Acc 29, Acc14 and Acc 20 were on par with Acc 2. The number of pods plant$^{-1}$ was highest for Acc 18 (26). The only genotype statistically on par with Acc 18 was Acc 1. Acc 9 had the lowest number of pods plant$^{-1}$ (15).The pod characters *viz*., pod length, pod weight and number of seeds pod$^{-1}$ differed significantly among varieties. Pod length ranged from 29.67 cm (Acc29) to 54 cm (Acc 25). Acc 23 and Acc 1 are statistically on par with Acc 29. Comparatively higher pod weight was recorded for Acc 27 (17.33g). Pod weight was minimum for Acc 29 (10.30 g) while Acc 27 (17.33) recorded maximum weight. Number of seeds pod$^{-1}$ was maximum for Acc 2 (18.67). The genotypes Acc 18 and Acc 27 were on par with Acc 2. Seeds pod$^{-1}$ recorded lowest values for the varieties Acc 23 and Acc 29. Acc 18 (15.87) recorded highest value for 100 seed weight while it was lowest for Acc 9 (13.27). Length of harvesting period was maximum for Acc 26 (28.33) and minimum for Acc 25 (23.67). Acc 1 was the genotype that has extended crop duration (84.33) and Acc 2 was the genotype with least duration (74.67). The varieties Acc 20, Acc 29, Acc 23, Acc 13 and Acc 26 was on par with Acc 1.

The yield or vegetable pods plant$^{-1}$ ranged from 176.97 g (Acc 9) to 485.03 g (Acc 18). The results indicated the superiority of Acc 18 over the other varieties. Wide variation was evident for the characters like days taken for 50 per cent flowering and crop duration.

Yield is the vital character considered for selection. Pod yield plant$^{-1}$ showed remarkable variation among genotypes. The highest pod yield plant$^{-1}$ was recorded for Acc 18 (Puthuppady local). Characters like number of pods plant$^{-1}$, length of pod and weight of pod also showed significant variation between genotypes.

## Coefficient of Variation

An estimate of the magnitude of variability present in a population is of great importance as it provides the basis for effective selection. The components used to measure the variability present in a population are PCV and GCV. The GCV provides a valid basis for comparing and assessing the range of genetic variability for quantitative characters and PCV measures the extend of total variation.

**Fig.1** Cluster diagram showing average intra and inter cluster distance

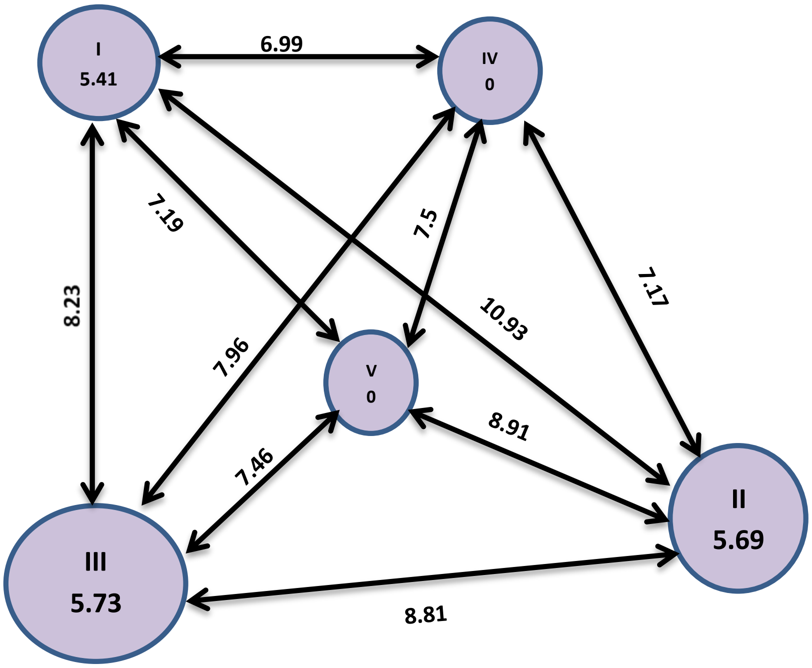

**Table.1** List of genotypes used in the study

| SI No | Genotype No | Source |
|---|---|---|
| 1 | Acc. 14 | Vijayanthi, Variety from KAU |
| 2 | Acc. 9 | NBPGR Accession |
| 3 | Acc. 20 | NBPGR Accession |
| 4 | Acc. 1 | NBPGR Accession |
| 5 | Acc. 27 | Githika, Variety from KAU |
| 6 | Acc. 26 | NBPGR Accession |
| 7 | Acc. 18 | Puthuppady local |
| 8 | Acc. 29 | Wayanad local, MSSRF |
| 9 | Acc.2 | Adityapuram local, MSSRF |
| 10 | Acc. 13 | NBPGR Accession |
| 11 | Acc. 25 | NBPGR Accession |
| 12 | Acc. 23 | NBPGR Accession |

