GENETIC DIVERGENCE IN CLUSTER BEAN
[*Cyamopsis tetragonoloba* (L.) Taub.]

ANANDHI, K.

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Department of Plant Breeding and Genetics
COLLEGE OF AGRICULTURE
VELLAYANI, THIRUVANANTHAPURAM 695 522

DECLARATION

I hereby declare that this thesis entitled **"Genetic divergence in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.]"** is a bonafide record of research work done by me during the course of research and that the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar title, of any other university or society.

Vellayani,
7-1-2006.

K. Anandhi
ANANDHI, K
(2003-11-44)

CERTIFICATE

Certified that this thesis entitled "**Genetic divergence in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.]**" is a record of research work done independently by Ms. Anandhi, K. (2003-11-44) under my guidance and supervision and that it has not previously formed the basis for the award of any degree, fellowship or associateship to her.

Vellayani,
7-1 -2006.

Dr. SUNNY K. OOMMEN
(Chairman, Advisory Committee)
Associate Professor,
Department of Plant Breeding and Genetics,
College of Agriculture, Vellayani,
Thiruvananthapuram-695 522.

Approved by

Chairman:

Dr. SUNNY K. OOMMEN
Associate Professor,
Department of Plant Breeding and Genetics,
College of Agriculture, Vellayani,
Thiruvananthapuram-695522.

7.1.2006

Members :

Dr. P. MANJU
Associate Professor and Head,
Department of Plant Breeding and Genetics,
College of Agriculture, Vellayani,
Thiruvananthapuram-695522.

7.01.06

Dr. D. WILSON
Associate Professor,
Department of Plant Breeding and Genetics,
College of Agriculture, Vellayani,
Thiruvananthapuram-695522.

7/1/06

Dr. VIJAYARAGHAVAKUMAR
Associate Professor,
Department of Agricultural Statistics,
College of Agriculture, Vellayani,
Thiruvananthapuram-695522.

07/01/06

External Examiner :

7/1/06

Dr. P. Vivekanandan,
Professor & Head
Dept. of Plant Breeding & Genetics
Agrl. College and Research Institute
Madurai

Dedicated to

My Beloved Sister

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Introduction

1. INTRODUCTION

Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] popularly known as guar is one of the most important legumes grown for vegetable, fodder, green manure and seed purposes. Tender pods are used as vegetable. The analysis of tender pods revealed that 100g of edible portion contains 81.0g moisture, 10.8g carbohydrates, 3.2g protein and 0.4g fat. Besides it contains appreciable quantities of vitamin A, B and C and minerals (Aykroyd, 1963).

The crop is widely cultivated in India, Pakistan, Indonesia and other parts of southern and southeastern Asia as a vegetable and fodder crop for a long time (Whyte *et al.*, 1953; ICAR, 1970). It has also assumed profound industrial importance as the gum obtained from seeds is extensively used in paper, mining, explosive, food, pharmaceutical, cosmetic, textile and oil industries around the world.

Inspite of its economic importance as a common vegetable consumed by many people in Peninsular India, especially in the south, attempts to improve vegetable pod yield and pod quality utilizing the genetic variability in the species were meagre. Advances in guar breeding is being reviewed and attempts to improve yield has to be taken up (Henry, A, 2003; Singh *et al* 2003). The crop improvement attempts were mostly directed towards enhancing seed yield in view of the industrial importance. Efforts to develop fodder types also received considerable attention.

Collection of clusterbean genotypes and evaluation of variability for vegetable pod yield and yield component characters is the initial step in the endeavour to develop high yielding types. Phenotypic selection can be relied upon only if the heritability of the character in question is high. Hence the estimation of heritability and genetic advance of yield and its contributing characters is a prerequisite for developing high yielding varieties.

Knowledge of inter-relationships of yield and other traits from correlation studies would facilitate effective selection for simultaneous improvement of one or many yield contributing characters. Assessing the direct and indirect effects of each component towards yield will help in selecting the characters to which attention is to be given in crop improvement efforts.

Grouping of genotypes based on genetic distance between them with respect to important characters would provide a way to identify the parents for further crop improvement programmes.

Keeping all these in view, the present investigation was undertaken with the following objectives

a. To study genetic variability for different characters by estimating phenotypic and genotypic coefficients of variation.

b. To estimate heritability and genetic advance for different characters.

c. To study the association between yield and its components by estimating the correlation coefficients

d. To understand the direct and indirect effects of yield contributing characters by path coefficient analysis

e. To group varieties into clusters and

f. To identify promising genotypes.

Review of Literature

2. REVIEW OF LITERATURE

The present investigation aimed at the study of variability in clusterbean and attempted to group varieties into clusters using Mahalanobis D^2 statistic. The literature pertinent to the study is reviewed and presented hereunder. Efforts on genetic improvement of the crop has been much less compared to other legumes. The work done on the crop being meagre, the review at times considers other leguminous crops. However the studies on the crop indicate the existence of high genetic variability and ample scope for improvement of the crop.

2.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

Heritability and genetic advance are very important parameters in selection. High heritability coupled with high genetic advance is indicative of additive genetic variance (Johnson et al., 1955).

Genetic variability for yield and yield contributing traits in the base population is essential for successful crop improvement (Allard, 1960). Greater the variability, more the chances for selection of better genotypes. The genetic parameters like coefficient of variation, heritability and genetic advance provide an exact picture of variability in a population.

Mital *et al.* (1969) in a study with 73 guar genotypes observed wide variability for total number of pods per plant, plant height and yield while seeds per pod showed very low magnitude of variation.

Chaudhary *et al.* (1975) reported wide range of variability at both phenotypic and genotypic levels for flowering and number of seeds per pod but only low range for number of branches per plant. High GCV was observed for pod yield.

Vashistha *et al.* (1981) reported wide range of variation for plant height at phenotypic and genotypic levels. High GCV was recorded for number of pods per cluster and pod yield. Heritability was high for pod length and pod yield while it was low for plant height and pods per cluster.

Dabas *et al.* (1982) reported high coefficient of variation for branch number, cluster number and pod number and low for days to 50 per cent flowering and seeds per pod. High heritability was observed for branch number, pod number and plant height.

Variability analysis by Sidhu *et al.* (1982) revealed wide range of variation both at genotypic and phenotypic levels for plant height, number of branches per plant and pod length. Heritability estimates were high for pod length, number of seeds per pod and pod yield while low heritability estimates were observed for plant height and number of branches per plant.

Reddy and Gupta (1984) in a study of variability in 40 strains of guar observed high heritability and genetic gain for branches per plant, pods per plant and clusters per plant.

Henry *et al.* (1986) reported high GCV for days to 50 per cent flowering in a study conducted with 36 genotypes.

Vijay (1988) studied variability among 113 cultivars of clusterbean and reported high GCV for pod yield and pod number.

Gipson and Balakrishnan (1990) in a variability study with 56 genotypes noted high variability for yield per plant, pods per plant, plant height, branches per plant, days to flowering, pods per cluster and pod length. Estimated heritability was highest for pods per cluster followed by branches per plant and pod length. Heritability and genetic gain were high for pods per plant, plant height and pod weight.

In a study with 64 genotypes, Lokesha and Shivashankar (1990) reported high heritability for days to maturity, number of branches and pod length and high genetic gain for days to maturity and pods per plant.

Arumugarangarajan (1997) reported maximum GCV and PCV for pod yield followed by number of branches. Heritability estimate was maximum for pod length among the characters studied. Moderate genetic advance as percentage of mean was reported for pod yield and number of branches while other traits showed low genetic advance.

Dwivedi *et al.* (1997) observed wide range of variability for number of branches, days to flowering and maturity, clusters per plant, pods per cluster and plant and seeds per pod.

In a study with 231 germplasm lines, Mitra *et al.* (2000) observed high variability for pods per plant followed by clusters per plant. Seeds per pod showed the lowest variability. Pods per plant showed the highest value for heritability followed by clusters per plant, seeds per pod and pod length.

Ajith (2001) reported high heritability coupled with high genetic advance in cowpea for length of main stem, number of primary branches, pod weight, number of pod clusters per plant, pod length and number of seeds per pod.

Singh *et al.* (2001) reported high heritability and high genetic advance for plant height, number of branches per plant, number of pods per plant and yield per plant.

Amrendrakumar and Jain (2003) in a study with 36 pea cultivars observed high variability for pod yield per plant, plant height, number of primary branches and pod weight. Heritability estimate was high for plant height.

Chaudhary and Sharma (2003) studied green pod yield and its components in garden pea and reported high heritability coupled with high genetic advance for pod yield per plant, plant height and number of pods per plant.

Pal *et al.* (2003) reported high PCV and GCV for plant height, number of pods per plant, number of primary branches per plant and green pod yield in cowpea.

2.2 CORRELATION STUDIES

Yield is a complex character determined by several component characters. Knowledge of the relationship of yield with other traits is essential for selection programmes aimed at yield improvement. Research work done in clusterbean to bring out the degree of association between yield and yield components is briefly reviewed.

Sanghi and Sharma (1964) in a study conducted with 64 indigenous varieties of clusterbean found that green pod yield was positively correlated with clusters per plant, branches per plant and pod length.

Mital and Thomas (1969) reported positive correlation of pod yield with pods per plant, clusters per plant, number of branches, plant height and days to maturity and negative correlation with pod length. Plant height had positive correlation with number of branches.

Mital *et al.* (1971) reported negative correlation between seed yield and pod length and seed size and seed weight.

Tikka (1975) in a study with 30 genotypes of clusterbean found significant and positive correlation of grain yield with number of clusters per plant, number of pods, pod length and number of grains per pod. It was also observed that the component characters had positive correlation with each other. Pod length was positively correlated with number of seeds per pod. The correlation coefficients were high between clusters per plant and pod number and between pod length and grains per pod and low for the remaining combinations.

Nath and Saini (1980) found that seed yield was positively correlated with plant height, number of branches per plant and number of clusters per plant.

Vashistha *et al.* (1981) reported that number of pods per cluster had positive correlation with length of pod. They also reported that length of pod showed negative correlation with number of seeds per pod, number of primary branches and number of pods per cluster.

Seiler and Stafford (1985) reported that grain yield was positively correlated with number of seeds per pod. They also reported positive and significant correlation between plant height and number of branches per plant.

Positive and significant correlation of grain yield with days to 50 per cent flowering, plant height, number of branches per plant, number of clusters per plant and number of pods per cluster was found by Henry *et al.* (1986). The number of pods per plant was positively correlated with several characters studied i.e. plant height, number of branches per plant and number of clusters per plant.

Vijay (1988) in a study with 113 cultivars of clusterbean reported positive significant correlation of pod yield with pod number, pod weight, number of clusters per plant, pod length and days to flowering.

Vahidy and Yousufzai (1991) in a study with 12 accessions of guar found that seed yield had strong positive association with plant height, number of primary branches, number of clusters per plant and number of pods per plant. Number of pods was correlated to plant height, number of primary branches and number of clusters per plant.

Positive correlation of grain yield with plant height, number of branches per plant, number of clusters per plant and number of seeds per plant was reported by Lokesha and Shivashankar (1992). They observed significant positive correlation between pod yield and number of clusters per plant. Number of clusters per plant was positively correlated with plant height and number of branches per plant. They also reported that number of seeds per pod was positively correlated with number of branches per plant.

Green pod yield was found to be positively correlated with plant height at final harvest, number of branches per plant, days to flowering, days to maturity, pod length, pod weight, seeds per pod and pods per plant at both genotypic and phenotypic levels in a study conducted by Brindha *et al.* (1997) with 60 genotypes.

Saini *et al.* (2001b) studied correlation of grain yield with several other characters in 18 genotypes of clusterbean. They reported positive correlation of 100 grain weight and number of pods per plant with grain yield. Days to flowering and plant height were negatively correlated with yield.

Singh *et al.* (2002) in a study with 43 genotypes of clusterbean found positive and significant correlation of grain yield with number of branches per plant, number of clusters per plant and number of pods per plant. Pods per plant was positively correlated with days to 50 per cent flowering, plant height, number of branches per plant and number of clusters per plant. They also reported positive correlation of number of clusters per plant with number of branches per plant and days to 50 per cent flowering with plant height.

Pod yield was found to be positively correlated with pod length, number of grains per pod and number of pods per plant in garden pea by Chaudhary and Sharma (2003).

Kutty *et al.* (2003) found that yield was positively correlated with number of pods per plant, average weight of pods and pod length in vegetable cowpea.

Venkatesan *et al.* (2004) found positive association among days to flowering, plant height, number of pods per plant and pod length. Negative association was observed for number of pods per cluster with pods per plant, pod length and number of seeds per pod in cowpea.

2.3 PATH ANALYSIS

Path coefficient is a standardized partial regression coefficient, which measures the direct influence of one variable upon another and permits the separation of correlation coefficients into components of direct and indirect effects (Dewey and Lu, 1959). The information obtained from path analysis helps in indirect selection for genetic improvement of yield.

Tikka (1975) observed that number of clusters per plant and number of seeds per pod had direct positive effect on seed yield per plant.

Menon *et al.* (1977) reported that pods per plant and number of clusters per plant had direct effect on grain yield.

Studies conducted by Sohoo and Bharatwaj (1985) and Henry *et al.* (1986) indicated that number of pods per plant had high direct effect on grain yield.

Stafford and Seiler (1986) found that pods per plant and 100 seed weight had high direct effect on grain yield.

Singh *et al.* (1988) observed that plant height, number of branches and number of leaves per plant had direct effect on green forage yield.

Path analysis of green pod yield by Vijay (1988) indicated that pod number and seeds per pod exhibited positive direct effect on pod yield. Negative direct effect was observed for the traits viz., pod weight, number of clusters per plant, pod length and days to flowering.

Gipson (1990) found that pod length had direct positive effect on seed yield.

Path analysis by Lokesha and Shivashankar (1992) suggested clusters per plant had maximum positive direct effect and number of branches had maximum negative direct effect on seed yield.

Brindha *et al.* (1995) conducted path analysis and found that the pod length exerted the strongest positive direct effect on pod yield followed by pod weight.

Path analysis conducted by Saini *et al.* (2001b) revealed that number of pods per plant, number of branches per plant and early flowering had positive direct effect on grain yield.

Singh *et al.* (2002) revealed that days to 50 per cent flowering followed by number of clusters per plant, 100 seed weight and number of pods per plant had positive direct effect on seed yield in clusterbean while negative direct effect was observed for plant height.

Path analysis in garden pea by Chaudhary and Sharma (2003) revealed that number of grains per pod, pod length, number of pods per plant and 100 seed weight had high direct effect on pod yield while negative direct effect was exerted by days to 50 per cent flowering, number of pods per plant and number of grains per pod.

Kutty *et al.* (2003) found that in vegetable cowpea number of pods per plant followed by average weight of pods had high direct effect on yield while pod length had low direct effect.

2.4 GENETIC DIVERGENCE

Genetic divergence measures the degree of diversity present in a germplasm collection or genetic stock. Clustering of genotypes determines the relative proportion of each component character to the total divergence and groups the less divergent ones whereas more divergent ones are placed in different clusters. This helps to choose genetically divergent parents for hybridization to produce new gene combinations in F_2 and later generations.

Henry *et al.* (1986) in a study with 36 diverse genotypes reported that clustering was not related to geographical origin. The genotypes were divided into five clusters and cluster I had 27 genotypes.

In a divergence study by Henry and Krishna (1990) with 24 genotypes, cultivars were divided into 10 groups, which did not reliably reflect geographical origin.

