GENETIC VARIABILITY IN YARD LONG BEAN

(*Vigna unguiculata* subsp. *sesquipedalis*

(L.) Verdcourt)

By

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THESIS

Submitted in partial fulfilment of the
requirement for the degree
MASTER OF SCIENCE IN HORTICULTURE
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Kerala Agricultural University

Department of Horticulture

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DECLARATION

I hereby declare that this thesis entitled "**Genetic variability in yard long bean (***Vigna unguiculata*** subsp. *sesquipedalis* (L.) Verdcourt)**" 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 to me of any degree, diploma, associateship, fellowship or other similar title of any other University or Society.

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CERTIFICATE

Certified that the thesis entitled "**Genetic variability in yard long bean** (*Vigna unguiculata* **subsp.** *sesquipedalis* **(L.) Verdcourt)**" is a record of research work done independently by Mrs. Resmi P.S. (Admission No: 95-12-07) 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.

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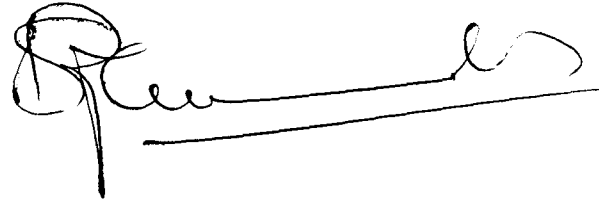Vellayani

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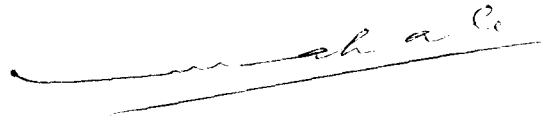College of Agriculture
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Introduction

1. INTRODUCTION

Yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) also known as Asparagus bean or vegetable cowpea is one of the most popular leguminous vegetable crops of Southern Kerala. The tender, green pods used as a delicious vegetable is much in protein, minerals vitamins and dietary fibre. The crop is thought to be originated in central Africa and is distributed in India, Indonesia, Philippines and Srilanka (Sampson, 1936). The crop has a simple cytotaxonomy and the diploid chromosome number is 22 (Steele, 1976). The crop is of trailing or climbing habit and grown with proper staking. The pods have great demand in gulf countries and large quantities are exported to the middle east.

Despite its nutritive value and popularity as a leguminous vegetable, very little attention has been paid for the genetic improvement of this crop. No serious attempts has been made to identify superior types and upgrade its productivity. The types that are under cultivation at present are non-descript ones. This necessitates a need based programme for developing high yielding varieties suited for different agroclimatic conditions. Development of cultivars resistant/tolerant to major pests and diseases is also a great necessity.

The aim of any crop improvement programme is to evolve superior genotypes with high yield, increased quality and resistance to pests and diseases. The success of any such programme largely depends on the extent of genetic variability available in a breeding population. Also the degree of transmission of these characters from one generation to next can be ascertained by partitioning the total variability into heritable and non heritable components, with the aid of suitable genetic parameters like coefficient of variation; heritability and genetic advance. An estimate of interrelationship between yield with other traits is of immense help to a breeder. Correlation studies would facilitate effective

selection for simultaneous improvement of one or many yield contributing components. Apart from these, path analysis and discriminant function analysis help to determine the extent of improvement that could be made in yield contributing characters. Further, the estimation of genetic divergence in the population helps to locate ideal parents for future hybridisation programmes.

Describing the available genotypes using descriptors which are internationally accepted, helps in easy exchange of information about the germplasm available in different parts of the world. Yard long bean is susceptible to an array of pathogens and insect pests. A scoring scale for the incidence of the major pests and diseases will help assess the suitability of genotype for disease prone or pest prone areas.

Hence, the present investigation was attempted using 30 yard long bean genotypes with the objective of assessing the variability existing in the germplasm of yard long bean in yield attributes, morphological characters and pest and disease resistance and to identify suitable lines if any which can be utilised in further breeding programmes.

Review of Literature

2. REVIEW OF LITERATURE

Yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) is one of the most important leguminous vegetable crops of Kerala. Despite its wide genetic variability, nutritional and economic importance, very little attention has been paid to the improvement of this crop. The studies specific to yard long bean are very limited and therefore the available literature on variability studies in cowpea in general are reviewed here under the following heads.

2.1 Genetic variability, heritability and genetic advance

2.2 Correlation studies

2.3 Path analysis and selection index

2.4 Genetic divergence

2.1 Genetic variability, heritability and genetic advance

The availability of an array of diverse genotypes is a basic requisite for any breeding programme for producing better types. The occurrence of larger variability ensures better chances of identifying improved forms in any crop. It also enables the breeder to determine the method of crop improvement. Superior genotypes can be selected only when major part of the variability of the trait is genetic. Many workers studied the extent of variability in cowpea by working out the genotypic and phenotypic coefficient of variation.

Singh and Mehndiratta (1969) reported maximum genotypic coefficient of variation for pods/plant followed by pod clusters/plant and grain yield/plant in cowpea. Days to flowering recorded high heritability (88.8) followed by pod length (80.5) and days to maturity (78.3) seed yield/plant had the lowest hertiability (31.6).