**Table.2** Mean values of 10 biometric characters of yard long bean

| Treatment No | Days to 50 per cent flowering | Days to first harvest | Pods plant$^{-1}$ | Length of pod | Pod yield plant$^{-1}$ | Weight of pod | Seeds pod$^{-1}$ | 100 seed weight | Length of harvest period | Crop duration |
|---|---|---|---|---|---|---|---|---|---|---|
| V27 | 42.33 | 51.33 | 22.00 | 45.33 | 394.83 | 17.33 | 18.33 | 14.77 | 25.67 | 75.67 |
| V26 | 50.67 | 58.00 | 16.33 | 37.67 | 242.15 | 13.00 | 14.67 | 15.13 | 28.33 | 83.33 |
| V23 | 50.00 | 50.67 | 18.33 | 33.00 | 225.67 | 12.00 | 15.33 | 12.13 | 25.67 | 82.00 |
| V13 | 48.00 | 57.67 | 20.67 | 45.67 | 312.33 | 15.07 | 16.67 | 13.50 | 27.33 | 83.67 |
| V25 | 47.67 | 54.33 | 18.67 | 54.00 | 231.00 | 11.40 | 15.33 | 13.77 | 23.67 | 75.00 |
| V18 | 45.33 | 54.67 | 26.00 | 43.67 | 485.03 | 16.23 | 17.67 | 15.87 | 27.33 | 75.00 |
| V1 | 50.67 | 57.33 | 24.67 | 32.00 | 305.13 | 11.80 | 16.33 | 14.70 | 25.00 | 84.33 |
| V29 | 44.67 | 54.67 | 17.67 | 29.67 | 210.00 | 10.30 | 15.33 | 14.57 | 26.33 | 80.67 |
| V9 | 48.67 | 57.67 | 15.00 | 48.00 | 176.97 | 13.53 | 15.67 | 13.27 | 26.00 | 76.67 |
| V2 | 44.34 | 50.00 | 20.33 | 44.67 | 298.14 | 13.67 | 18.67 | 14.03 | 27.33 | 74.67 |
| V14 | 47.33 | 54.67 | 18.67 | 43.00 | 213.00 | 14.43 | 15.67 | 15.30 | 25.33 | 77.33 |
| V20 | 40.67 | 51.33 | 17.33 | 44.67 | 246.67 | 13.13 | 16.00 | 14.33 | 25.67 | 78.67 |
| Mean | 46.69 | 54.36 | 19.64 | 41.78 | 278.41 | 13.49 | 16.31 | 14.28 | 26.14 | 78.92 |
| ±SE | 0.94 | 0.85 | 0.95 | 2.09 | 25.39 | 0.59 | 0.37 | 0.29 | 0.37 | 1.07 |
| CD(0.05) | 3.15 | 4.75 | 3.65 | 5.38 | 81.14 | 1.64 | 1.21 | .55 | NS | 6.46 |

**Table.3** Components of variance for the 10 characters in yard long bean

| SI No. | Characters | GCV% | PCV% |
|---|---|---|---|
| 1 | Days to 50 per cent flowering | 6.52 | 7.69 |
| 2 | Days to first harvest | 4.52 | 6.86 |
| 3 | Pods plant$^{-1}$ | 9.18 | 13.84 |
| 4 | Length of pod (cm) | 16.72 | 18.37 |
| 5 | Pod yield plant$^{-1}$ | 29.99 | 34.58 |
| 6 | Weight of pod (g) | 14.53 | 16.20 |
| 7 | Seeds pod$^{-1}$ | 7.45 | 8.64 |
| 8 | 100 seed weight (g) | 6.99 | 7.35 |
| 9 | Length of harvest period (days) | 2.40 | 7.73 |
| 10 | Crop duration (days) | 3.77 | 6.13 |

**Table.4** Clustering pattern of 12 genotypes of yard long bean

| Cluster No. | No of genotypes | Genotypes |
|---|---|---|
| I | 3 | Acc. 14 (Vijayanthi), Acc. 26(NBPGR Accession), Acc. 18(Puthuppady local) |
| II | 4 | Acc. 9(NBPGR Accession), Acc. 13(NBPGR Accession), Acc. 25(NBPGR Acc), Acc. 23(NBPGR Accession) |
| III | 3 | Acc. 20(NBPGR Accession), Acc. 29(Wayanad local), Acc. 2(Adityapuram local) |
| IV | 1 | Acc. 1(NBPGR Accession) |
| V | 1 | Acc. 27(Githika) |

**Table.5** Average intra and inter cluster distances between the five clusters of Twelve genotypes of yard long bean

| | I | II | III | IV | V |
|---|---|---|---|---|---|
| I | 29.28<br>(5.41) | 119.42<br>(10.93) | 67.76<br>(8.23) | 48.81<br>(6.99) | 51.67<br>(7.19) |
| II | | 32.39<br>(5.69) | 78.60<br>(8.87) | 51.43<br>(7.17) | 79.44<br>(891) |
| III | | | 32.87<br>(5.73) | 55.65<br>(7.46) | 62.79<br>(7.92) |
| IV | | | | 0 | 56.28<br>(7.50) |
| V | | | | | 0 |