Gipson and Balakrishnan (1992) grouped 56 genotypes into eight clusters including two single variety clusters. Clusters III and VIII showed high genetic divergence. Among 15 characters studied number of pods per plant and number of pods per cluster gave the highest contribution towards genetic divergence.

Lima *et al.* (2000) studied the genetic divergence among 30 cultivars and concluded that for the formation of base population aimed at intra population improvement, the cultivar pairs (205,142) and (142, 203) were most divergent.

Mitra *et al.* (2000) grouped 213 germplasm lines into 12 clusters and observed maximum genetic divergence between clusters V and IX whereas clusters III and VIII were the closest ones. Pods per plant exhibited highest contribution to divergence.

Saini *et al.* (2001a) in a genetic divergence study among 18 genotypes, showed that plant height contributed the most towards genetic divergence followed by grain yield per plant. The genotypes were grouped into five clusters and high genetic divergence was observed between clusters V and III followed by clusters III and I.

Singh *et al.* (2003) studied the degree of divergence in 60 genotypes and grouped them into three clusters. Cluster I contained 55 genotypes and III was a single genotype cluster. Maximum intercluster distance was observed between clusters II and III. Maximum intracluster distance was found in cluster II.

Venkatesan *et al.* (2004) grouped 20 genotypes of cowpea into six clusters. Maximum intracluster distance was given by V and minimum by II. Maximum intercluster distance was given by II and VI.

Materials and Methods

3. MATERIALS AND METHODS

The present study aimed at evaluating a collection of clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.) genotypes for yield and related characters was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during the period 2004. The materials used and methods adopted are discussed hereunder.

3.1 MATERIALS

The materials for the study comprised of 29 genotypes, which included the released variety Pusa Navbahar and a local cultivar from Tamil Nadu. The test entries are assigned accession numbers Ct 1 to Ct 29. The source and some of the important morphological features of the genotypes are presented in Table 1. The variation in pod characters is shown in Plate 1 and those in pod clusters is evident from Plate 2. The differences in branching are given in Plates 3 and 4.

3.2 METHODS

3.2.1 Layout and Conduct of the Experiment

The experimental crop was raised during the period July to November 2004. The 29 genotypes were planted in a field experiment in randomized block design with three replications. The land was well prepared incorporating farmyard manure at the rate of 20 t / ha. The field was divided into three blocks of 29 plots each. Treatments were allotted to the plots in each block at random. Plot size was 2.8 m^2. Spacing was 70 cm between rows and 20 cm between plants in a row. Fertilizers were applied at the rate of 20 kg N, 60 kg P_2O_5 and 80 kg K_2O per hectare.

Need based application of plant protection chemicals was done to protect the crop from pests and diseases. Plate 6 shows the general view of the experiment.

Table 1. Clusterbean genotypes used in the study, their sources and some of the morphological features

Acc No.	Genotypes	Source	Growth habit	Duration	Raceme clustering habit	Pod pubescence	Pod shape
Ct 1	IC 38-1	NBPGR, regional research station, Jodhpur	Indeterminate	Long	Clusters not at each node	Non hairy	Straight
Ct 2	IC 44-A	NBPGR, regional research station, Jodhpur	Indeterminate	Long	Clusters not at each node	Non hairy	Straight
Ct 3	IC 439	NBPGR, regional research station, Jodhpur	Determinate	Short	Clusters not at each node	Non hairy	Crescent
Ct 4	IC 3118/P1	NBPGR, regional research station, Jodhpur	Indeterminate	Long	Clusters not at each node	Hairy	Straight
Ct 5	IC 3267	NBPGR, regional research station, Jodhpur	Indeterminate	Long	Clusters not at each node	Non hairy	Straight
Ct 6	IC 3773	NBPGR, regional research station, Jodhpur	Determinate	Medium	Clusters not at each node	Non hairy	Straight
Ct 7	IC 8423	NBPGR, regional research station, Jodhpur	Indeterminate	Long	Clusters not at each node	Non hairy	Straight
Ct 8	IC 9007/P2	NBPGR, regional research station, Jodhpur	Indeterminate	Long	Clusters not at each node	Non hairy	Straight
Ct 9	IC 10327	NBPGR, regional research station, Jodhpur	Determinate	Short	Clusters not at each node	Non hairy	Straight
Ct 10	IC 10339	NBPGR, regional research station, Jodhpur	Determinate	Short	Clusters at each node	Non hairy	Straight
Ct 11	IC 10350	NBPGR, regional research station, Jodhpur	Determinate	Medium	Clusters not at each node	Non hairy	Straight
Ct 12	IC 10356	NBPGR, regional research station, Jodhpur	Determinate	Short	Clusters at each node	Non hairy	Straight
Ct 13	IC 11354	NBPGR, regional research station, Jodhpur	Indeterminate	Long	Clusters not at each node	Non hairy	Straight
Ct 14	IC 11357	NBPGR, regional research station, Jodhpur	Determinate	Medium	Clusters at each node	Non hairy	Straight
Ct 15	IC 11388	NBPGR, regional research station, Jodhpur	Determinate	Short	Clusters not at each node	Non hairy	Straight
Ct 16	IC 11704	NBPGR, regional research station, Jodhpur	Determinate	Short	Clusters not at each node	Non hairy	Straight

Table 1 Continued

Acc No.	Genotypes	Source	Growth habit	Duration	Raceme clustering habit	Pod pubescence	Pod shape
Ct 17	IC 13496	NBPGR, regional research station, Jodhpur	Determinate	Medium	Clusters not at each node	Non hairy	Straight
Ct 18	IC 33705	NBPGR, regional research station, Jodhpur	Indeterminate	Long	Clusters not at each node	Non hairy	Straight
Ct 19	IC 40040	NBPGR, regional research station, Jodhpur	Determinate	Medium	Clusters not at each node	Non hairy	Straight
Ct 20	IC 51063	NBPGR, regional research station, Jodhpur	Determinate	Medium	Clusters at each node	Non hairy	Crescent
Ct 21	PLG 519	NBPGR, regional research station, Jodhpur	Indeterminate	Long	Clusters at each node	Hairy	Straight
Ct 22	PLG 528	NBPGR, regional research station, Jodhpur	Determinate	Medium	Clusters not at each node	Non hairy	Straight
Ct 23	PLG 530	NBPGR, regional research station, Jodhpur	Determinate	Medium	Clusters not at each node	Non hairy	Straight
Ct 24	PLG 534	NBPGR, regional research station, Jodhpur	Indeterminate	Long	Clusters not at each node	Non hairy	Straight
Ct 25	Pusa Navbahar	NBPGR, regional research station, Jodhpur	Determinate	Short	Clusters at each node	Non hairy	Straight
Ct 26	Local variety	Villupuram District, Tamil Nadu	Determinate	Short	Clusters at each node	Non hairy	Straight
Ct 27	GJCBS 2000-6	JAU, Junagadh	Indeterminate	Long	Clusters at each node	Non hairy	Straight
Ct 28	GJCBS 2002-2	JAU, Junagadh	Indeterminate	Long	Clusters at each node	Non hairy	Straight
Ct 29	GJCBS 2003-1	JAU, Junagadh	Indeterminate	Long	Clusters at each node	Non hairy	Straight

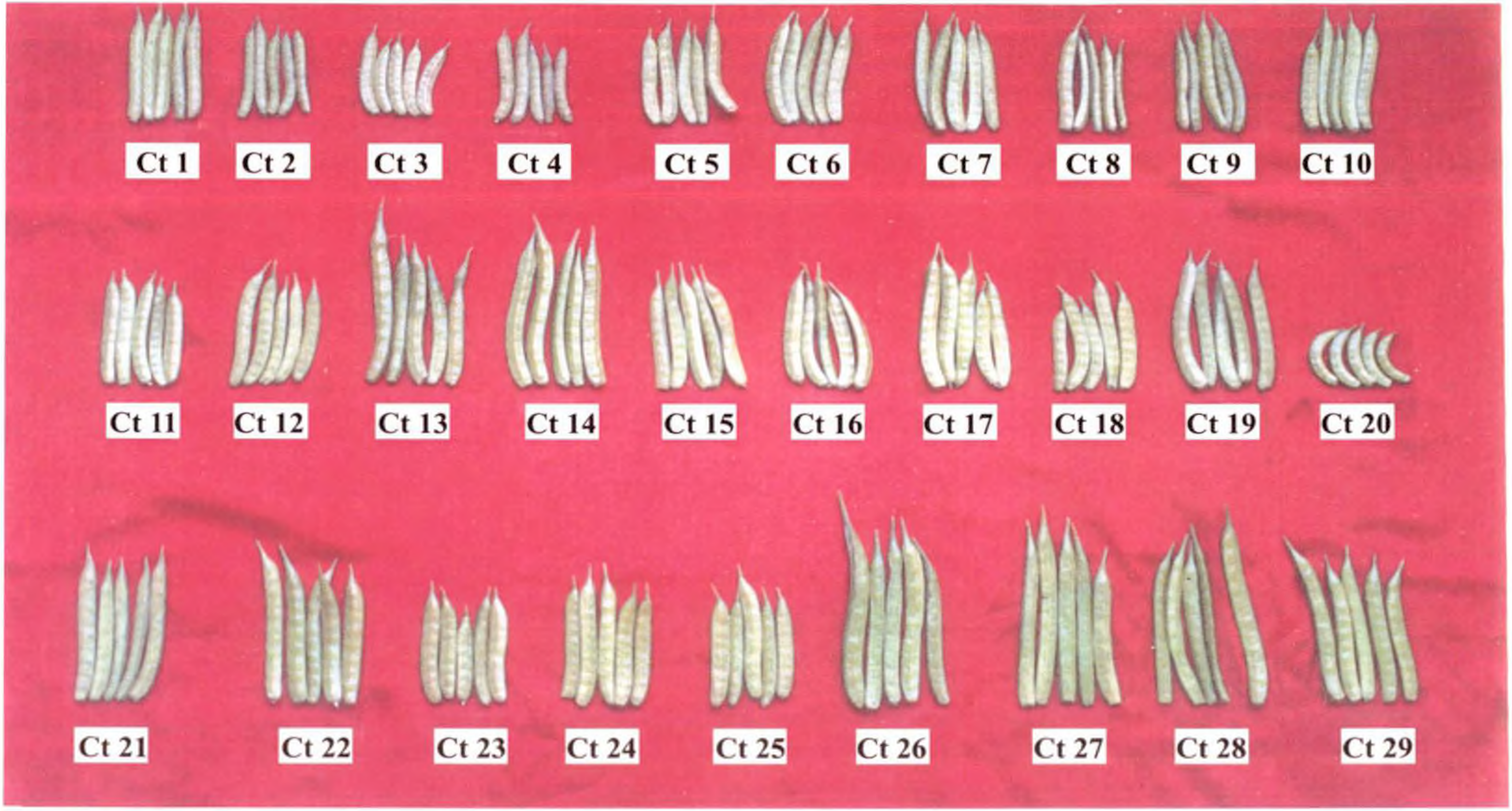


Plate 1. Variation in pod characters

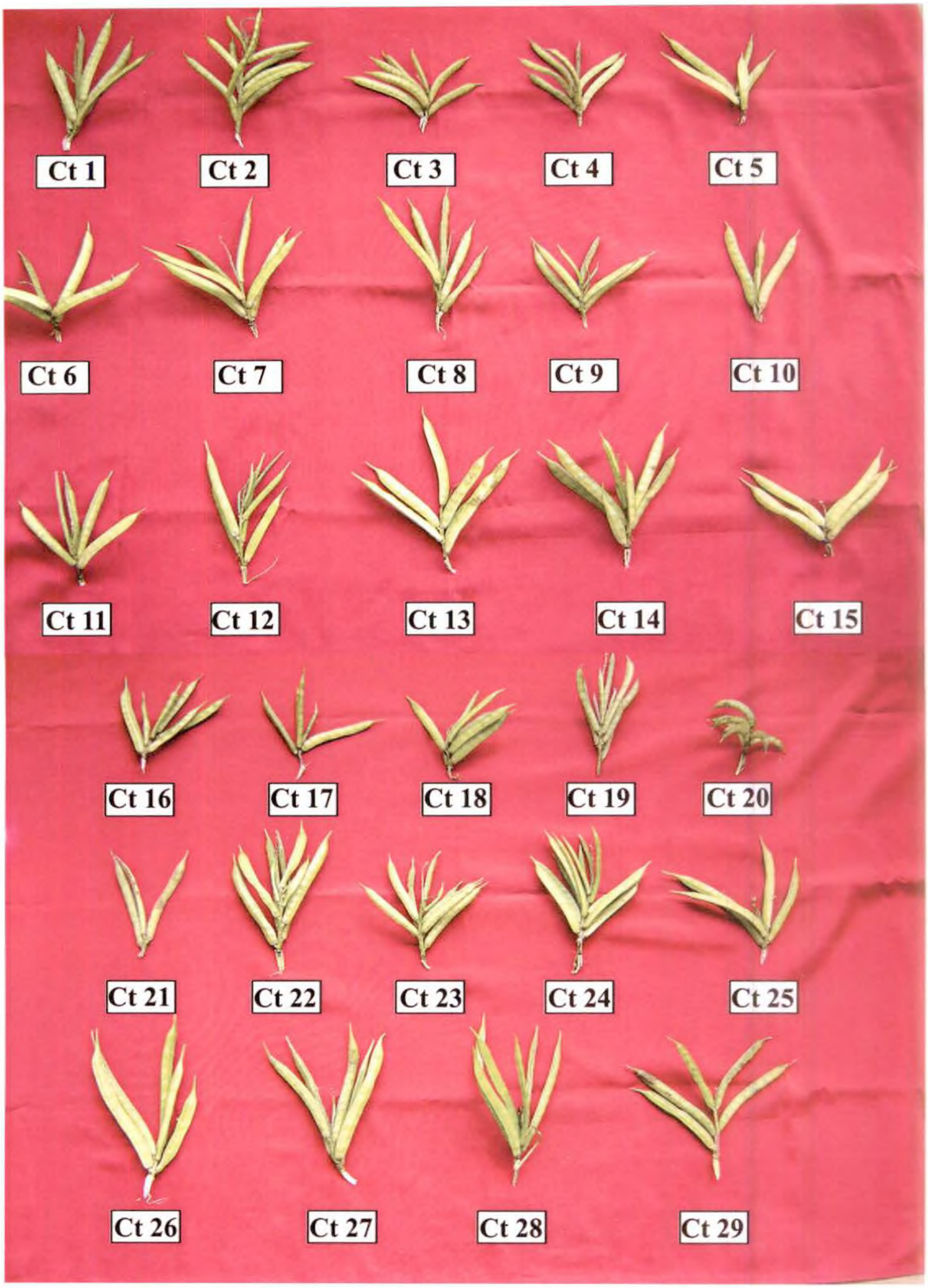


Plate 2. Variation in pod clusters

Plate 3. GJCBS 2002-2 Non-branching type

Plate 4. IC 11354 Branching type

Plate 5. Field view - Evaluation of genotypes for yield and yield component characters

3.2.2 Biometric Observations

a. Days to 50 per cent flowering

Number of days taken from sowing to 50 per cent of the plants in each plot to attain flowering was recorded.