Among 12 varieties of cowpea, wide variability was noticed for many characters (Lakshmi and Goud, 1977). The genotypic coefficient of variation was higher for plant height, grain yield, pods/plant and 100 grain weight. Heritability was very high for plant height, pod length and 100 grain weight. Pod length was associated with high genetic advance.

Angadi *et al* (1978) studied 50 types of cowpea and obtained a genotypic coefficient of variation of 81.58 for pod number, and 30.48 for seeds/pod. Number of pod clusters, pod number and 100 seed weight also recorded high genotypic coefficient of variation whereas seeds/pod recorded the lowest. Heritability values ranged from 68.35% for number of branch to 98.92% for seed weight. High genetic advance was recorded in respect of pod number, seed yield, pod yield and seed weight. Number of branches and seeds/pod exhibited high heritability and low genetic advance.

Rajendran *et al* (1979) reported high heritability for all characters like area of primary leaf, plant height, plant spread, days to first flowering, days to 50% flowering, flowers/bunch, pod set/bunch, 100 seed weight, length of peduncle, number of peduncles, number of primary branches, number of seeds/pod and seed yield/plant in cowpea.

Chandrika (1979) observed variability for all the important economic characters in cowpea. Except for primary branches/plant, the major portion of the variability was genetic. Forty three diverse genotypes of cowpea were studied by Sreekumar *et al* (1979) and found that the lowest genotypic coefficient of variation was for total duration (4.48%) followed by days to flowering (6.14%). Grain yield and 100 grain weight had high heritability and genetic advance.

In a study on selected cowpea genotypes, Ramachandran *et al* (1980) reported that the range of variation for varietal means was quite large in respect of days to first harvest, weight of pods, seeds/pod, pods/plant and yield/plant. Genotypic coefficient of variation

was highest for yield/plant followed by pods/plant. Days to flowering had the highest heritability followed by days to harvest. Genetic advance as percentage of mean was maximum for seeds/pod followed by yield/plot and pods/plant.

Jalajakumari (1981) studied genetic variability in 17 cowpea varieties and reported highly significant variation for all the characters. Variability studies in eleven cowpea varieties by Jana *et al* (1982) revealed high genotypic coefficient of variation for vegetable yield and pods/plant. Heriability and genetic advance were high for the characters 1000 grain weight and days to flower. A study on genetic variability for six traits in 40 genotypes of cowpea revealed significant differences for all the characters except pods/cluster (Pandita *et al*, 1982). Yield/plant had the highest genotypic and phenotypic coefficient of variation. High heritability estimates and high percentage of genetic gain were also recorded for yield/plant.

Radhakrishnan and Jebaraj (1982) reported maximum genotypic coefficient of variation for pod clusters and branches/plant in cowpea.

Vaid and Singh (1983) observed high phenotypic coefficient of variation and genotypic coefficient of variation for branch clusters and yield/plant in cowpea. High heritability and genetic advance was reported for branch, clusters and yield/plant. Substantial genetic variability was observed among cowpea cultivars of Malaysia. (Yap, 1983). He also reported high heritability for pod length and low heritability for pod yield and seed protein content.

In a study of 40 genotypes of cowpea, Dharmalingam and Kadambavana sundaram (1989) obtained high heritability for pod length (87.37), 100 seed weight (85.38) and harvest index (69.58%).

Chikkadyavaiah (1985) studied 11 related characters in 207 indigenous and 117 exotic genotypes in cowpea and reported maximum variability for plant spread in Kharif

and plant height in summer seasons. Heritability and genetic advance were high for plant height in both Kharif and summer season.

De Mooy (1985) observed high variability in flowering, plant habit, number of pods/plant and seed characters in cowpea germplasm.

High estimates of heritability was reported for 100 seed weight, seeds / pod and days to maturity in cowpea by Apte *et al* (1987). Percentage of genetic gain was greatest for 100 seed weight followed by plant height, branches/plant and seeds/pod.

Patil and Baviskar (1987) observed maximum variability for seed yield/plant followed by pods/plant, pod clusters per plant and days to maturity. The phenotypic coefficient of variation and genotypic coefficient of variation were highest for pods/plant, pod clusters/plant, seed yield and 100 seed weight. Heritability was the highest for 100 seed weight, followed by days to maturity and pod length.

Patil and Patil (1987) reported moderate to high heritability estimates for yield/plant and six other yield related characters. Expected genetic advance was moderate to high for all traits except 100 seed weight and seed number/pod.

High heritability for pod length, flowering date and length of flowering period was observed in cowpea by Ye and Zhang (1987). Sharma *et al* (1988) reported maximum genotypic coefficient of variation for dry matter yield followed by plant height, green forage yield, pods/plant, seed weight and green pod yield. Heritability ranged from 46.9% for green pod yield to 98% for days to 50% maturity.