**Table.6** Cluster means of the ten biometric characters in yard long bean

| SI No | Character | Clusters | | | | |
|---|---|---|---|---|---|---|
| | | I | II | III | IV | V |
| 1 | Days to 50 per cent flowering | 47.778 | 48.58 | 43.22 | 50.67 | 42.33 |
| 2 | Days to first harvest | 55.78 | 55.08 | 52 | 57.33 | 51.33 |
| 3 | Pods plant$^{1}$ | 20.33 | 18.17 | 18.44 | 24.67 | 22 |
| 4 | Length of pod | 41.44 | 45.17 | 39.67 | 32 | 45.33 |
| 5 | Pod yield plant$^{1}$ | 313.39 | 236.49 | 251.60 | 305.13 | 394.83 |
| 6 | Weight of pod | 14.55 | 13 | 12.37 | 11.8 | 17.33 |
| 7 | Seeds pod$^{1}$ | 16 | 15.75 | 16.67 | 16.33 | 18.32 |
| 8 | 100 seed weight | 15.43 | 13.17 | 14.31 | 14.7 | 14.77 |
| 9 | Length of harvest period | 27 | 25.67 | 26.44 | 25 | 25.67 |
| 10 | Crop duration | 78.55 | 79.33 | 78 | 84.33 | 75.67 |

In the present study, high values of PCV and GCV were observed for pod yield plant$^{-1}$. Moderate PCV and GCV were recorded for length of pod and weight of pod. Pods plant$^{-1}$ recorded high PCV but low GCV. GCV and PCV values are presented in Table3. The study thus revealed that the character with high PCV and GCV contributes to maximum variability.

Improvement of these characters through selection is desirable. These results were in agreement with earlier reports in cowpea by Panicker (2000), Selvam *et al.,* (2000), Jyothi (2001), Kutty *et al.,* (2003), Madhukumar (2006), Sivakumar *et al.,* (2014) and Litty and Celine (2015). Low GCV and PCV were recorded for days to 50 per cent flowering, days to first harvest, seeds pod$^{-1}$, 100 seed weight, length of harvest period and crop duration indicating low variability which limits the scope for improvement of these characters through selection. Similar results were reported by Lovely (2005), Manju (2006), Sivakumar *et al.,* (2014) and Litty and Celine (2015).

## Genetic divergence studies

Divergence analysis is performed to identify the most diverse genotypes for a rational choice of potential parents for breeding programme. It was observed that the twelve genotypes of yard long bean were distributed at random among the clusters based on their genetic distance. Resmi *et al.,* (2005), Muhmudul *et al.,* (2012) and Sivakumar *et al.,* (2014) performed divergence analysis in yard long bean.

The twelve genotypes were grouped into five clusters (Table 4). Cluster II is the largest with four genotypes followed by cluster I and III each with three genotypes. Cluster IV and V are solitary clusters. The cluster means reveal the best cluster for various characters. Depending upon the aim of breeding, potential lines can be selected from different clusters as parents in a hybridization programme. Table 7 represents the cluster means. Cluster V showed the highest cluster mean for the characters *viz.,* pod yield plant$^{-1}$, length of pod, weight of pod and seeds pod$^{-1}$. Cluster V also showed the lowest cluster mean for days to 50 per cent flowering and days to first harvest.

The highest cluster mean for days to 50 per cent flowering, days to first harvest, pods plant $^{-1}$ and crop duration were noticed in cluster IV. It also had lowest cluster mean for length of harvest period, length of pod and weight of pod. Cluster II and III have recorded intermediate cluster means. Cluster I had highest cluster mean for 100 seed weight and length of harvest period. For crop improvement programmes, intercrossing of genotypes from those clusters with outstanding mean performance would be effective.

Maximum divergence would be shown by clusters which possess maximum intercluster distance between them (Table 6).. Fig. 1 represents the cluster diagram. The inter cluster distance was maximum between cluster I and cluster II. The least intercluster distance was recorded between cluster I and cluster IV.

The average inter and intracluster distances are presented in Table. The inter cluster distance was maximum for cluster I and cluster II (10.93) followed by cluster II and cluster V (8.91) and cluster II and cluster III (8.87).

The least intercluster distance was recorded between cluster I and cluster IV. The intracluster distance was highest for cluster III followed by cluster II and cluster I. The intracluster distances was least and zero for cluster IV and cluster V as they are the solitary ones. The genotype Acc 18 was identified as the highest pod yielder. Hybridisation of this genotype with genotypes from other clusters having high pods per plant and pod weight is desirable.

In conclusion, the study revealed the average performances of different genotypes to various yield contributing characters, contribution of various characters towards variability and the genetic distance between various genotypes. PCV and GCV estimates showed that the character yield plant$^{-1}$ showed high variability and the importance of this character for character. The twelve genotypes were clustered into five groups. It would be desirable to attempt hybridisation between genotypes belonging to distant clusters to obtain highly heterotic crosses. The inter cluster distance was maximum for cluster I and cluster II followed by cluster II and cluster V and cluster II and cluster III. Therefore, genotypes from these clusters can be selected for hybridization programme to get desirable recombinants. The cluster means reveal the best cluster for various characters. Depending upon the aim of breeding, potential lines can be selected from different clusters as parents in a hybridization programme.

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