The observations on the following characters were recorded from five randomly selected plants in each plot. Statistical analysis was done with mean values worked out thereafter.

b. Plant height

Length of main stem from ground level to its tip was recorded at peak harvest.

c. Number of primary branches

Primary branches were counted at the full maturity stage of the plant.

d. Number of pod clusters per plant

The number of pod clusters on each observational plant was recorded.

e. Number of pods per plant

Total number of pods harvested from each observational plant was separately counted and the average worked out.

f. Number of pods per cluster

The total number of pods in five randomly chosen clusters in the observational plants were counted and average worked out.

g. Yield of green pods per plant

Weight of pods from observational plants at each harvest was taken using a top loading balance and added to get the total yield and the average worked out.

h. Pod characters

Pod length (cm) and pod weight (g) at vegetable maturity stage and number of seeds per pod from dried pods were recorded from 10 randomly selected pods from each plot and mean value for each character worked out.

i. Incidence of pests and diseases

The crop was periodically examined for the incidence of pests and diseases.

3.2.3 Statistical Analysis

The data collected were subjected to the following statistical analyses.

3.2.3.1 Analysis of Variance

The analysis of variance was carried out for various characters (Panse and Sukhatme, 1967)

i. To test the significance of differences among the genotypes with respect to various characters and

ii. To estimate the variance components and other genetic parameters like coefficients of variation, heritability and genetic advance.

Estimation of components of variance

1. Variance (for a trait X)

Environmental variance, $\sigma^2 e_x = E_{xx}$

Genotypic variance, $\sigma^2 g_x = \dfrac{G_{xx} - E_{xx}}{r}$

Phenotypic variance, $\sigma^2 p_x = \sigma^2 g_x + \sigma^2 e_x$

where

E_{xx} = observed mean square for error

G_{xx} = observed mean square for genotype

2. Coefficient of variation

Phenotypic and genotypic coefficients of variations (PCV and GCV) for a trait X were estimated as suggested by Singh and Chaudhary (1979).

$$GCV = \frac{\sigma g_x}{\bar{X}} \times 100$$

$$PCV = \frac{\sigma p_x}{\bar{X}} \times 100$$

where

σg_x = genotypic standard deviation

σp_x = phenotypic standard deviation

$\bar{X}$ = mean of the character under study

3. Heritability (broad sense)

Heritability (H^2) was calculated to estimate the proportion of heritable component of variation

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

where H^2 is the heritability expressed in percentage (Jain, 1982).

Heritability was categorized as low (<30 per cent) moderate (31-60 per cent) and high (>60 per cent) as suggested by Johnson *et al.* (1955).

4. Genetic advance as percentage of mean

To estimate the change in the mean genotypic value of population brought about by selection, genetic advance is calculated as

$$\text{GA (as \% of mean)} = \frac{k\ H^2 \sigma p}{\underline{X}} \times 100$$

where k is the standardized selection differential with value 2.06 at 5 per cent selection intensity (Miller *et al.*, 1958).

3.2.3.2 Covariance Analysis

Covariance analysis was done for the estimation of correlation coefficients, path analysis and genetic divergence.

Table 2. Analysis of variance / covariance for two traits X and Y

Source	Degrees of freedom	Observed mean square for X	Expected mean square for X	Observed mean square for Y	Expected mean square for Y	Observed mean sum of products for X & Y	Expected mean sum of products for X & Y
Block	r-1	B_{xx}		B_{yy}		B_{xy}	
Genotype	v-1	G_{xx}	$\sigma^2e_x+\sigma^2g_x$	G_{yy}	$\sigma^2e_y+r\sigma^2g_y$	G_{xy}	$\sigma e_{xy}+r\sigma g_{xy}$
Error	(v-1)(r-1)	E_{xx}	σ^2e_x	E_{yy}	σe_{xy}	E_{xy}	σe_{xy}
Total	(vr-1)						

where r = number of replications

v = number of treatments

The covariances are estimated for two traits as

$$\text{Environmental covariance } (\sigma e_{xy}) = E_{xy}$$

$$\text{Genotypic covariance } (\sigma g_{xy}) = \frac{G_{xy} - E_{xy}}{r}$$

$$\text{Phenotypic covariance } (\sigma p_{xy}) = \sigma g_{xy} + \sigma e_{xy}$$

3.2.3.3 *Correlation Analysis*

The correlation coefficients (phenotypic, genotypic and environmental) were worked out as based on the formulae given by Singh and Chaudhary (1985).

$$\text{Genotypic correlation } (r_{gxy}) = \frac{\sigma g_{xy}}{\sigma g_x \times \sigma g_y}$$

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{\sigma p_{xy}}{\sigma p_x \times \sigma p_y}$$

$$\text{Environmental correlation } (r_{exy}) = \frac{\sigma e_{xy}}{\sigma e_x \times \sigma e_y}$$

3.2.3.4 *Path Analysis*

The path analysis was done by the method developed by Wright (1954) to study the cause and effect relationship among a system of variables which helps to measure the direct influence along each separate path in such a system and to find the degree to which the variation of a given effect is determined by each particular cause.

The simultaneous equations that give the estimates of path coefficients are as follows.

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ \cdot \\ \cdot \\ \cdot \\ r_{iy} \\ \cdot \\ \cdot \\ \cdot \\ r_{ky} \end{pmatrix} = \begin{pmatrix} 1 & r_{12} & r_{13} & \cdots & r_{1j} & \cdots & r_{1k} \\ & 1 & r_{23} & \cdots & r_{2j} & \cdots & r_{2k} \\ & & & & \cdot & & \cdot \\ & & & & \cdot & & \cdot \\ & & & & \cdot & & \cdot \\ & & & & r_{ij} & & r_{ik} \\ & & & & \cdot & & \cdot \\ & & & & \cdot & & \cdot \\ & & & & \cdot & & \cdot \\ & & & & & & 1 \end{pmatrix} \times \begin{pmatrix} P_1 \\ P_2 \\ \cdot \\ \cdot \\ \cdot \\ P_i \\ \cdot \\ \cdot \\ \cdot \\ P_k \end{pmatrix}$$

$$i.e., \underline{R}_y = \underset{\sim}{R}_x \cdot \underline{P}$$

$$\underline{P} \doteq \underset{\sim}{R}_x^{-1} \cdot \underline{R}_y$$

where R_y is the vector of r_{iy}, the genotypic correlation between i^{th} trait with yield Y.

$i,j = 1,2,\ldots k$

R_x is the matrix of r_{ij}, the genotypic correlation between i^{th} trait with j^{th} trait.

P_i = path coefficient of X_i

The residual factor (h) which measures the contribution of other factors not defined in the casual scheme was estimated by the formula

$$h = \sqrt{\left[1 - \sum_{i=1}^{k} P_i r_{iy}\right]}$$

Indirect effect of different characters on yield is obtained as Pirij for the ith character via jth character.

3.2.3.5 D^2 Analysis

Genetic divergence was studied using Mahalanobis D^2 statistic as described by Rao (1952). The genotypes were clustered by Tocher's method.

3.2.3.6 Selection Index

The various genotypes were discriminated based on nine characters using the selection index developed by Smith (1937) using the discriminant function of Fisher (1936).

The selection index is described by the function $I = b_1x_1 + b_2x_2 + \ldots + b_kx_k$. The function $H = a_1G_1 + a_2G_2 + \ldots + a_kG_k$ where H denotes the genetic worth of the plant and $G_1, G_2, \ldots G_k$ are the genotypic values of the plant with respect to the characters $X_1, X_2, \ldots X_k$. . The economic weightages assigned to each character is assumed to be equal to unity i.e., $a_1, a_2, \ldots a_k = 1$. The regression coefficients $b_1, b_2, \ldots b_k$ are estimated in such a way that the correlation between H and I is maximum. The procedure will reduce to an equation of the form $b = P^{-1}G_a$, where P is the phenotypic and G is the genotypic variance covariance matrix respectively from which the b values were solved out.

Results

4. RESULTS

Twenty nine genotypes of clusterbean were collected and evaluated at the College of Agriculture, Vellayani. Data collected on 10 characters were subjected to statistical analysis. The results are presented in this chapter.

4.1 ANALYSIS OF VARIANCE

The analysis of variance (Table 3) revealed significant differences among the 29 varieties for all the characters studied. These characters include days to 50 per cent flowering, plant height, number of primary branches, number of pod clusters per plant, number of pods per cluster, pod weight, pod length, number of seeds per pod, number of pods per plant, yield per plant.

4.2 MEAN PERFORMANCE OF THE GENOTYPES

The mean values of each of the 29 genotypes for the 10 characters studied are presented in Table 4. Days to 50 per cent flowering ranged from 29.33 to 33.00 days and Ct 20 was the earliest. Ct 3, Ct 5, Ct 6, Ct 10, Ct 12, Ct 16, Ct 17, Ct 20, Ct 22, Ct 23 and Ct 25 were statistically on par with it. Ct 29, Ct 28, Ct 27, Ct 19 and Ct 2 were the latest to attain 50 per cent flowering. Ct 9 and Ct 4 were statistically on par with them.

The growth characters viz., plant height and number of primary branches showed wide variation among the cultivars. Plant height ranged from 78.07 to 161.53 cm. The tallest was Ct 1 with Ct 28 statistically on par with it. Ct 15 was the shortest and no other cultivar was statistically on par with it.

The genotypes could be categorized as branching and non-branching types. Among the 21 branching types the range was 5.60 to

12.53 for Ct 23 and Ct 16 respectively and both were significantly different from all the other cultivars.

The genotype Ct 11 had the maximum number of pod clusters per plant (71.53) and none was statistically on par with it. The minimum number of pod clusters per plant was recorded by Ct 27 (9.40). Ct 22 and Ct 24 were statistically on par with Ct 27.

Regarding number of pods per cluster, the highest value (12.47) was for Ct 2 and none of the genotypes was statistically on par with it. The least value (4.33) was recorded by Ct 21. However, Ct 8, Ct 9, Ct 10 and Ct 17 were statistically on par with it.

Pod characters viz., pod weight, pod length and number of seeds per pod differed significantly among the genotypes. Pod weight ranged from 1.47 (Ct 20) to 4.77 (Ct 26). Ct 25, Ct 27, Ct 28 were statistically on par with Ct 3 and Ct 26 was statistically on par with Ct 20. The maximum value for pod length (14.39 cm) was shown by Ct 28 and Ct 13, Ct 26 and Ct 27 were statistically on par with it. The minimum value was recorded by Ct 20 (4.94 cm). None of the varieties was statistically on par with Ct 20 for the character. Number of seeds per pod was maximum for Ct 7 (9.97) and Ct 12, Ct 15, Ct 17, Ct 22 and Ct 28 were on par with it. Ct 3 gave the minimum number of seeds per pod (7.10) and showed significant difference from all the other genotypes.

The number of pods per plant was the highest (303.07) for Ct 11. The lowest value for number of pods per plant was recorded by Ct 27 (45.53). None of the varieties was statistically on par with either the minimum or maximum value for the character.

The yield per plant ranged from 117.33g (Ct 8) to 383.33g (Ct 11). Significantly Ct 11 (Plate 6) was superior to other varieties in pod yield.

Table 3. Analysis of variance of 10 characters in 29 clusterbean genotypes

Sl. No	Character	Mean square		
		Replication	Genotypes	Error
1	Days to 50 per cent flowering	0.355	5.165**	0.261
2	Plant height	119.750*	1591.808**	35.721
3	Number of primary branches◈	0.099	7.906**	0.233
4	Number of pod clusters per plant	32.842*	414.409**	7.769
5	Number of pods per cluster	0.723*	10.957**	0.224
6	Pod weight	0.028	1.987**	0.068
7	Pod length	0.619	13.186**	0.659
8	Number of seeds per pod	0.003	1.412**	0.048
9	Number of pods per plant	164.500	7547.750**	266.984
10	Yield per plant	66.250	11041.810**	457.013

* Significant at 5 per cent level **Significant at 1 per cent level

◈Excluding non-branching types

Table 4. Mean values for 10 biometric characters in 29 clusterbean genotypes

Genotypes	Days to 50% flowering	Plant height (cm)	Number of primary branches	Number of pod clusters per plant	Number of pods per cluster	Pod weight (g)	Pod length (cm)	Number of seeds per pod	Number of pods per plant	Yield per plant (g)
Ct 1	31.33	161.53	7.47	25.93	6.33	3.30	9.61	9.30	84.07	180.00
Ct 2	33.00	135.47	7.53	17.13	12.47	2.77	9.78	9.47	91.27	161.33
Ct 3	29.67	87.87	6.60	25.13	6.33	1.63	7.44	7.10	173.73	172.00
Ct 4	32.33	122.13	8.00	24.00	7.13	2.37	8.89	8.67	96.07	155.33
Ct 5	29.67	121.87	7.67	30.80	6.27	3.40	9.34	9.27	116.80	160.00
Ct 6	29.67	140.73	7.20	23.20	5.13	3.30	9.93	9.10	97.87	247.33
Ct 7	31.33	103.87	8.53	31.67	6.00	3.57	9.57	9.97	156.80	341.33
Ct 8	31.00	94.60	8.27	30.53	5.07	2.17	8.21	8.27	95.80	117.33
Ct 9	32.33	93.00	7.73	39.33	4.40	3.13	9.47	9.27	161.53	200.67
Ct 10	29.67	103.27	10.93	26.20	4.40	2.97	8.86	9.20	95.60	205.33
Ct 11	31.33	92.87	9.33	71.53	5.53	3.10	9.26	9.37	303.07	383.33
Ct 12	29.67	91.13	8.40	24.73	6.00	3.30	9.42	9.77	128.07	206.67
Ct 13	31.00	102.67	11.00	23.40	7.27	3.07	13.28	8.90	159.40	246.67
Ct 14	31.67	103.80	7.60	32.13	5.47	2.97	12.15	8.73	138.87	216.00
Ct 15	31.67	78.07	7.67	26.07	5.40	2.97	9.67	9.80	115.07	198.67
Ct 16	29.67	95.20	12.53	26.40	5.20	2.57	9.73	8.23	133.33	184.00
Ct 17	29.67	98.13	9.33	28.67	4.80	3.07	11.13	9.80	120.93	270.00
Ct 18	32.00	92.80	7.40	18.60	7.53	2.17	8.38	7.90	111.00	164.00
Ct 19	33.00	125.27	0.00	19.80	8.67	3.13	11.33	8.70	149.53	211.33
Ct 20	29.67	135.87	7.53	40.33	7.73	1.47	4.94	8.03	212.87	143.33
Ct 21	31.00	102.20	6.67	24.13	4.33	3.17	10.76	9.20	92.87	172.00
Ct 22	29.67	97.47	0.00	11.47	10.07	4.23	11.71	9.73	77.87	252.00
Ct 23	29.67	135.47	5.60	22.67	5.40	2.80	8.95	8.10	112.73	262.00
Ct 24	30.67	94.00	0.00	10.20	10.40	3.23	9.08	9.30	104.47	234.67
Ct 25	29.67	113.00	0.00	15.80	5.87	4.53	10.28	8.80	84.20	276.00
Ct 26	29.33	121.53	0.00	15.47	5.53	4.77	14.36	9.53	78.40	236.67
Ct 27	33.00	143.87	0.00	9.40	5.27	4.67	14.17	9.60	45.53	218.67
Ct 28	33.00	159.00	0.00	17.73	5.67	4.50	14.39	9.63	72.40	155.33
Ct 29	33.00	148.33	0.00	16.80	6.67	3.13	11.29	8.83	85.07	118.00
CD (0.05)	0.837	9.784	0.798	4.563	0.774	0.426	1.329	0.360	26.749	34.997

Plate 6. IC 10350 - The highest green pod yielder

4.3 VARIABILITY STUDIES

The phenotypic, genotypic and environmental variance and coefficients of variation for the 10 characters are presented in Table 5. Fig 1 shows the phenotypic and genotypic coefficients of variation for the 10 characters.