In a variability study for yield and other traits Kandaswamy *et al* (1989) obtained increased yield through selection for pods/plant, seeds/pod and 100 seed weight. A study by Thiyagarajan (1989) showed high heritability and genetic advance for plant height seeds/pod and 100 seed weight. Roquib and Patnaik (1990) also reported high heritability for these characters and for primary branches, pod length and breadth, days to 50%

flowering, maturity and yield in cowpea. Most of these traits exhibited high estimates of genetic advance.

Gowda *et al* (1991) reported that an F_2 population of cowpea showed high estimate of genotypic component of variation for pods/plant and seed yield/plant followed by 100 seed weight.

Savithramma (1992) reported high genotypic variances for all the characters except seeds/pod in cowpea. Seeds/pod had a genotypic coefficient of variation of 7.94 and plant height recorded a genotypic coefficient of variation of 31.86. Seed weight/plant, 100 seed weight and petiole length showed high genotypic coefficient of variation. High heritability values was observed for plant height, pod length and 100 seed weight. High genetic advance was recorded in respect of plant height, seed weight per plant and 100 seed weight.

Aghora *et al* (1994) studied 19 diverse vegetable cowpea lines and found that wide variability existed among the genotypes with respect to the protein content.

Weight of seeds/plant, number of pods/plant and 100 seed weight recorded high heritability of 94.4%, 85.9% and 83.3% respectively as reported by Damarany (1994).

Ram *et al* (1994) observed wide range of variability particularly for plant height and seed yield/plant in cowpea. High heritability and genetic advance as % of mean were estimated for plant height, seed yield/plant and pods/plant.

Sawant (1994) reported moderate to high heritability for all characters in cowpea except branches/plant inflorescence/plant and seed/plant.

Sobha (1994) observed significant differences among 31 genotypes of cowpea. pods/kg., pod weight and yield had highest genotypic coefficient of variation. High heritability and genetic advance was observed for pods/kg, pod weight, yield, days to harvest, pod length, pod girth, pod weight and yield.

Backiyarani and Nadarajan (1995) reported highest genotypic coefficient of variation, phenotypic coefficient of variation and genetic advance for leaf area followed by leaf breadth. Estimates of heritability and genetic advance were high for 100 seed weight, plant height and harvest index in cowpea (Rewale *et al*, 1995).

Sreekumar (1995) observed high heritability for days to 50% flowering, weight of 100 seeds and seed protein content, medium heritability for length of pods and number of pods/plant and low heritability for plant dry weight and grain yield. Genetic advance as percentage of mean was high for characters like number of pods/plant and 100 seed weight. Moderate genetic advance was observed for grain yield and low genetic advance for number of days to flower, length of pod and seed protein content.

Sreekumar *et al* (1996) studied 18 vegetable cowpea genotypes and obtained the maximum genotypic coefficient of variation for green pod yield (45.06) followed by pod length (43.99). The relative magnitude of difference between phenotypic coefficient of variation and genotypic coefficient of variation was low for characters such as days to flower, days to first picking, pod length and seeds/pod indicating low degree of environmental influence on these characters and this difference was high for characters like number of fruiting points, pods/plant and yield of green pods indicating the high influence of environment on these two characters. Pod length had the highest heritability value, followed by number of days to first picking, number of seeds/pod and days to flower. High genetic advance was obtained for pod length and number of seeds/pod.

2.2 Correlation Studies

Yield in any crop is a complex character determined by many component characters. Selection for specific characters result in correlated response for some other

characters. Interrelationship between yield and its contributing characters have been reported by many workers in cowpea.

Singh and Mehndiratta (1969) reported high positive genotypic correlation among number of pods/plant, number of pod clusters/plant, days to flowering and days to maturity in cowpea. Negative genotypic correlation was reported for length of pods with number of pod clusters/plant and number of pods/plant. Positive correlation of pod yield with branches/plant, pod length, pod thickness, days to flowering and days to maturity was obtained by Kumar *et al* (1976).

Hanchinal *et al* (1979) obtained high correlation between 100 seed weight and number of pods and number of branches in cowpea. Jana *et al* (1982) found that pod yield was positively and significantly correlated with primary branches/plant. Primary branches/plant was negatively correlated with days to flower and pod length, but positively correlated with vegetable pod yield/plant.

Negative correlation was obtained between pods/plant and seeds/pod in cowpea (Patil and Bhapkar, 1987). Ye and Zhang (1987) observed the existence of positive correlation between pod yield, protein yield, dry matter yield and their components in cowpea.

Green pod yield was positively and highly correlated with pods/plant, days to first flowering, seeds/pod and plant height (Sharma *et al*, 1988).

Perrino *et al* (1993) obtained high positive correlation (r = 0.9) between flowering time and ripening time in cowpea accessions. Peduncle length was not correlated with any of the other traits.

Samiullah and Imtiaz (1993) found that green pod yield/plant was significantly and positively correlated with pod number at the genotypic level only. It was suggested that the

fruiting branches and days to flowering were the reliable and effective selection criteria for the improvement of pod yield in cowpea.

Sobha (1994) obtained high and positive correlation between pod yield and days to harvest, pod length, pod girth, pod weight, pods/kg, seeds/pod and 100 seed weight in cowpea.