Number of pod clusters per plant showed the maximum value for GCV (46.29) followed by number of pods per plant (40.88), number of pods per cluster (29.46) and yield per plant (28.29). GCV values were low for days to 50 per cent flowering (4.13) and number of seeds per pod (7.48).

The highest PCV was observed for number of pod clusters per plant (47.60) followed by number of pods per plant (43.06), number of pods per cluster (30.37) and yield per plant (30.06). The magnitude of PCV was low for days to 50 per cent flowering and number of seeds per pod.

The difference between phenotypic and genotypic coefficients of variation was least for days to 50 per cent flowering (0.31%) succeeded by number of seeds per pod (0.38%) and was relatively high for number of pods per plant (2.18%) and yield per plant (1.77%).

4.4 HERITABILITY AND GENETIC ADVANCE

The estimates of heritability and genetic advance are given in Table 6 and Fig 2. All the characters showed high heritability and the highest estimate was recorded by number of pod clusters per plant (94.58%) followed by number of pods per cluster (94.11%), plant height (93.56%), number of primary branches (91.65%) and pod weight (90.43%). Among the characters studied the minimum value was observed for days to 50 per cent flowering (86.22%) succeeded by pod length (86.37%).

Expected genetic advance as percentage of mean was the highest for number of pod clusters per plant (92.72) followed by number of pods per plant (79.92), number of pods per cluster (58.88), yield per plant

Table 5. Components of variance for the ten characters in clusterbean

Sl. No	Character	Mean± SE	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	GCV%	PCV%
1	Days to 50 per cent flowering	30.98±0.295	1.90	1.63	0.26	4.13	4.44
2	Plant height	113.62±3.451	554.42	518.70	35.72	20.02	20.73
3	Number of primary branches◈	8.23±0.237	2.80	2.56	0.23	19.43	20.29
4	Number of pod clusters per plant	25.15±1.609	143.32	135.55	7.77	46.29	47.60
5	Number of pods per cluster	6.42±0.273	3.80	3.58	0.22	29.46	30.37
6	Pod weight	3.15±0.150	0.71	0.64	0.07	25.40	26.71
7	Pod length	10.18±0.469	4.83	4.18	0.66	22.63	24.35
8	Number of seeds per pod	9.02±0.127	0.50	0.45	0.05	7.48	7.86
9	Number of pods per plant	120.52±9.434	2693.91	2426.92	266.98	40.88	43.06
10	Yield per plant	210.00±12.342	3985.28	3528.27	457.01	28.29	30.06

$\sigma^2 g$ – genotypic variance

$\sigma^2 p$ – phenotypic variance

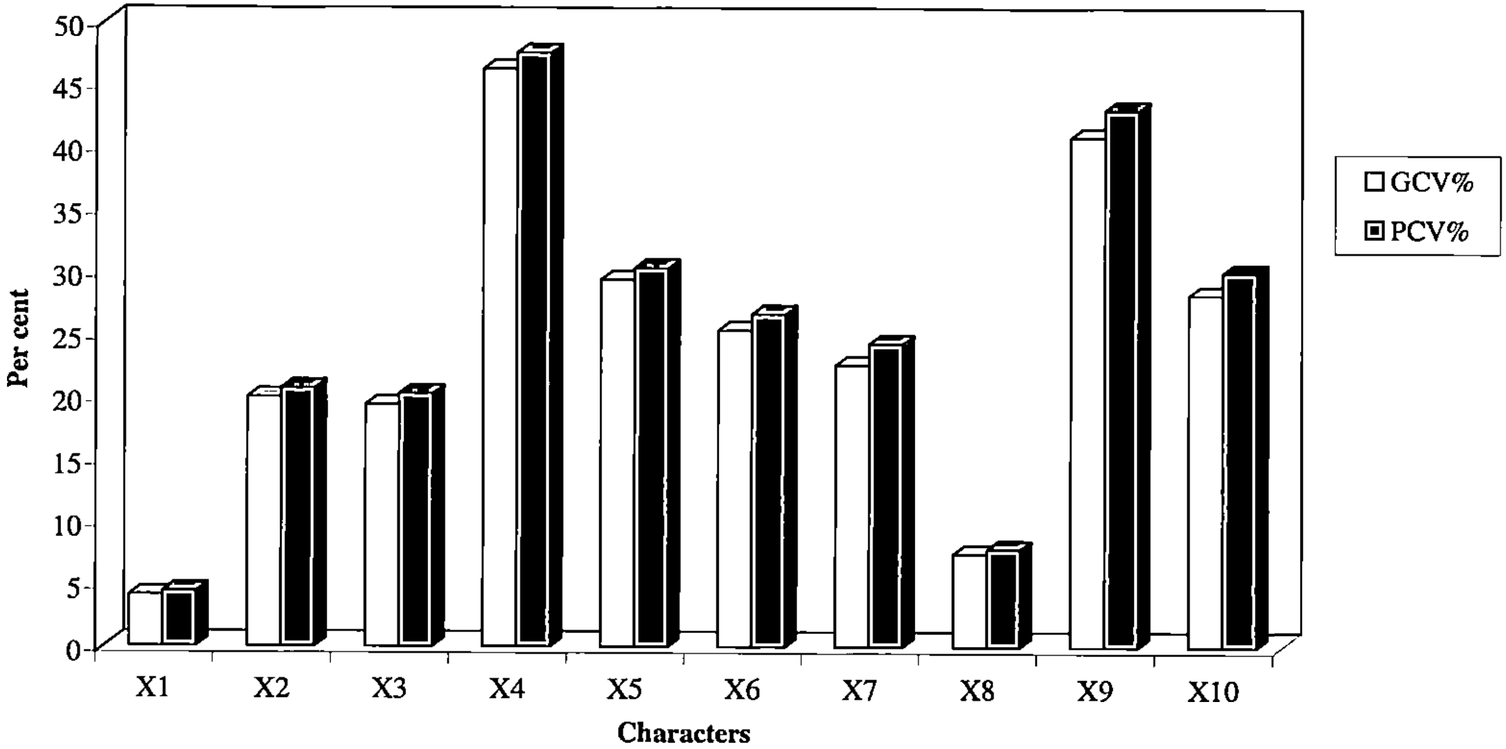
$\sigma^2 e$ – environmental variance

SE – standard error of mean

GCV – genotypic coefficient of variation

PCV – phenotypic coefficient of variation

◈Excluding non-branching types



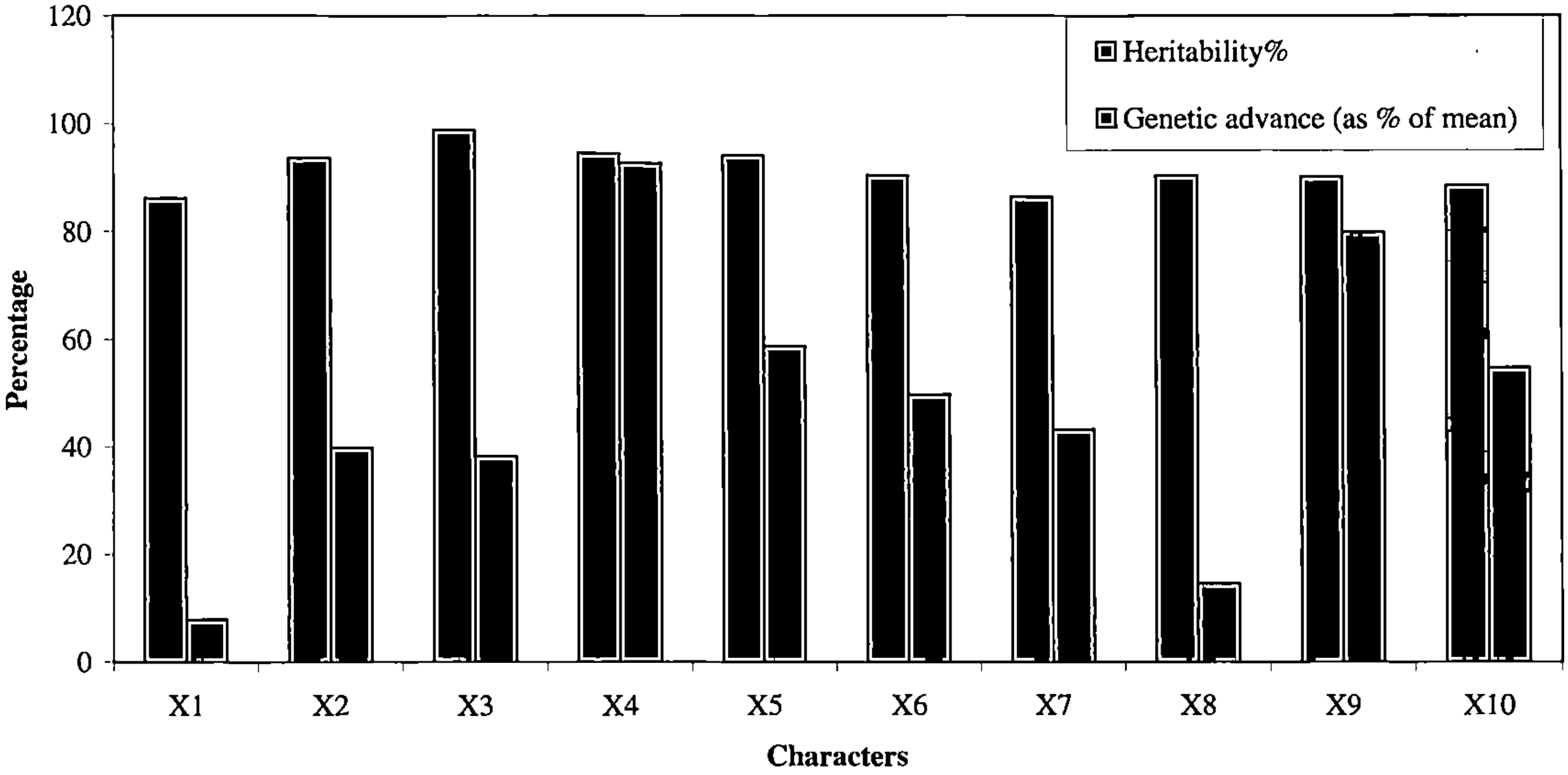
X1	Days to 50 percent flowering	X6	Pod weight
X2	Plant height	X7	Pod length
X3	Number of primary branches	X8	Number of seeds per pod
X4	Number of pod clusters per plant	X9	Number of pods per plant
X5	Number of pods per cluster	X10	Yield/plant

Fig. 1. Phenotypic and genotypic coefficients of variation for different characters

Table 6. Heritability and genetic advance for the 10 characters in clusterbean

Sl. No	Character	Heritability (%)	Genetic advance (at 5% selection)	Genetic advance (as % of mean)
1	Days to 50 per cent flowering	86.22	2.44	7.88
2	Plant height	93.56	45.38	39.95
3	Number of primary branches◈	91.65	8.16	38.32
4	Number of pod clusters per plant	94.58	23.32	92.72
5	Number of pods per cluster	94.11	3.78	58.88
6	Pod weight	90.43	1.57	49.84
7	Pod length	86.37	3.91	43.30
8	Number of seeds per pod	90.36	1.32	14.63
9	Number of pods per plant	90.09	96.32	79.92
10	Yield/plant	88.53	115.13	54.83

◈Excluding non-branching types



X1	Days to 50 percent flowering	X6	Pod weight
X2	Plant height	X7	Pod length
X3	Number of primary branches	X8	Number of seeds per pod
X4	Number of pod clusters per plant	X9	Number of pods per plant
X5	Number of pods per cluster	X10	Yield/plant

Fig. 2. Heritability and genetic advance (as percentage of mean)

(54.83), pod weight (49.84), pod length (43.30), plant height (39.95) and number of primary branches (38.32). Number of seeds per pod and days to 50 per cent flowering exhibited low values with the least value of 7.88 for days to 50 per cent flowering.

High heritability coupled with high genetic advance was observed for plant height, number of pod clusters per plant, number of pods per cluster, pod weight, pod length, number of pods per plant and yield per plant.

4.5 CORRELATION ANALYSIS

The phenotypic, genotypic and environmental correlation coefficients were estimated for all the pairs of characters. The results are given under the following subtitles.

a. Correlation between yield and other characters

b. Correlation among the yield component characters

a. Correlation between yield and other characters

The phenotypic, genotypic and environmental correlation coefficients of yield with other characters are presented in Table 7. Correlation diagram is given with genotypic correlation coefficients between yield and other characters as Fig 3.

Significant positive phenotypic correlation was recorded for number of pods per plant (0.3969) and number of seeds per pod (0.3527).

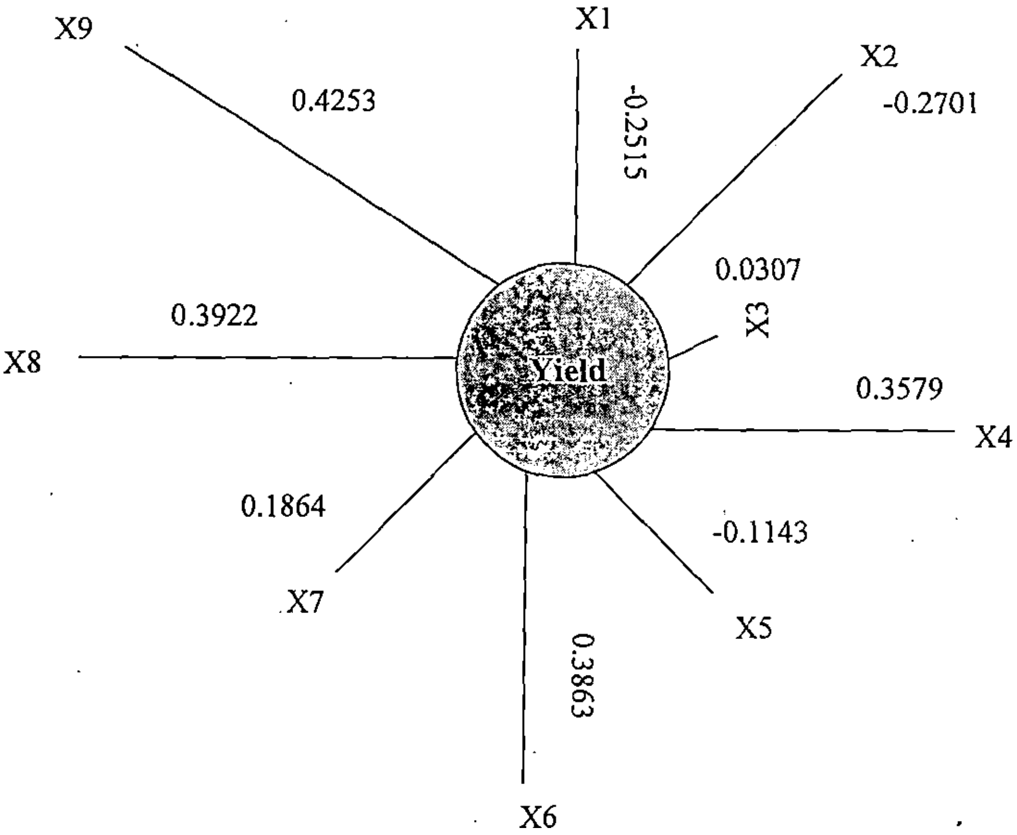
Genotypic correlation was found to be positive and significant for number of pods per plant (0.4253), number of seeds per pod (0.3922), pod weight (0.3863) and number of pod clusters per plant (0.3579).

Environmental correlation was non significant for all the characters.

Table 7. Phenotypic, genotypic and environmental correlation coefficients between pod yield per plant and other characters

Sl. No	Character	Correlation coefficient		
		Phenotypic	Genotypic	Environmental
1	Days to 50 per cent flowering	-0.2486	-0.2515	-0.2292
2	Plant height	-0.2320	-0.2701	0.1610
3	Number of primary branches	0.0355	0.0307	0.1969
4	Number of pod clusters per plant	0.3221	0.3579*	-0.0685
5	Number of pods per cluster	-0.1047	-0.1143	-0.0040
6	Pod weight	0.3479	0.3863*	0.0215
7	Pod length	0.1422	0.1864	-0.1665
8	Number of seeds per pod	0.3527*	0.3922*	0.0181
9	Number of pods per plant	0.3969*	0.4253*	0.1603

* Significant at 5 per cent level **Significant at 1 per cent level



Variables
X1. Days to 50 percent flowering
X2. Plant height
X3. Number of primary branches
X4. Number of pod clusters per plant
X5. Number of pods per cluster
X6. Pod weight
X7. Pod length
X8. Number of seeds per pod
X9. Number of pods per plant

Fig 3. Genotypic correlation of yield with other characters (not to scale)

b. Correlation among the yield component characters

The phenotypic, genotypic and environmental correlation coefficients among yield component characters are presented in Tables 8, 9 and 10 respectively.

Days to 50 per cent flowering

Correlation coefficients of days to 50 per cent flowering with other characters at phenotypic, genotypic and environmental levels were found to be non significant.

Plant height

Significant negative correlation was observed with number of primary branches both at phenotypic (-0.3776) and genotypic (-0.3945) levels.

Number of primary branches

High positive phenotypic correlation was found with number of pod clusters per plant (0.5606) and for number of pods per plant (0.4268) while high negative correlation was seen with pod weight (-0.5840) followed by pod length (-0.4474) and plant height (-0.3776). High negative genotypic correlation was observed for pod weight (-0.6173), pod length (-0.4737) and plant height (-0.3945) and positive genotypic correlation was shown by number of pod clusters per plant (0.5780) and number of pods per plant (0.4496).

Number of pod clusters per plant

High positive phenotypic correlation was seen with number of pods per plant (0.8178) and number of primary branches (0.5606) and a negative correlation with pod length (-0.3843). Positive genotypic correlation was observed with number of pods per plant (0.8846) followed by number of primary branches (0.5780) while negative correlation was found with pod length (-0.4148) and pod weight (-0.3854).

Table 8. Phenotypic correlation coefficients among the yield component characters

Character	Days to 50% flowering	Plant height	Number of primary branches	Number of pod clusters per plant	Number of pods per cluster	Pod weight	Pod length	Number of seeds per pod	Number of pods per plant
Days to 50 percent flowering	1.0000								
Plant height	0.2914	1.0000							
Number of primary branches	-0.2285	-0.3776*	1.0000						
Number of pod clusters per plant	-0.0696	-0.2533	0.5606**	1.0000					
Number of pods per cluster	0.2048	0.1124	-0.2888	-0.3179	1.0000				
Pod weight	0.0635	0.2708	-0.5840**	-0.3413	-0.0824	1.0000			
Pod length	0.2985	0.2333	-0.4474*	-0.3843*	-0.1064	0.7277**	1.0000		
Number of seeds per pod	0.1522	0.0573	-0.1538	-0.0530	-0.0023	0.6330**	0.4816**	1.0000	
Number of pods per plant	-0.0786	-0.3345	0.4268**	0.8178**	-0.0402	-0.4311*	-0.4029*	-0.2037	1.0000

* Significant at 5 per cent level **Significant at 1 per cent level

Table 9. Genotypic correlation coefficients among the yield component characters

Character	Days to 50% flowering	Plant height	Number of primary branches	Number of pod clusters per plant	Number of pods per cluster	Pod weight	Pod length	Number of seeds per pod	Number of pods per plant
Days to 50 percent flowering	1.0000								
Plant height	0.3150	1.0000							
Number of primary branches	-0.2447	-0.3945*	1.0000						
Number of pod clusters per plant	-0.0802	-0.2746	0.5780**	1.0000					
Number of pods per cluster	0.2313	0.1065	-0.3001	-0.3531	1.0000				
Pod weight	0.0637	0.2866	-0.6173**	-0.3854*	-0.0976	1.0000			
Pod length	0.2990	0.2815	-0.4737**	-0.4148*	-0.0862	0.8244**	1.0000		
Number of seeds per pod	0.1432	0.0677	-0.1587	-0.0549	0.0083	0.7193**	0.5121**	1.0000	
Number of pods per plant	-0.1237	-0.3882	0.4496*	0.8846**	-0.0628	-0.4767**	-0.4483**	-0.2395	1.0000

* Significant at 5 per cent level **Significant at 1 per cent level

Table 10. Environmental correlation coefficients among the yield component characters

Character	Days to 50% flowering	Plant height	Number of primary branches	Number of pod clusters per plant	Number of pods per cluster	Pod weight	Pod length	Number of seeds per pod	Number of pods per plant
Days to 50 percent flowering	1.0000								
Plant height	0.0906	1.0000							
Number of primary branches	-0.0657	0.0754	1.0000						
Number of pod clusters per plant	0.0329	0.0843	0.0589	1.0000					
Number of pods per cluster	-0.0391	0.2018	0.0309	0.2709	1.0000				
Pod weight	0.0638	0.0924	0.0004	0.2105	0.1017	1.0000			
Pod length	0.2953	-0.2106	-0.2500	-0.1101	-0.3198	-0.0071	1.0000		
Number of seeds per pod	0.2235	-0.0623	-0.1154	-0.0313	-0.1322	-0.1799	0.2547	1.0000	
Number of pods per plant	0.2606	0.2744	0.0742	0.0169	0.2306	-0.0082	-0.0637	0.1269	1.0000

* Significant at 5 per cent level **Significant at 1 per cent level

Number of pods per cluster

Phenotypic, genotypic and environmental correlation coefficients were non significant with all the other yield components

Pod weight

High positive phenotypic correlation was found with pod length (0.7277) followed by number of seeds per pod (0.6330) and high negative correlation was seen with number of primary branches (-0.5840) and number of pods per plant (-0.4311). High positive genotypic correlation was registered by pod length (0.8244) followed by number of seeds per pod (0.7193) and high negative correlation was given by number of primary branches (-0.6173), number of pods per plant (-0.4767) and number of pod clusters per plant (-0.3854).

Pod length

Pod length showed high positive phenotypic correlation with pod weight (0.7277) and number of seeds per pod (0.4816) and was negative with number of pods per plant (-0.4029). At the genotypic level, positive correlation was high for pod weight (0.8244) and number of seeds per pod (0.5121) and negative correlation was recorded for number of pods per plant (-0.4483).

Number of seeds per pod

Number of seeds per pod showed positive phenotypic correlation with pod length (0.4816) and pod weight (0.6330). At genotypic level, the positive correlation was found with pod weight (0.7193) and pod length (0.5121).

Number of pods per plant

Number of pods per plant showed high positive phenotypic correlation with number of pod clusters per plant (0.8178) and number of primary branches (0.4268) while the correlation was negative with pod weight (-0.4311) and pod length (-0.4029). Genotypic correlation was positive and high with number of pod clusters per plant (0.8846) and number of primary branches (0.4496). It was negative with pod weight (-0.4767) and pod length (-0.4483).

4.6 PATH ANALYSIS

The genotypic correlation coefficients of yield with yield contributing characters were partitioned into different components to find the direct and indirect contribution of each character to green pod yield (Table 11). Path coefficient analysis was done taking into account the characters having high genotypic correlation with yield viz., days to 50 per cent flowering, plant height, number of pod clusters per plant, pod weight, number of seeds per pod and number of pods per plant.

The direct effect and correlation were positive for number of pods per plant, pod weight and number of seeds per pod and both were negative for days to 50 per cent flowering and plant height. Number of pod clusters per plant showed positive correlation but negative direct effect.

Number of pods per plant had the highest direct effect (1.0394) as well as high positive genotypic correlation (0.4253) with yield. The negative indirect effects were high for number of pod clusters per plant (-0.3169) and pod weight (-0.3240), which accounted for the high direct effect.

Days to 50 per cent flowering and plant height expressed a negative direct effect and negative genotypic correlation with yield. Negative genotypic correlation of these characters with yield is due to their high negative indirect effect via number of pods per plant.

Number of pod clusters per plant had negative direct effect (-0.3583) and positive genotypic correlation (0.3579) but had high indirect effect (0.9195) via number of pods per plant, which nearly accounts for the total correlation.

Table 11. Direct and indirect effect of yield component characters on yield

Characters	Days to 50% flowering	Plant height	Number of pod clusters per plant	Pod weight	Number of seeds per pod	Number of pods per plant	Genotypic correlation with yield
Days to 50% flowering	-0.1831	-0.0357	0.0287	0.0433	0.0238	-0.1286	-0.2515
Plant height	-0.0577	-0.1134	0.0984	0.1948	0.0113	-0.4035	-0.2701
Number of pod clusters per plant	0.0147	0.0311	-0.3583	-0.2400	-0.0091	0.9195	0.3579
Pod weight	-0.0117	-0.0325	0.1265	0.6797	0.1197	-0.4955	0.3863
Number of seeds per pod	-0.0262	-0.0077	0.0197	0.4889	0.1664	-0.2489	0.3922
Number of pods per plant	0.0226	0.0440	-0.3169	-0.3240	-0.0399	1.0394	0.4253

$h^2 = 0.2816$

The direct effect of pod weight is positive and the correlation is positive and high (0.6797) and the correlation is also positive (0.3863).

The direct effect of number of seeds per pod is positive (0.1664). The correlation is also positive (0.3922).

Number of pods per plant and pod weight are the main characters which influence the yield directly and indirectly. Hence these characters may be considered during selection programmes to identify high yielding clusterbean genotypes.

The residual effect (h^2 = 0.2816) indicates that the selected characters explain the total correlation well and the remaining characters have only minor contribution in the variability of pod yield.

4.7 GENETIC DIVERGENCE ANALYSIS

Following Mahalanobis statistic, the 29 genotypes of clusterbean were subjected to D^2 analysis based on the 10 characters *viz.*, days to 50 per cent flowering, plant height, number of primary branches, number of pod clusters per plant, number of pods per cluster, pod weight, pod length, number of seeds per pod, number of pods per plant, yield per plant.

The 29 genotypes study were grouped into four clusters (Table 12).

Cluster II was having 10 genotypes followed by cluster I and cluster III with 9 genotypes each. Cluster IV had only one genotype.

The cluster means of the 10 characters are presented in Table 13.

Cluster I showed the highest cluster mean for days to 50 per cent flowering (31.81), plant height (126.44 cm) and number of pods per cluster (6.83) and lowest for number of primary branches (7.57)

The maximum value of cluster mean for pod weight (3.70g) and pod length (10.80) was recorded in cluster II.

The highest cluster mean for number of primary branches (9.93), number of pod clusters per plant (71.53), number of seeds per pod (9.37),

Table 12. Clustering pattern

Clusters	Number of genotypes	Accessions
I	9	Ct 1, Ct 2, Ct 4, Ct 5, Ct 8, Ct 18, Ct 21, Ct 28, Ct 29
II	10	Ct 6, Ct 7, Ct 10, Ct 17, Ct 22, Ct 23, Ct 24, Ct 25, Ct 26, Ct 27
III	9	Ct 3, Ct 9, Ct 12, Ct 13, Ct 14, Ct 15, Ct 16, Ct 19, Ct 20
IV	1	Ct 11

Table 13. Cluster means for the various characters

Character	Clusters			
	I	II	III	IV
Days to 50 per cent flowering	31.81	30.23	30.93	31.33
Plant height	126.44	115.03	101.43	92.87
Number of primary branches◈	7.57	8.32	8.63	9.93
Number of pod clusters per plant	22.85	19.47	28.59	71.53
Number of pods per cluster	6.83	6.29	6.27	5.53
Pod weight	3.00	3.70	2.69	3.10
Pod length	10.07	10.80	9.71	9.26
Number of seeds per pod	8.95	9.31	8.72	9.37
Number of pods per plant	93.93	97.44	152.49	303.07
Yield per plant	153.70	254.40	197.70	383.33

◈Excluding non-branching types

number of pods per plant (303.07) and yield per plant (383.33g) and the lowest cluster mean for plant height (92.87 cm), number of pods per cluster (5.53) and pod length (9.26 cm) was recorded by cluster IV.

Cluster II exhibited the minimum value for days to 50 per cent flowering (30.23) and number of pod clusters per plant (19.47) and cluster I for number of pods per plant (93.93) and yield per plant (153.70g).

Cluster III recorded the minimum value for pod weight (2.69g) and number of seeds per pod (8.72)

The average inter and intracluster distances are furnished in Table 14.

The average inter and intracluster distances were estimated based on the total D^2 values. The intracluster distances varied from 172.17 to 239.64 whereas the intercluster distances ranged from 365.98 to 1004.02. The minimum intracluster distance was observed in cluster I (172.17). The maximum intercluster distance was noticed between clusters I and IV (1004.02) while the minimum was between clusters II and III (365.98).

The relative contribution of different characters to genetic divergence showed that yield per plant contributed the maximum (50.98 per cent) followed by number of pods per plant (38.42 per cent) and plant height (10.59 per cent). The rest of the traits did not contribute to total divergence (Table 15).

4.8 SELECTION INDEX

Discriminant function technique was adopted for the construction of selection index for yield using pod yield per plant and the component characters viz., days to 50 per cent flowering, plant height, number of primary branches, number of pod clusters per plant, number of pods per cluster, pod weight, pod length, number of seeds per pod and number of pods per plant.

Table 14. Average intra and intercluster distances (D values)

Clusters	I	II	III	IV
I	172.17	389.32	521.92	1004.02
II		239.64	365.98	816.45
III			220.29	768.30
IV				0

Table 15. Contribution of different characters towards divergence

Sl. No	Characters	% Contribution (1^{st} rank)	% Contribution (2^{nd} rank)
1	Days to 50 percent flowering	0.00	0.00
2	Plant height	10.59	26.11
3	Number of primary branches	0.00	0.25
4	Number of pod clusters per plant	0.00	3.94
5	Number of pods per cluster	0.00	0.98
6	Pod weight	0.00	0.00
7	Pod length	0.00	0.00
8	Number of seeds per pod	0.00	0.00
9	Number of pods per plant	38.42	39.16
10	Yield per plant	50.98	29.56

The b coefficients calculated for these characters are as follows.

Characters	b coefficients
X_1	-2.4719
X_2	0.5841
X_3	-0.8476
X_4	3.4098
X_5	4.2797
X_6	-5.7385
X_7	5.6500
X_8	-3.0274
X_9	0.4929
X_{10}	0.8704

The index value for each genotype was determined and the genotypes were ranked accordingly. The selection indices are presented in Table 16 according to the rank of each genotype. The highest index value was recorded by the genotype IC 10350 (Ct11) followed by Ct 7. These were identified to be genotypically superior.