High positive correlation between the number of pods/plant and seed production was obtained by Sudhakumari (1994) in cowpea. Tamilselvam and Das (1994) reported positive correlation of plant height with days to 50% flowering, number of clusters/plant, pod length and 100 seed weight. Pod length was positively correlated with number of seeds/pod and 100 seed weight. Number of seeds/pod was positively correlated with 100 seed weight. Number of clusters and pods/plant were negatively correlated with pod length and 100 seed weight. It was concluded that number of flower clusters and pods/plant and 100 seed weight should be used as selection criteria in the development of high yielding genotypes.

Leaf length and breadth in cowpea had positive correlations with leaf area (Backiyarani and Nadarajan, 1995).

Hussein and Farghali (1995) obtained significant phenotypic correlation between pod length and 100 seed weight. There was significant genotypic correlation between days to flowering and each of pod length, number of seeds/pod and seed yield.

Kar et al (1995) observed strong association of pod yield with fibre percentage and seeds/pod. Pod length and 100 seed weight had significant positive phenotypic correlation in cowpea (Shakarad et al, 1995). A significant genotypic correlation was found between days to flowering and each of pod length, number of seeds/pod and seed yield.

Sreekumar (1995) obtained very strong negative correlation between weight of 100 seeds and seed protein content.

Sreekumar *et al* (1996) reported positive significant correlation between yield of green pods with number of pods/plant, pod length and number of seeds/pod, both at phenotypic and genotypic levels. The number of fruiting points/plant had also a positive significant association with yield of green pods. Number of pods/plant had negative correlation with number of days to first picking and also with number of days to flower. Number of pods/plants had significant correlation with number of fruiting points/plant. Number of seeds/pod had significant positive correlation with pod length and number of days to flower. Considering the correlation of characters with green pod yield, positively correlated charaters like number of fruiting points, number of pods/plant, pod length and number of seeds/pod can be utilized as selection criteria for yield improvement in vegetable cowpea.

2.3 Path analysis and selection index

Angadi *et al* (1978) concluded that in cowpea, individual plant selection for pod number, cluster number, seed yield, pod yield and 100 seed weight is effective for improvement.

Murthy (1982) observed pod number/plant as the major contributor to yield followed by pod length, seed number/pod and pod weight. Jana *et al* (1983) reported pod number/plant had the highest direct effect on pod yield/plant in cowpea.

Yap (1983) opined average selection index was more effective than visual pedigree or bulk population methods for developing high yielding lines in cowpea.

Obisesan (1985) revealed through path coefficient analysis that the most important yield components were pods/plant, 100 seed weight and seeds/pod. The indirect effect of peduncles/plant, mean peduncle length and a vigour index were more important than their direct effects.

Improvement in cowpea should be based on 100 seed weight, pods/plant, pod clusters/plant and seed yield/plant (Patil and Baviskar, 1987).

Ye and Zhang (1987) reported that number of pods/inflorescence had the greatest direct effect on pod yield in vegetable cowpea. Selection for pods/plant, seeds/pod and 100 seed weight resulted in increased yield in cowpea (Kandaswamy *et al*, 1989).

Biradar *et al* (1991) found that pod weight had the highest positive direct effect on yield followed by plant height, and clusters/plant. Pod length, pods/plant and seeds/pod showed negative direct effect on yield. Pod weight/plant can be used as a reliable parameter for yield in cowpea.

Pod weight exerted the maximum direct positive effect on yield, followed by pod girth and 100 seed weight in cowpea (Sobha, 1994). Tamilselvam and Das (1994) concluded that number of clusters and pods/plant and 100 seed weight should be used as selection criteria in the development of high yielding genotypes in cowpea.

Kar *et al* (1995) observed that pod length and fibre content were the main determinants of pod yield in vegetable cowpea.

2.4 Genetic divergence

A knowledge of genetic diversity, its nature and degree is useful in the improvement of any heritable character. Chandrika (1979) could group 202 varieties of cowpea into 17 clusters based on the genetic distance using Mahalanobis D^2 analysis. Chikkadyavaiah (1985) studied 207 indigenous and 117 exotic genotypes in cowpea and assigned 23 stable diverse genotypes to one cluster.

Marangappanvar (1986) concluded that inter-cluster spatial patterns were not consistent with varietal geographic distribution following clustering studies in cowpea. Patil and Bhapkar (1987) did not obtain any relationship between genetic diversity and

geographic origin. Thiyagarajan (1989) reported that days to flowering, 100 seed weight and plant height contributed most to genetic divergence.

Dharmalingam and Kadambavanasundaram (1989) reported wide genetic diversity among the 13 clusters formed from 40 genotypes of cowpea. Among them Co-2 and C-5 were the widest which were identified for heterosis breeding. Based on their intracluster mean values and wide genetic diversification, the types suitable for hybridisation among themselves and the selection for the desirable traits have been identified. Thiyagarajan (1989) reported that days to flowering, 100 seed weight and plant height contributed most to genetic divergence. Thirty geographically diverse cowpea accessions could be grouped into four clusters by Thiyagarajan *et al* (1989). Pods/plant, seeds/pod and seed yield/plant gave the largest contribution to genetic divergence. They also did not obtain relationship between geographic distribution and genetic diversity. Renganayaki and Rangaswamy (1991) could cluster 6 genotypes of cowpea into 4 clusters. Hundred seed weight, pod length and seed yield contributed most towards genetic divergence.