Table 16. Selection indices arranged in descending order

Acc.No	Genotypes	Selection index
11	IC 10350	2177.117
7	IC 8423	1462.348
13	IC 11354	1226.026
17	IC 13496	1213.899
20	IC 51063	1185.411
23	PLG 530	1185.094
14	IC 11357	1171.637
9	IC 10327	1147.613
6	IC 3773	1131.039
19	IC 40040	1120.624
25	Pusa Navbahar	1076.476
26	Local variety	1033.404
22	PLG 528	1007.797
3	IC 439	995.171
1	IC 38-1	994.235
12	IC 10356	991.589
5	IC 3267	975.740
16	IC 11704	975.332
24	PLG 534	956.218
10	IC 10339	950.772
15	IC 11388	931.275
2	IC 44-A	897.260
27	GJCBS 2000-6	882.216
28	GJCBS 2002-2	879.764
4	IC 3118/P1	870.086
21	PLG 519	865.546
18	IC 33705	818.880
8	IC 9007/P2	767.046
29	GJCBS 2003-1	763.856

Discussion

5. DISCUSSION

The improvement of any crop depends on altering the genetic make up of the existing varieties. The choice of the most suitable breeding method for improvement of yield and its components largely depends on the available variability, heritability of the character, genetic advance under selection and the association among the characters. There exists great diversity among the genotypes of clusterbean with respect to the various traits. Genetic diversity plays an important role in plant breeding because the more diverse the parents within a reasonable range, the more would be the chances of improving the characters in question. Hence, the present study was contemplated to investigate the genetic parameters, association among the characters and genetic divergence in clusterbean. The results are discussed below.

5.1 VARIABILITY STUDIES

An insight into the magnitude of variability present in a crop species is valuable as it provides the basis for effective selection. As the observed variability is the sum of genotypic and environmental effects, knowledge on the nature and magnitude of genetic variation contributing to gain under selection is of utmost importance (Allard, 1960). Of the various estimates of quantitative variability, range and variation around the mean are very basic ones.

There were significant differences among the 29 genotypes of clusterbean for all the characters considered in the present study viz., days to 50 per cent flowering, plant height, number of primary branches, number of pod clusters per plant, number of pods per cluster, pod weight, pod length, number of seeds per pod, number of pods per plant and yield per plant. Mital *et al.* (1969), Arumugarangarajan (1997) and Singh *et al.*

(2003) reported the existence of high variability for several characters in clusterbean.

There was remarkable variation in yield ranging from 117.33g to 383.33g. Studies by Mital *et al.* (1969) and Gipson and Balakrishnan (1990) also revealed high variation for the character. Ct 11 stands out among the varieties evaluated on account of its significant superiority in yield.

Conspicuous variation was noticed for pods per plant, its range being 72.40 to 303.07. Ct 11 was significantly superior to other varieties. Mital *et al.* (1969), Gipson and Balakrishnan (1990) and Dwivedi *et al.* (1997) reported wide variation for pods per plant.

Plant height showed high variability with mean values ranging from 78.07 to 161.53 cm. This is in accordance with the earlier reports of Mital *et al.* (1969), Vashistha *et al.* (1981), Sidhu *et al.* (1982) and Gipson and Balakrishnan (1990).

Wide variability was expressed for number of pod clusters per plant with mean values ranging from 9.40 to 71.53. Considerable variability for the character among varieties was earlier reported by Dwivedi *et al.* (1997).

Number of pods per cluster and pod length exhibited wide variation with range of 4.33 to 12.47 and 4.94 to 14.39 respectively. Sidhu *et al.* (1982) and Gipson and Balakrishnan (1990) reported existence of high degree of variability for these characters after evaluating varietal collections.

High magnitude of variability for number of primary branches was found in the present study. Similar reports by Sidhu *et al.* (1982), Gipson and Balakrishnan (1990) and Dwivedi *et al.* (1997) agree with the present findings.

Low magnitude of variation was found for number of seeds per pod. Similar reports by Mital *et al.* (1969) and Mitra *et al.* (2000) support the findings.

Variability is also expressed as the coefficient of variation. Coefficients of variation, phenotypic (PCV) and genotypic (GCV) are better indices for comparison of characters with different units of measurements. The GCV provides a valid basis for comparing and assessing the range of genetic variability for quantitative characters and PCV measures the extent of total variation. There was close relationship between genotypic and phenotypic coefficients of variation for almost all the characters. This similarity between phenotypic and genotypic coefficients of variation indicated low environmental influence and reflected the reliability of selection based on phenotypic performance. Mital *et al.* (1969), Lokesha and Shivashankar (1990) and Singh *et al.* (2001) earlier reported closeness of PCV and GCV for various characters in clusterbean.

In the present investigation, GCV ranged from 4.13 to 46.29 per cent for different characters. The highest GCV was for number of pod clusters per plant and was followed by pods per plant, number of pods per cluster and yield. High GCV for pod clusters per plant and pods per plant as in the present study was earlier reported by Dabas *et al.* (1982). High GCV for yield and number of pods per cluster were evident in the present study. Similar results were reported by Vashistha *et al.* (1981). High estimates of GCV for yield were also reported by Vijay (1988) and Arumugarangarajan (1997).

Low estimates of GCV for days to 50 per cent flowering and number of seeds per pod indicated limited scope for improvement of these characters through selection due to low magnitude as heritable variation.

High values of PCV with correspondingly high values of GCV were observed in the present study for number of pod clusters per plant, number of pods per plant, number of pods per cluster and yield, which indicated the presence of high degree of genetic variation and ample scope for improvement of these characters through selection. Corroborative reports on high PCV and GCV include those by Dabas *et al.* (1982) for pod clusters per plant, Dabas *et al.* (1982) and Vijay (1988) for number of pods per plant, Vashistha *et al.* (1981) for number of pods per cluster and Vashistha *et al.* (1981), Vijay (1988) and Arumugarangarajan (1997) for yield.

The difference between PCV and GCV was comparatively high for number of pods per plant revealing the importance of environment in the expression of the character. PCV and GCV estimates as well as the difference between them were low for days to 50 per cent flowering and number of seeds per pod. This indicates that low variability for these characters is the constraint for genetic improvement through selection inspite of the fact that the character expression is largely decided by genotype.

5.2 HERITABILITY AND GENETIC ADVANCE

Once the relative amount of variability in a population is assessed, it becomes necessary to partition the overall variability into heritable and non heritable components. Magnitude of heritability indicates the effectiveness with which selection of genotypes can be made based on phenotypic performance (Johnson et al., 1955). Allard (1960) suggested that gain from selection for a particular character depends largely on heritability of the character. Burton (1952) suggested that heritability along with GCV would provide a clear idea about the amount of genetic advance expected through selection. High value of heritability indicates that phenotype of the trait strongly reflects the genotype and suggests the major role of genotypic constitution in the expression of the character. Such traits are considered dependable from breeding point of view.

All the characters considered in this study exhibited high heritability ranging from 86.22 per cent for days to 50 per cent flowering to 94.58 per cent for number of pods per cluster.

High heritability for pod clusters per plant seen in the present investigation is in agreement with the findings of Reddy and Gupta (1984) and Mitra *et al.* (2000).

Heritability was high for pods per cluster in the present study. Gipson and Balakrishnan (1990) reported similar results.

Studies by Dabas *et al.* (1982), Gipson and Balakrishnan (1990) and Singh *et al.* (2001) supports the high heritability estimate for plant height observed in the present investigation.

Dabas *et al.* (1982), Reddy and Gupta (1984), Gipson and Balakrishnan (1990), Lokesha and Shivashankar (1990) and Singh *et al.* (2001) reported high heritability values for number of primary branches. This is in agreement with the present findings.

Pod weight exhibited high heritability, which is in accordance to the findings of Gipson and Balakrishnan (1990). Reports of Sidhu *et. al.* (1982) and Mitra *et al.* (2000) support the high heritability values recorded for number of seeds per pod.

High heritability for pods per plant observed in the present investigation is in agreement with the reports from Dabas *et al.* (1982), Reddy and Gupta (1984), Gipson and Balakrishnan (1990), Mitra *et al.* (2000) and Singh *et al.* (2001).

High heritability for yield noticed in this study is supported by similar results reported by Vashistha *et al.* (1981), Sidhu *et al.* (1982) and Singh *et al.* (2001).

Earlier reports of high heritability for pod length by Vashistha *et al.* (1981), Sidhu *et al.* (1982), Gipson and Balakrishnan (1990), Lokesha and Shivashankar (1990), Arumugarangarajan (1997) and Mitra *et al.* (2000)

and for days to 50 per cent flowering by Henry *et al.* (1986) supports the findings in the present study.

High genetic advance as percentage of mean is seen for number of pod cluster per plant followed by number of pods per plant, yield, pod weight, plant height and number of primary branches per plant.

High genetic advance as percentage of mean for number of pod clusters per plant is supported by Reddy and Gupta (1984). Earlier reports of Reddy and Gupta (1984), Gipson and Balakrishnan (1990), Lokesha and Shivashankar (1990) and Singh *et al.* (2001) supports high genetic gain for number of pods per plant.

The high genetic gain for yield is in accordance with the findings by Arumugarangarajan (1997) and Singh *et al.* (2001) and pod weight with the findings of Gipson and Balakrishnan (1990).

Studies by Gipson and Balakrishnan (1990) and Singh *et al.* (2001) support the high genetic gain for plant height while those by Reddy and Gupta (1984), Arumugarangarajan (1997) and Singh *et al.* (2001) supports similar findings for number of primary branches per plant.

High heritability along with high genetic advance indicates additive gene action for the characters under consideration, which implies the possibility for its genetic improvement through selection (Panse, 1957). In the present study, high heritability coupled with high genetic advance was observed for number of pod clusters per plant, pods per plant, pod yield, pod weight, plant height, number of pods per cluster and number of primary branches per plant. These are in conjunction with the reports by Reddy and Gupta (1984) for number of pod clusters per plant, Reddy and Gupta (1984), Gipson and Balakrishnan (1990) and Singh *et al.* (2001) for number of pods per plant, Singh *et al.* (2001) for pod yield, Gipson and Balakrishnan (1990) for pod weight, Gipson and Balakrishnan (1990) and

Singh *et al.* (2001) for plant height, Reddy and Gupta (1984) and Singh *et al.* (2001) for number of primary branches per plant.

From the foregoing discussion it is evident that the characters *viz.*, yield per plant, number of pods per plant, number of pod clusters per plant and number of pods per cluster present immense scope for improvement through selection on account of their high magnitude of heritability and exceptionally high genetic advance.

5.3 CORRELATION STUDIES

Correlation studies in crop plants have got enormous practical value as they reveal the magnitude of the relationship between different characters. This gives a broad idea of the effect of one character on the other and finally on the yield and thereby, suggests the relative importance of different characters in increasing the production. The genotypic correlation between characters provides a reliable measure of the genotypic association between characters and helps to differentiate the vital association useful in breeding from non vital ones (Falconer, 1981).

In the present investigation the characters having high positive genotypic correlation with vegetable pod yield were number of pods per plant, number of seeds per pod, pod weight and number of pod clusters per plant. The earlier reports of positive association of yield with number of pods per plant (Vijay, 1988 and Lokesha and Shivashankar, 1992), number of seeds per pod (Lokesha and Shivashankar, 1992 and Brindha et al., 1997), pod weight (Vijay, 1988 and Brindha et al., 1997) and number of pod clusters per plant (Vijay, 1988; Lokesha and Shivashankar, 1992) corroborate the present findings.

The characters showing strong negative genotypic correlation with yield in the present study were plant height and days to 50 per cent flowering. This suggests that selection of dwarf and early flowering genotypes would result in better yielding types.

High genotypic as well as phenotypic correlation of yield with number of pods per plant and number of seeds per pod evident in the present study is endorsed by the findings of Brindha *et al.* (1997). The above mentioned characters also showed high heritability. Hence it implies that selection for these characters would simultaneously lead to the improvement of pod yield as their phenotypic values genuinely reflect the genotypic worth.

It is noteworthy that the environmental correlation coefficients with pod yield per plant were meager for all the characters studied. In general, the magnitude of genotypic correlation coefficients were greater than the corresponding phenotypic correlation coefficients which indicated that the environment had only small effects on the characters studied.

For selection based on yield component to be successful, knowledge of interrelationships among yield components is necessary as it gives more reliable information for effective selection.

Number of primary branches had positive correlation with number of pod clusters per plant and number of pods per plant. This is in conformity with the findings of Sanghi and Sharma (1964), Henry *et al.* (1986) and Singh *et al.* (2001). Negative association of pod weight and pod length with number of primary branches was evident in this study. Sanghi and Sharma (1964) earlier reported such relationship between number of primary branches and pod length.

Number of pod clusters per plant had strong positive association with number of pods per plant, which is in conformity with several earlier reports (Sanghi and Sharma, 1964; Henry *et al.*, 1986; Singh *et al.*, 2002).

Positive correlation of pod length with number of seeds per pod as found in the present study was earlier reported by Sanghi and Sharma (1964) and Tikka (1975). However pod length was negatively associated with number of pods per plant similar to the earlier report by Sanghi and Sharma (1964).

The discussion given above suggests the selection of number of pods per plant and number of seeds per pod would improve yield by their direct influence and also by their indirect influence through number of pod clusters per plant and pod weight respectively.

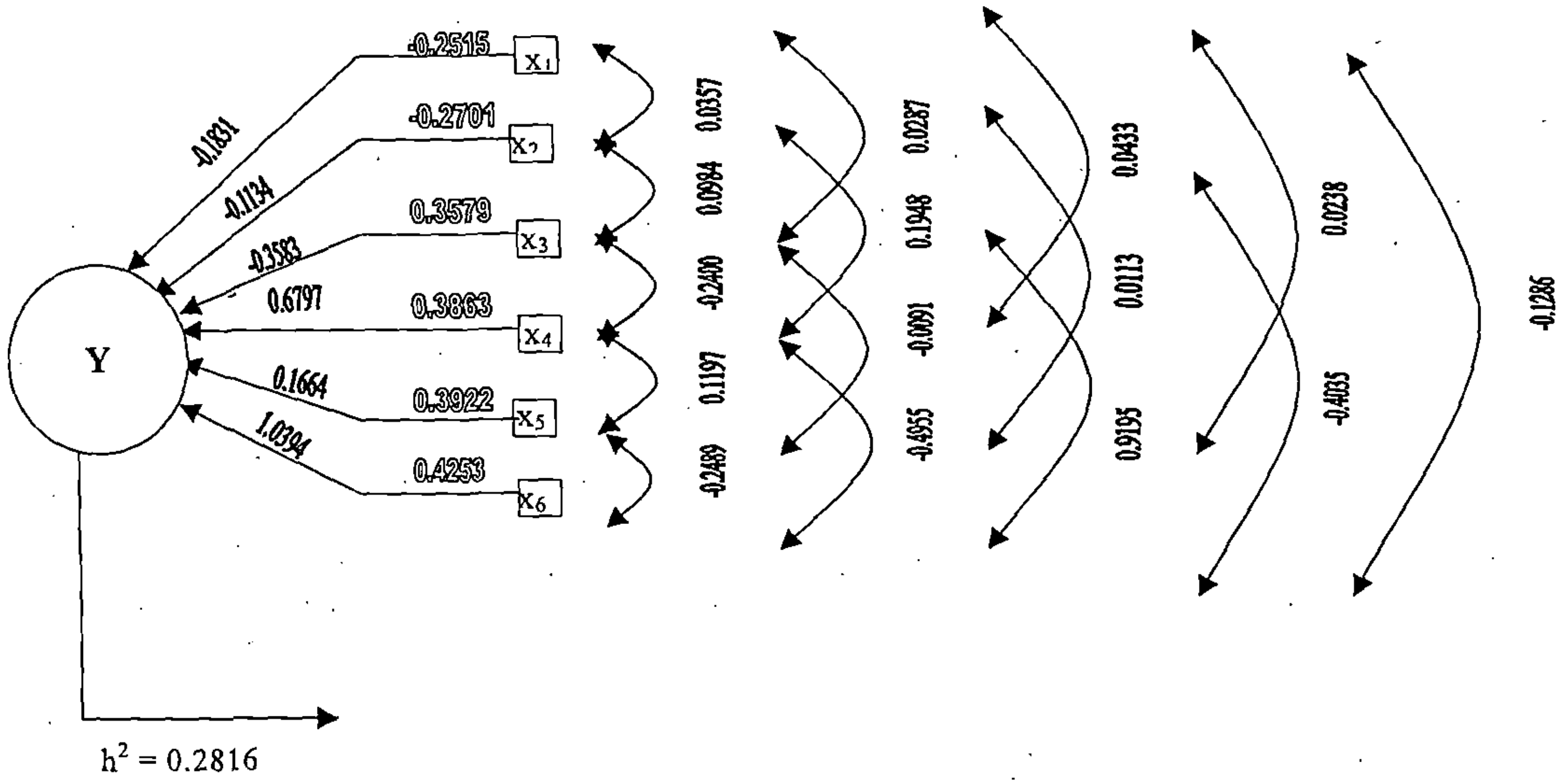
5.4 PATH ANALYSIS

Plant breeders have to deal mostly with correlated characters during crop improvement programmes. Although correlation studies between yield and its components are useful, it does not give an exact picture of the relative importance of various yield attributes. Rate of improvement is expected to be rapid if differential emphasis is laid on component characters during selection. Evans (1978) opined that selection based on yield alone is not as efficient as that based on its components as well. Path coefficient analysis provides the knowledge of the paths through which a component character influences the expression of an economic character like yield. It helps in partitioning the genotypic correlation coefficients into direct and indirect effects of the component characters on yield on the basis of which improvement programmes can be devised effectively.

In the present study, the maximum direct effect on yield was shown by number of pods per plant (1.0394) followed by pod weight (0.6797) and number of seeds per pod (0.1664) (Fig.4). Number of pods per plant also exerted positive indirect effect through number of pod clusters per plant while pod weight exerted positive indirect effect via number of seeds per pod.

High direct effects of number of pods per plant was reported by Vijay (1988) and pod weight by Brindha *et al.* (1995) on green pod yield.

Based on the correlation and path coefficient analysis number of pods per plant and pod weight can be identified as the major characters



Direct effects given in straight lines and correlations in curved lines

X1	Days to 50% flowering	X4	Pod weight
X2	Plant height	X5	Number of seeds per pod
X3	Number of pod clusters/plant	X6	Number of pods per plant

Fig. 4. Path diagram showing direct and indirect effects of components on yield

contributing towards pod yield and selection based on these characters can be effective for developing high yielding varieties of clusterbean genotypes.

5.5 GENETIC DIVERGENCE

Hybridisation has been and will continue to be the most important tool in the hands of the breeder in releasing useful variability for subsequent use. The hybridisation programme aims at the recombination of characters, which depends on the genetic diversity of the parents. The genetic divergence among the different types available is to be known as crosses between genetically divergent parents are likely to produce high heterotic effects and that the crosses involving distantly related parents within the same species produce a wide spectrum of variability. However, the maximum heterosis generally occurs at an optimal or intermediate level of diversity.

One of the potent techniques of measuring genetic divergence is the D^2 statistic (Mahalanobis, 1936). This technique measures the force of differentiation at the intracluster and intercluster levels and thus provides a reasonable basis for selection of genetically divergent parents in breeding programmes. A number of pioneering workers (Moll et al., 1962 and Murthy and Arunachalam, 1966) have utilized this method of quantifying the degree of divergence between biological populations at genotypic level and its role in breeding improved types.

The 29 accessions of clusterbean were subjected to Mahalanobis D^2 analysis based on the 10 characters considered in the study. They were grouped into four clusters on the basis of relative magnitude of D^2 values. The greater the distance between two clusters, greater is the divergence between accessions belonging to the two clusters and vice versa.

Cluster IV exhibited the maximum mean value for yield per plant, number of pods per plant and number of clusters per plant indicating that this cluster is superior to the others with respect to these characters. Cluster II was superior for pods per cluster, pod weight and days to 50 per cent flowering. For the rest of the characters the variation between the mean values of the various clusters was meagre.

The cluster means for various characters are illustrated in metroglyph as depicted in fig 6. In the illustration also the cluster IV, a single variety (Ct 11) cluster is distinctively seen followed by cluster II with high yielder Ct 7.

The clusters, which are separated by the greatest statistical distance, show the maximum divergence. The highest intercluster distance was observed between clusters I and IV while the least proximity was noticed between the clusters II and III (Fig 5). The intracluster distance for cluster I was minimum indicating homogeneity among the accessions grouped in it as compared to other clusters.

The result of contribution of various characters towards the expression of genetic divergence indicated that yield per plant, number of pods per plant and plant height alone contributed to the total divergence in the 29 genotypes of clusterbean. None of the other characters contributed towards the total divergence. Gipson and Balakrishnan (1992) and Mital *et al.* (2000) reported that pods per plant gave the highest contribution towards total divergence. Saini *et al.* (2001a) showed that plant height contributed the most towards genetic divergence followed by grain yield per plant.

5.6 SELECTION INDEX

Selection index worked out considering several yield related characters would be more efficient in identifying a superior genotype. Use of selection index enables more efficient selection for yield improvement than straight selection for yield alone.

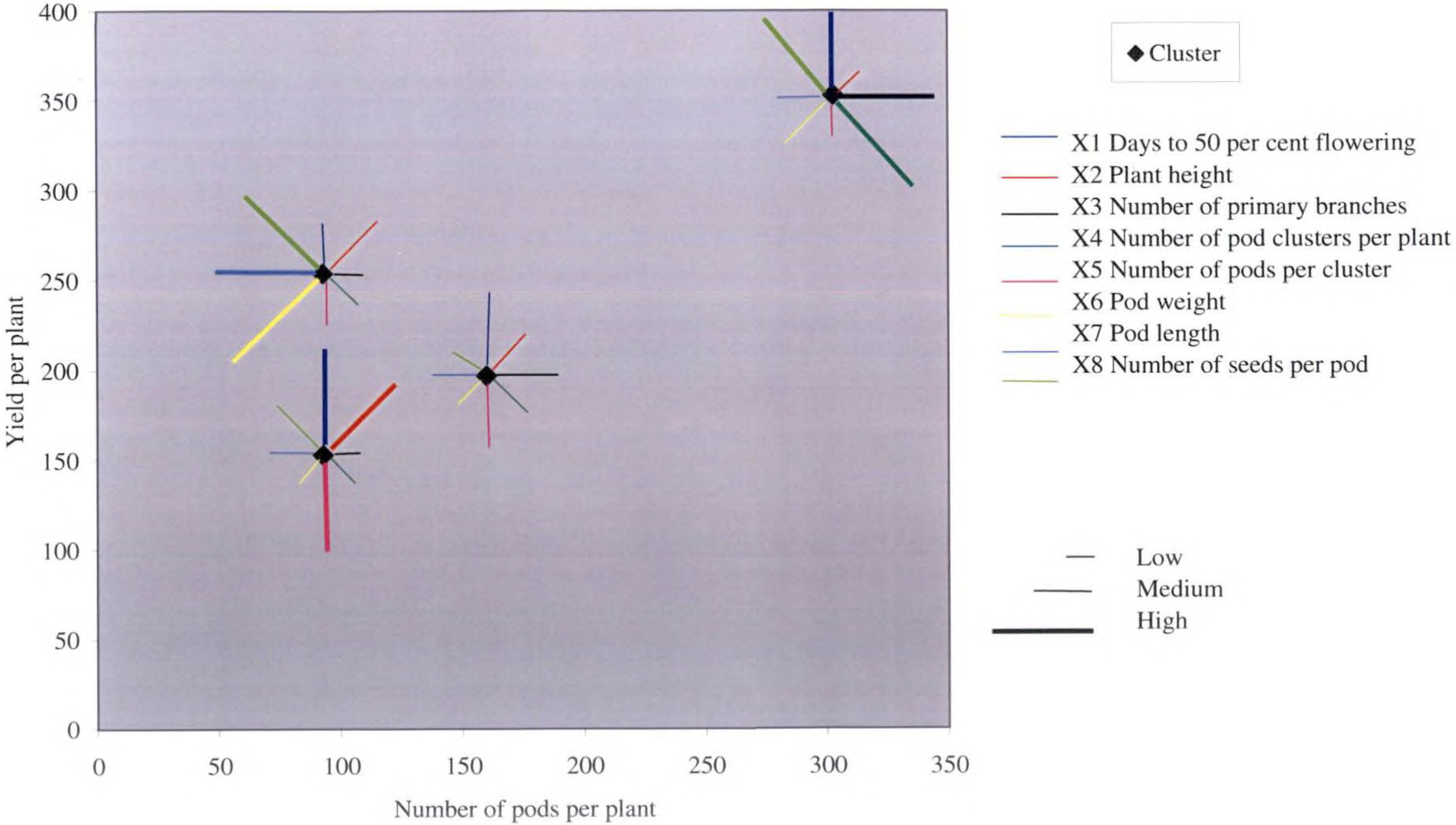


Fig. 6. Metroglyph

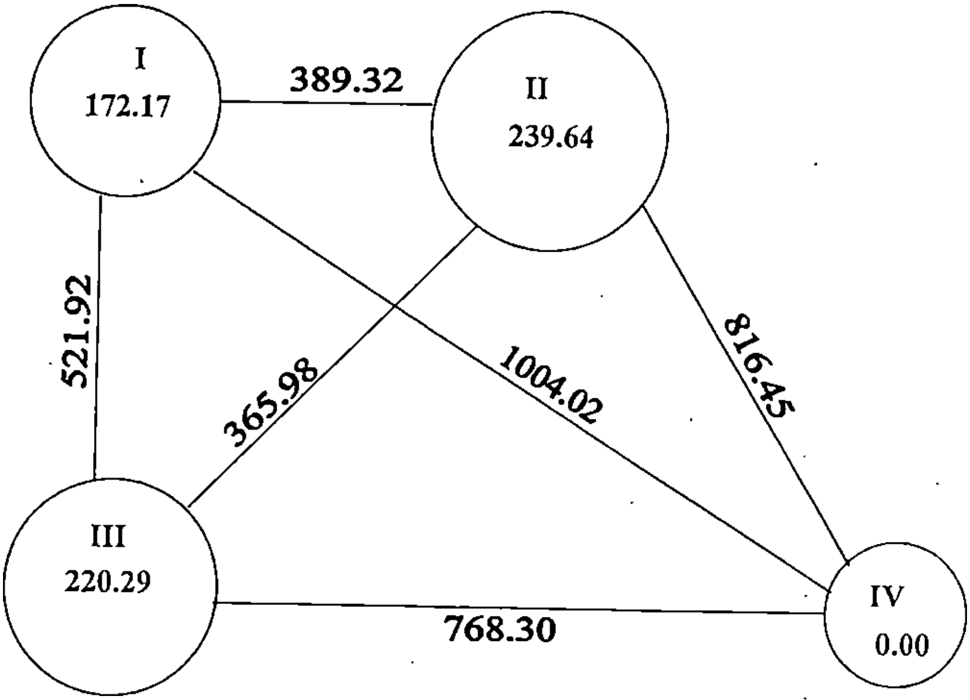


Fig. 5. Cluster diagram

In the present study, selection index was constructed based on all the characters studied viz., days to 50 per cent flowering, plant height, number of primary branches, number of pod clusters per plant, number of pods per cluster, pod length, pod weight, number of seeds per pod, number of pods per plant and yield.

The genotype IC 10350 (Ct 11) recorded highest index value and it formed a single variety cluster. The released variety Pusa Navbahar (Ct 25) had lesser index value compared to other high yielders. The genotypes GJCBS 2003-1 (Ct 29), IC 9007/P2 (Ct 8), IC 33705 (Ct 18), PLG 519 (Ct 21), IC 3118/P1 (Ct 4) and GJCBS 2002-2 (Ct 28) having low values were found to be grouped together in cluster I.

Thus it is evident from the above discussion that in the present material there exists considerable amount of genetic variability in respect of different characters as evident from the highly significant differences except for days to 50 per cent flowering and number of seeds per pod. Close values of PCV and GCV explain less environmental influence. Heritability was high for all the traits. However, estimate of genetic advance indicated additive gene action in many of the traits. Pods per plant, seeds per pod, pod weight and clusters per plant had positive association with yield. Pods per plant and pod weight had positive direct effect on yield. There was considerable genetic diversity in the material studied and only yield, pods per plant and plant height contributed for the divergence. The genotypes Ct 11 belonging to cluster IV and Ct 7 belonging to cluster II were the top ranking genotypes on the basis of selection index values. It is therefore inferred that these genotypes will help us further crop improvement programmes.

Summary

6. SUMMARY

The present study entitled "Genetic divergence in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.)" was conducted at Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during the period 2003-2004.

Twenty nine genotypes of clusterbean, which included a released variety Pusa Navbahar and a local cultivar from Tamil Nadu were evaluated for yield and yield component characters in a field experiment in randomized block design with three replications. Observations were recorded on 10 characters viz., days to 50 per cent flowering, plant height, number of primary branches, number of pod clusters per plant, number of pods per cluster, pod weight, pod length, number of seeds per pod, number of pods per plant and yield per plant.

Analysis of variance revealed significant differences among the varieties for all the 10 characters studied. The cultivar Ct 11 recorded the highest green pod yield and number of pods per plant.

The genotypic variance made up the major portion of phenotypic variance for all the characters studied. High values of PCV with correspondingly high values of GCV were observed in the present study for number of pod clusters per plant, number of pods per plant, number of pods per cluster and yield, which indicated the presence of high degree of genetic variation and ample scope for improvement of these characters through selection but both were low for days to 50 per cent flowering and number of seeds per pod.

The heritability estimates were high for all the 10 characters. High values of heritability coupled with high genetic advance was observed for number of pod clusters per plant, pods per plant, pod yield and number of pods per cluster suggesting additive gene action for these traits. There is immense scope for improvement of number of pod cluster per plant and number of pods per plant through selection on account of their high magnitude of heritability and exceptionally high genetic advance.

At genotypic level, pod yield per plant showed high positive correlation with number of pods per plant, number of seeds per pod, pod weight and number of pod clusters per plant. The inter correlations suggested that the selection for number of pods per plant and pod weight would improve yield by their direct influence and also by their indirect influence through number of pod clusters per plant and number of seeds per pod respectively.

Path coefficient analysis revealed number of pods per plant and pod weight as the characters with high direct effect as well as high indirect effect through other characters. Hence these characters can be identified as the major characters contributing towards pod yield and selection based on these characters would be effective for developing high yielding varieties of clusterbean.