Hazra *et al* (1993) studied the genetic divergence among cowpea genotypes belonging to 3 cultigroups, - viz. unguiculata, biflora and sesquipedalis under two environments using D^2 statistics. The genotypes were grouped into 4 clusters in both the environments. No close correspondence was observed between geographic distribution and genetic divergence. Maximum genetic divergence was observed between the genotypes of cultigroups, sesquipedalis and those of biflora.

Thiyagarajan and Rajasekharan (1993) conducted metroglyph analysis in cowpea and divided the genotypes into low, medium and high yielding groups. Grouping according to plant height produced three groups - four genotypes under dwarf group, seven under medium group and eight under tall group.

Sudhakumari and Gopimony (1994) studied genetic divergence in cowpea using Mahalanobis D^2 technique. They grouped 59 cowpea varieties into eight clusters. The maximum divergence was observed between clusters V and VII which contained two and one genotype each respectively.

Sobha (1994) could group 31 cowpea gentoypes into six clusters and observed strict parallelism between genetic diversity and geographic distribution.

Materials and Methods

3. MATERIALS AND METHODS

The present study on genetic variability in yard long bean (*Vigna unguiculata subsp. sesquipedalis* (L.) Verdcourt) was carried out at the Department of Horticulture, College of Agriculture, Vellayani during 1996-97.

The experimental material consisted of 30 diverse accessions of yard long bean collected from southern parts of Kerala. The details of the accessions and their source is presented in table 1. These included genotypes varying in vegetative and productive characters. Selfed seeds of each accession were used for the study.

The experiment was laid out in randomized block design with three replications. The spacing adopted was 1m x 0.75m. Ten plants were maintained per plot in two rows of five each. The crop received timely management practices as per Package of Practices Recommendations of Kerala Agricultural University (KAU, 1993).

3.1 Observations recorded

All the observations were recorded from plants selected at random in each replication and the mean was taken for further analysis. The observations on the following characters were recorded.

3.1.1. Plant characters

3.1.1.1 Length of vine (cm)

3.1.1.2 Number of primary branches

3.1.2. Leaf characters

3.1.2.1 Petiole length (cm)

3.1.2.2 Length of terminal leaflet (cm)

Table 1 List of yardong bean accessions used for the study and their sources

Genotype	Source
VS-1 to VS-6	Sreekaryam, Trivandrum Dt.
VS-7	Nedinjil, Trivandrum Dt.
VS-8	Kanakkary, Kottayam Dt.
VS-9	KHDP Pilot Project Area, Nedumangad, Trivandrum Dt.
VS-10 (Sharika)	Kerala Agricultural University
VS-11 (Malika)	Kerala Agricultural University
VS-13	Kalliyoor, Trivandrum Dt.
VS-14	Karyavattom, Trivandrum Dt.
VS-15	Muttakkadu, Trivandrum Dt.
VS-16,VS-17	Kalliyoor, Trivandrum Dt.
VS-18 to VS-30	KHDP Pilot Project Area, Nedumangad, Trivandrum Dt.
VS-31	Muttakkadu, Trivandrum Dt.

3.1.7. Genetic catalogueing of genotypes

3.2 Details of biometrical observations

a. Plant characters

Length of vine (cm)

Length of the vines from ground level to the tip was measured in five randomly selected plants in each replication after the final harvest of the crop, the average worked out and presented in cm.

Number of primary branches

The total number of primary branches in each of the five observational plants was counted at full maturity of the plant.

b. Leaf characters

Petiole length (cm)

Length of petiole of five leaves was measured at random in each plant and their mean expressed in cm.

Length of terminal leaflet (cm)

Length of five terminal leaflets selected at random from each observational plant was measured and expressed in cm.

Breadth of terminal leaflet (cm)

Breadth of five terminal leaflets selected at random from the observational plants was measured in cm.

Length of lateral leaflet (cm)

Length of five randomly selected lateral leaves were measured in cm from each observational plant.

Breadth of lateral leaflet (cm)

Breadth of five randomly selected lateral leaves were measured in cm.

c. *Flowering observations*

Days to first flowering

Number of days taken for the appearance of the first flower from the date of sowing was recorded from the five observational plants.

Days to first harvest

Number of days taken from sowing to the first harvest of vegetable pods was recorded from the five observational plants.

Harvesting interval

Number of days taken between successive harvest of vegetable pods was recorded in the five observational plants.

d. *Pod characters*

Pod length (cm)

Length of ten randomly selected pods from each observational plant were measured using an ordinary scale, the average worked out and presented in cm.

Pod girth (mm)

The same pods used for measuring length was used for measuring the girth in mm.