Genetic diversity studies using Mahalanobis D^2 statistic indicated considerable diversity among the 29 cultivars of clusterbean. The clustering pattern indicated that cluster II was having 10 genotypes followed by cluster I and cluster III with nine genotypes each. Cluster IV was a single genotype cluster. The highest Intercluster distance was observed between clusters I and IV (1004.02) while very close proximity was noticed between the clusters II and III (365.98). The intracluster distance was the lowest for cluster I

Cluster mean values suggested that cluster IV having the single variety Ct 11 recorded the highest values for yield of green pods, number of pods per plant, number of pod clusters per plant and number of seeds per pod. The cluster II had the highest pod weight and pod length and included the high yielding genotypes Ct 7 and Ct 25. Plant height, number of pods per plant and yield per plant were the characters that contributed towards total divergence.

Selection index was constructed based on all the 10 characters studied and the genotypes were ranked based on this. The grouping of genotypes by selection indices were similar to their clustering pattern. The genotype IC 10350 (Ct 11) recorded highest index value and it formed a single genotype cluster while the genotypes GJCBS 2003-1 (Ct 29), IC 9007/P2 (Ct 8), IC 33705 (Ct 18), PLG 519 (Ct 21), IC 3118/P1 (Ct 4) and GJCBS 2002-2 (Ct 28) having low values were found to be grouped together in cluster I.

The genotypes Ct 11 belonging to cluster IV and Ct 7 belonging to cluster II were the top ranking genotypes on the basis of selection index values. It is therefore inferred that crossing between these varieties can be effected for evolving high yielding clusterbean genotypes.

References

7. REFERENCES

Ajith, P.M. 2001. Variability and path analysis in bush type vegetable cowpea (*Vigna unguiculata* (L.) Walp.). M.Sc.(Ag.) Thesis. Kerala Agricultural University, Thrissur. 64 p.

Allard, R.W. 1960. *Principles of Plant Breeding.* John Wiley and Sons, Inc. New York, 485 p.

Amrendrakumar and Jain, B.P. 2003. Genetic variability in pea (*Pisum sativum*). *J.* ~~*r*~~R*es.* 15: 55-59

Arumugarangarajan, S. 1997. Studies on variability and stability analysis in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). M.Sc. (Ag.) Thesis. Tamil Nadu Agricultural University, Coimbatore, 108 p.

*Aykroyd, W. R. 1963. Indian Council of Medical Research, Special Report Ser. No. 42, sixth Edition, New Delhi, 32 p.

Brindha, S., Ponnuswami, V. and Thamburaj, S. 1995. Path coefficient analysis in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). *South Indian Hort.* 43: 131-133

Brindha, S., Ponnuswami, V. and Thamburaj, S. 1997. Correlation studies in clusterbean (*Cyamopsis tetragonoloba). South Indian Hort.* 45: 59-60

Burton, G. W. 1952. Quantitative inheritance in grasses. Proc.6th Int. Grassld. Congr., 1:277-283.

Chaudhary, B. D., Bhatt, P. N. and Singh, V. P. 1975. Genetic variability in clusterbean. *Indian J. agric. Sci.* 45: 530-535.

Chaudhary, D. K. and Sharma, R. R. 2003. Genetic variability, correlation and path analysis for green pod yield and its components in garden pea. *Indian J. Hort.* 60: 251-256

Dabas, B. S., Mital, S. P. and Arunachalam, V. 1982. An evaluation of germplasm accessions in guar. *Indian J. Genet.* 42: 56-59

Dewey, D. R. and Lu, K. H. 1959. A correlation and path co-efficient analysis of crested wheat grass seed production. *Agron. J.* 51: 515-518

*Dwivedi, N. K., Bhandari, D. C., Bhatnagar, N., Dabas, S. and Chandel, K. P. S. 1997. Conservation of genetic diversity of arid legumes. *Recent advances in management of arid ecosystem.* Proceedings of a symposium held in India. (Eds. Faroda, A. S., Joshi, N. L., Kathju, S. and Kar, A.), pp. 49-56

Evans, L. T. 1978. *Crop physiology.* Cambridge University Press, Cambridge, London, 355 p.

Falconer, D. S. 1981. *Introduction to Quantitative Genetics.* Third edition. Longman, New York, 438 p.

Fisher, R.H. 1936. The use of multiple measurement in taxonomic problems. *Ann. Eugen.* 7: 179-188

Gipson, A. 1990. Biometrical studies in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). M.Sc. (Hort.) Thesis. Tamil Nadu Agricultural University, Coimbatore, 128 p.

Gipson, A. and Balakrishnan, R. 1990. Variability studies in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). *South Indian Hort.* 38: 311-315

Gipson, A. and Balakrishnan, R. 1992. Genetic diversity in clusterbean. *Indian J. Hort.* 49: 70-74

Henry, A., Daulay, H. S. and Krishna, G. V. S. R. 1986. Correlation, path coefficient analysis and genetic diversity in clusterbean. *Madras agric. J.* 73: 11-16

Henry, A. and Krishna, G. V. S. R. 1990. Genetic divergence in clusterbean. *Madras agric J.* 77: 116-120

Henry, A. 2003. Clusterbean : an industrial crop for arid zone. *Human impact on desert environment* (eds. Narain, P., Kathju, S., Kar, A., Singh, M. P. and Praveenkumar) Arid zone research association of India, Jodhpur, pp. 280-286.

ICAR. 1970. *Pulse crops in India.* Indian Council of Agricultural Research, New Delhi, 226 p.

Jain, J. P. 1982. *Statistical Techniques in Quantitative Genetics.* Tata Mc Hill Co. New Delhi, 281 p.

Johnson, H. W., Robinson, H. D. and Comstock, R. E. 1955. Estimates of genetical and environmental variability in soyabeans. *Agron. J.* 47: 314-318.

Kutty, C. N., Mili, R. and Jaikumaran, U. 2003. Correlation and path coefficient analysis in vegetable cowpea (*Vigna unguiculata* (L.) Walp.). *Indian J. Hort.* 60: 257-261

*Lima, W. A. A. de, Pertal, J., Sediyama, T. and Miranda, G. V. 2000. Genetic divergence in guar (*Cyamopsis tetragonoloba* (L.) Taub.). *Revisterceres.* 47 (271): 253-262

Lokesha, R. and Shivashankar, G. 1990. Analysis of genetic variability and character association in clusterbean. *Mysore J. agric. Sci.* 24: 316-320

Lokesha, R. and Shivashankar, G. 1992. Character association and path analysis in clusterbean. *Mysore J. agric. Sci.* 26: 230-235

Mahalanobis, P. C. 1936. On the generalized distance in statistics. *Proc. Nat. Inst. Sci., (India)*: 12-49

Menon, U., Dubey, M. M. and Kala, K. O. 1977. Path coefficient analysis in guar (*Cyamopsis tetragonoloba* (L.) Taub.). *Indian J. Heredity.* 9 (2): 21-23

Miller, P. A., Williams, V. C., Robinson, H. P. and Comstock, R. E. 1958. Estimation of genotypic and environmental variances and covariance in upland cotton and their implications in selection. *Agron. J.* 5: 126-131

Mital, S. P. and Thomas, T. A. 1969. Correlation and selection indices in improvement of seed yield on guar. *Indian J. Genet.* 29: 10-17

Mital, S. P., Swarup, V., Kohli, M. M. and Singh, H. B. 1969. Variability in guar. *Indian J. Genet.* 29: 98-103

Mital, S. P., Thomas, T. A., Dabas, B. S. and Lal, B. M. 1971. Gum content as related to seed yield and other characters in guar. *Indian J. Genet.* 31: 228-232

Mitra, J., Natarajan, S., Jain, R. K. and Singh, V. P. 2000. Genetic divergence for seed yield in a large collection of clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). *Indian J. Pl. Genet. Resour.* 13: 230

Moll, R.H., Salhuana, W.H. and Robinson, H.F. 1962. Heterosis and genetic diversity in variety crosses of maize. *Crop Sci.* 2: 197-198

Murthy, B.R. and Arunachalam, V. 1966. The nature of divergence in relation to breeding system in some crop plants. *Indian J. Genet.* 26: 188-198

Nath, R. and Saini, M. L. 1980. Correlation and path coefficient analysis in clusterbean. *Forage Res.* 6: 1-5

Pal, A. K., Maurya, A. N., Singh, B., Ram, D. and Kumar, S. 2003. Genetic variability, heritability and genetic advance in cowpea *(Vigna unguiculata* (L.) Walp.). *Orissa J. Hort.* 31(1): 94-97

Panse, V. G. 1957. Genetics of quantitative characters in relation to plant breeding. *Indian J. Genet.* 17: 318-328

Panse, V. G. and Sukhatme, P. V. 1967. *Statistical Methods for Agricultural Workers*. ICAR, New Delhi, pp. 280-297

Rao, C.R. 1952. *Advanced Statistical Methods in Biometrical Research.* John Wiley and Sons Inc., New York, 390 p.

Reddy, J. N. and Gupta, S. C. 1984. Variability parameters in guar. *Madras agric J.* 71: 361-364

Robinson, H. F., Comstock, R. E. and Harvey, P. H. 1949. Estimates of heritability and the degree of dominance in corn. *Agron. J.* 14: 352-359

Saini, K. S., Brar, K. S. and Brar, W.S. 2001a. Genetic diversity in clusterbean. *Ann. Agri Bio Res.* 6 (1): 39-41

Saini, K. S., Brar, K. S., Tharkar Singh and Aujla, M. S. 2001b. Analysis of correlation and path coefficients for grain yield in clusterbean. *Ann. Agri Bio Res.* 6 (1): 43-45

Sanghi, A. K. and Sharma, S. K. 1964. Correlation studies on guar. *Indian J. Genet.* 24: 282-285

Seiler, G. J. and Stafford, R. E. 1985. Factor analysis of components of yield in guar. *Crop Sci* 25: 905-908

Sidhu, A. S. M. L., Pandita, S. K., Arora, S. K. and Vashistha, R. N. 1982. Studies on genetic variability and correlation coefficients in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). *Haryana Agrl. Univ. J. Res.* 12: 225-230

Singh, J. V., Subhashchander, Punia, A. and Jatasra, D. 2001. Studies on variability, heritability and genetic advance in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). *Ann. Biol.* 17: 177-178

Singh, J. V., Subhashchander and Punia, A. 2002. Studies on character association in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). *Nat. J. Pl. Improv.* 4(1): 71-74

Singh, J. V. and Arora, R. N. Guar breeding: What has been done and what lies ahead? . *Human impact on desert environment* (eds. Narain, P., Kathju, S., Kar, A., Singh, M. P. and Praveenkumar) Arid zone research association of India, Jodhpur, pp. 287-293.

Singh, K., Hazra, C. R. and Kumar, A. 1988. Correlation and path coefficient analysis in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). *Ann. agric. Res.* 9: 43-46

Singh, N. P., Chaudhary, A. K. and Chaudhary, S. P. S. 2003. Genetic divergence in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). *Indian J. agric. Sci.* 73: 356-357

Singh, R. K. and Choudhary, B. D. 1979. *Biometrical Methods in Quantitative Genetic Analysis.* Kalyani Publishers, New Delhi, pp. 39-79

Smith, F.H. 1937. A discriminant function for plant selection. *Ann. Eugen.* 7: 240-250

Stafford, R. E. and Seiler, G. J. 1986. Path coefficients of yield components in guar. *Fld Crop Res.* 14 (2): 171-179.

Sohoo, M. S. and Bharatwaj, B. L. 1985. Path coefficient analysis of seed yield in clusterbean. *Crop improv.* 12: 85-86.

Tikka, S. B. S. 1975. Interrelationship between yield and components in clusterbean. *Indian J. Genet.* 35: 340-343

Vahidy, A.A and Yousufzai, A. S. 1991. Variation and correlation studies of vegetative and reproductive characteristics in twelve accessions of guar (*Cyamopsis tetragonoloba* (L.) Taub.). *J. Islam. Acad. Sci.* 4: 245-248.

Vashistha, R. N., Pandita, M. L. and Sidhu, A. S. 1981. Variability and interrelationship between yield and its components in guar under dry farming condition. *Haryana J. Hort. Sci.* 10: 131-135

Venkatesan, M., Veeramani, N., Thangavel, P. and Ganesan, J. 2004. Genetic divergence in cowpea (*Vigna unguiculata* (L.) Walp.). *Legume Res.* 27: 223-225

Vijay, O. P. 1988. Genetic variability, correlation and path analysis in clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.) (guar). *Indian J. Hort.* 45: 126-132

Whyte, R.O., Nilsson-Leissner, G. and Trumble, H.C. 1953. *Legumes in Agriculture.* FAO Agricultural studies No.21. Food and Agriculture Organisation of the United Nations, Rome, 367 p.

Wright, S. 1954. The interpretation of multivariate systems. *Statistics and Mathematics in Biology.* (Eds. Kempthorn, O., Bancroft, T. A., Gowen, J. W. and Lush, J. L). State University Press, Iowa, pp. 11-13

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GENETIC DIVERGENCE IN CLUSTER BEAN
[*Cyamopsis tetragonoloba* (L.) Taub.]

ANANDHI, K.

Abstract of the
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Department of Plant Breeding and Genetics
COLLEGE OF AGRICULTURE
VELLAYANI, THIRUVANANTHAPURAM 695 522

ABSTRACT

The present study aimed at evaluating a collection of clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.) genotypes for yield and related characters and grouping of genotypes was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during the period 2003-2004.

Twenty nine genotypes of clusterbean were evaluated for yield and yield related characters in randomized block design with three replications. The analysis of variance revealed significant differences among the varieties for all the characters studied which include days to 50 per cent flowering, plant height, number of primary branches, number of pod clusters per plant, number of pods per cluster, pod weight, pod length, number of seeds per pod, number of pods per plant and yield per plant.

High values of PCV with correspondingly high values of GCV were observed in the present study for number of pod clusters per plant, number of pods per plant, number of pods per cluster and yield, which indicated the existence of high degree of genetic variation and ample scope for improvement of these characters through selection. High values of heritability coupled with high genetic advance was observed for number of pod clusters per plant, pods per plant, pod yield and number of pods per cluster suggesting additive gene action for these traits. There is immense scope for improvement of number of pod clusters per plant and number of pods per plant through selection on account of their high magnitude of heritability and exceptionally high genetic advance.

Vegetable pod yield showed high positive genotypic correlation with the characters number of pods per plant, number of seeds per pod, pod weight and number of pod clusters per plant.

Path coefficient analysis revealed number of pods per plant and pod weight are the characters with high direct effect. These two characters had got high indirect effect on yield through number of pod clusters per plant and number of seeds per plant respectively. Hence these characters can be identified as the major characters contributing towards pod yield and selection based on these characters would be effective for developing high yielding varieties of clusterbean genotypes.

Based on Mahalanobis statistic, the 29 genotypes of clusterbean were grouped into four clusters. Cluster II was the largest with 10 genotypes. Intercluster distance was observed maximum between clusters I and IV while the close proximity was noticed between the clusters II and III. Cluster IV having the single variety Ct 11 exhibited the maximum mean value for yield per plant, number of pods per plant and number of clusters per plant indicating that this cluster is superior to the others with respect to these characters. Cluster II having Ct 7 was superior for pods per cluster, pod weight and days to 50 per cent flowering. On the basis of selection index the genotypes IC 10350 (Ct 11) and IC 8423 (Ct 7) recorded highest index value. Hybridization of the superior genotype Ct 11 of cluster IV with Ct 7 of cluster II having high pod weight would be beneficial for evolving high yielding genotypes.