Pod weight (g)

Individual pods which were used for measurement of length and girth were weighed and expressed in grams.

Beans pod

Beans were extracted from each pod, counted and recorded.

Length of peduncle (cm)

Length of peduncle was measured in cm from five random inflorescence in each observational plant.

Number of inflorescence plant

The total number of inflorescence in each observational plant was recorded.

Number of pods inflorescence

Number of pods set in each of the five inflorescence were counted and recorded.

Number of pods kg

Number of pods which make one kg was noted in the observational plants.

Pods plant

The total number of pods in each observational plant were counted during each harvest and recorded.

Yield plant (kg)

The total yield of green pods from each observational plant was taken and expressed in kilograms.

Hundred seed weight (g)

One hundred dried seeds from each genotype were weighed using an electronic balance and weight recorded in grams.

e. Pod quality

Fibre content of pods (%)

Crude fibre content of whole dried pods along with seeds was estimated by acid and alkali digestion method (Sadasivam and Manickam, 1992).

Crude protein content of pods (%)

Dried pod samples were subjected to nitrogen analysis by the modified microkjeldahl method (Jackson, 1967). The crude protein was estimated by multiplying the nitrogen percentage with a factor 6.25 (Simpson *et al*, 1965).

Keeping quality (days)

The harvested pods were kept under ordinary room conditions to study its shelf life and the number of days upto which the pods remained fresh for consumption without loss of colour and firmness were recorded.

f. Pest and disease scoring

The accessions were scored for the major pests and diseases in a 0-9 scale. The description for each scale is as follows

Score	Descriptor	Severity of symptoms
0	No incidence	No symptoms at all
3	Low incidence	Less than 25% of plants attacked
5	Medium incidence	25-50% of the plants attacked
7	High incidence	50-75% of plants attacked
9	Very high incidence	> 75% attacked

Scoring for the following major pests and diseases observed in the season was made.

f.1. Pests

f.1.1. American serpentine leaf miner - *Lyriomyza trifolii*

f.1.2. Pod bug - *Riptortus pedestris*

f.1.3. Cowpea Aphid - *Aphis craccivora*

f.2. Diseases

f.2.1. Cowpea rust - *Uromyces appendiculatus*

f.2.2. Cercospora Leafspot - *Cercospora canascens*

f.2.3. Anthracnose (Colletotrichum Leafspot) - *Colletotrichum lindemuthianum*

f.2.4. Fusarium wilt - *Fusarium oxysporum*

f.2.5. Cowpea mosaic - *Cowpea mosaic virus*

g. Genetic catalogueing

The genotypes were described morphologically using descriptors developed by IBPGR (IBPGR, 1983) and NBPGR for cowpea (table 2).

3.3 Statistical Analysis

The collected data were subjected to the following statistical analysis.

3.3.1 Analysis of variance and covariance

Analysis of variance and covariance were done (a) to test the significant difference among the genotypes with respect to various traits and (b) to estimate variance components and other parameters like correlation coefficients, heritability, genetic advance etc. (Singh and Choudhary, 1979).

3.3.1.1 Variance

	x	y
Environmental variance(σ_e^2)	$\sigma^2_{ex} = E_{xx}$	$\sigma^2_{ey} = E_{yy}$
Genotypic variance(σ^2_g)	$\sigma^2_{gx} = \dfrac{G_{xx} - E_{xx}}{r}$	$\sigma^2_{gy} = \dfrac{G_{yy} - E_{yy}}{r}$
Phenotypic variance(σ^2_p)	$\sigma^2_{px} = \sigma^2_{gx} + \sigma^2_{ex}$	$\sigma^2_{py} = \sigma^2_{gy} + \sigma^2_{ey}$

Analysis of variance and covariance is represented in table 3. From this table, the genetic parameters for any two traits x and y are estimable as follows.

Table 2 - Descriptors for yard long bean

1. Plant Data - Vegetative

1.1 Growth habit

Evaluated in the 6th week after sowing

1. Acute erect (branches form acute angle with main stem)

2. Erect (branching angle less acute than above)

3. Semi-erect (branches perpendicular to main stem, but do not touch ground)

4. Intermediate (most lower branches touch the ground)

5. Semi prostrate (main stem reaches 20 or more cm above ground)

6. Prostrate (plants flat on ground branches spread several meters)

7. Climbing

1.2 Growth pattern

Recording period near 50% flowering (Terminal or uppermost axial bud must have flowered)

1. Determinate (Terminal (apical) bud of main stem reproductive)

2. Indeterminate (uppermost raceme position is in the axial bud)

1.3 Plant vigour

To be recorded at complete vegetative growth stage

3. Non vigorous

4. Intermediate

7. Vigorous

9. Very vigorous

1.4 Leafiness   Recording period completion of vegetative growth

phase

1. Vigorously leafy

2. Leafy

3. Intermediate

4. Sparse, leaf size average or above

5. Sparse, leaf size small

1.5 Plant pigmentation   Recorded for stem, branches petioles, and peduncle

in the sixth week after sowing

0. None

1. Very slight

3. Moderate at the base and tip of petioles

5. Intermediate

7. Extensive

9. Solid

2.Inflorescence and Fruit Data

2.1 Flower pigment pattern   Of newly opened flowers

0. Not pigmented (white / cream)

1. Wing pigmented; standard with light v-shaped

	pattern of pigment at top centre
	2. Pigmented margins on wing and standard
	3. Wing pigmented; standard lightly pigmented
	4. Wing with pigmented upper margin standard is pigmented
	5. Completely pigmented
	6. Others
2.2 Calyx colour	0. Green
	3. Lightly pigmented
	5. Deeply pigmented
2.3 Calyx lobing	3. Light
	5. Medium
	7. Deep
2.4 Days to 50% flowering	Recorded from date of sowing to the appearance of first flower in 50% plants
	1. 40-45 days
	2. 45-50 days
	3. 50-55 days
2.5 Duration of flowering	Recorded from first flowering to the stage when 50% plants have finished flowering
	1. Asynchronous (> 30 days)
	2. Intermediate
	3. Synchronous (< 15 days)

2.6 Raceme position	Recorded when peduncles have reached full length
	1. Mostly above canopy
	2. In upper canopy
	3. Throughout canopy
2.7 Number of clusters/plant	Average of five plants to be recorded when pod formation is complete
	1. 25-40
	2. 40-55
	3. 55-70
2.8 Days to first mature pods	From sowing to stage when 50% of the plants have mature pods
	1. 52-58
	2. 58-64
	3. 64-70
2.9 Pod attachment to peduncle	Recorded at complete pod formation
	3. Pendant
	5. 30-90 degree from erect
	7. Erect
2.10 Immature pod pigmentation	Pattern of pigment distribution on full grown immature pods
	0. None
	1. Pigmented tip
	2. Pigmented sutures
	3. Pigmented valves; green sutures

	4. Splashes of pigment
	5. Uniformly pigmented
	6. Others
2.11 Pod length	Recorded at complete pod formation
	1. Extra long (> 45 cm)
	3. Medium (35-45 cm)
	5. Small (< 35 cm)
2.12 Pod curvature	Recording period at complete pod formation
	0. Straight
	3. Slightly curved
	5. Curved
	7. Coiled
2.13 Pod fibrousness	Recorded at vegetable harvestible stage
	1. Fibre less (1.40 to 2.0%)
	3. Moderately fibrous (2.0-2.6%)
	5. Highly fibrous (> 2.6%)
2.14 Number of locules/pod	Mean number of ten pods measured for length
	1. 12-15
	2. 15-18
	3. 18-21
2.15 Hundred seed weight	Average of 100 seeds drawn at random (g)
	1. 13-16
	2. 16-19
	3. 19-23

2. 16 Seed colour (descriptive)   Recorded within 3 months after harvest

1. Light brown

2. Light brown and white

3. Brown

4. Brown with stripes

5. Brown with white tip

6. Brown and white

7. Dark brown

8. Dark brown and white

9. Black

3. Plant duration

3.1 Senescence   Recorded at complete maturity of germplasm

population

1. Whole plant green

2. 70% plant green

3. 40% plant green

4. 10-15% plant green

5. Complete plant dried

3.2 Perenniality   Recorded as above

0. No regeneration

1. New leaves emerging

2. Leaves and flowers emerging

Flowers emerging

Table 3 Analysis of variance / covariance

Source		Observed mean square	Expected mean square	Observed mean sum of products	Expected mean sum of products	Observed mean square	Expected mean square
		xx	xx	xy	xy	yy	yy
Block	(r-1)	B_{xx}		B_{xy}		B_{yy}	
Genotype	(v-1)	G_{xx}	$\sigma^2_{ex} + r\sigma^2_{gx}$	G_{xy}	$\sigma_{exy} + r\sigma_{gxy}$	G_{yy}	$\sigma^2_{ex} + r\sigma^2_{gx}$
Error	(v-1)(r-1)	E_{xx}	σ^2_{ex}	E_{xy}	σ_{exy}	E_{yy}	σ^2_{ey}
Total	(rv-1)	T_{xx}		T_{xy}		T_{yy}	

3.3.1.2 Coefficient of variation

Phenotypic and genotypic coefficient of variation (PCV and GCV) were estimated as

$$GCV = \frac{\sigma_{gx}}{\bar{x}} \times 100 \text{ and}$$

$$PCV = \frac{\sigma_{px}}{\bar{x}} \times 100$$

where σ_{gx} - genotypic standard deviation, σ_{px} - phenotypic standard deviation and $\bar{x}$ is the mean of the character under study.

3.3.1.3 Heritability (Broad sense)

$$h^2 = \frac{\sigma^2_{gx}}{\sigma^2_{px}}$$

where h^2 is the heritability (Jain, 1982).

3.3.1.4 Genetic advance as percentage of mean

$$GA = \frac{kh^2\sigma_p}{\bar{x}} \times 100$$

where k is the standardised selection differential. $k = 2.06$ at 5% selection intensity (Miller et al, 1958)

3.3.2 Correlation

Genotypic correlation (r_{gxy}) $= \dfrac{\sigma_{gxy}}{\sigma_{gx} \times \sigma_{gy}}$

Phenotypic correlation (r_{pxy}) $= \dfrac{\sigma_{pxy}}{\sigma_{px} \times \sigma_{py}}$

Environmental correlation (r_{exy}) $= \dfrac{\sigma_{exy}}{\sigma_{ex} \times \sigma_{ey}}$

3.3.3 Path analysis

The path coefficients were worked out by the method suggested by Wright (1921) using ten characters which showed high correlation with yield. The simultaneous equations which give the estimates of path coefficients are as follows

$$
\begin{vmatrix} r_{1y} \\ r_{2y} \\ r_{iy} \\ r_{ky} \end{vmatrix}
=
\begin{vmatrix} 1 & r_{12} & r_{13} \cdots r_{1j} \cdots r_{1k} \\ & 1 & r_{23} \cdots\cdots\cdots r_{2k} \\ & & r_{ij} \cdots\cdots r_{ik} \\ & & 1 \end{vmatrix}
\times
\begin{vmatrix} p_1 \\ p_2 \\ p_i \\ p_k \end{vmatrix}
$$

i.e., $\underline{R}_y = R_x \underline{P}$ so that $\underline{P} = R_x^{-1} \underline{R}_y$

Where r_{ij} is the genotypic correlation between x_i and x_j ; i, j = 1, 2 ......, k ;

r_{iy} is the genotypic correlation between x_i and y and P_i is the path coefficient of x_i

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

$$ R = \sqrt{\left(1 - \sum_{i=1}^{k} P_i r_{iy}\right)} $$

Indirect effect of different characters on yield is obtained as $P_i\, r_{ij}$ for the ith character via j[th] character.

3.3.4 Selection index

The selection index developed by Smith (1937) using discriminant function of Fisher (1936) was used to discriminate the genotypes based on 13 characters.

The selection index is described by the function $I = b_1x_1 + b_2x_2 + \ldots \ldots b_kx_k$ and the merit of a plant is described by the function $H = a_1G_1 + a_2G_2 + \ldots \ldots + a_kG_K$ where $x_1, x_2 \ldots x_k$ are the phenotypic values and $G_1, G_2 \ldots G_k$ are the genotypic values of the plant with respect to characters, $x_1, x_2 \ldots x_k$ and H is the genetic worth of the plant. It is assumed that the economic weight assigned to each character is equal to unity. ie $a_1, a_2, \ldots, a_k = 1$. The b coefficients are determined such that the correlation between H and I is maximum.

3.3.5 Assessment of genetic divergence and grouping of genotypies

The genetic distances among 30 cowpea genotypes were assessed by determining Mahalanobis D^2 (Mahalanobis, 1928) values between every pair using 13 quantitative characters, selected for computation of selection index. Grouping of genotypes into clusters were done by Tocher's method (Rao, 1952).

Results

4. RESULTS

Different genotypes of yard long bean (30) were evaluated for various morphological and yield traits. The data on the observations recorded were statistically analysed and the results presented in this chapter.

4.1 Analysis of variance

The analysis of variance revealed significant differences among the thirty yard long bean genotypes for all the following twenty four characters studied.

1. Length of vine (cm)

2. Number of primary branches

3. Petiole length (cm)

4. Length of terminal leaflet (cm)

5. Breadth of terminal leaflet (cm)

6. Length of lateral leaflet (cm)

7. Breadth of lateral leaflet (cm)

8. Days to flowering

9. Days to first harvest

10. Harvesting interval

11. Pod length (cm)

12. Pod girth (mm)

13. Pod weight (g)

14. Beans per pod

Table 4 : Analysis of variance for 24 characters in 30 yard long bean genotypes (Mean squares are given)

Source	df	1	2	3	4	5	6	7	8
Replication	2	250.0	5.7986	0.8714	0.2344	0.0010	0.1084	0.1201	0.4063
Genotype	29	8044.3110**	1.2650**	3.5975**	2.8998**	1.7539**	3.5268**	1.9134**	16.5151**
Error	58	254.9483	0.3750	0.3279	0.2794	0.1111	0.3050	0.1287	0.6765

Source	df	9	10	11	12	13	14	15	16
Replication	2	0.2188	0.0272	0.9375	1.1445	4.6465	0.4932	0.5771	1.2422
Genotype	29	44.1272**	0.2467**	67.5436**	14.6599**	100.3194**	9.5503**	17.5557**	304.9812**
Error	58	0.8761	0.022	1.2724	0.2971	1.4203	0.3984	1.2469	6.5434

Source	df	17	18	19	20	21	22	23	24
Replication	2	1.0315	0.500	37.4219	0.0395	1.8457	0.0012	0.0122	0.0172
Genotype	29	4.7879**	422.4828**	58.1326**	0.8957**	15.3926**	0.2151**	0.2685**	1.0917**
Error	58	0.2243	0.4111	27.5140	0.0214	0.1013	0.0126	0.0170	0.0254

** Significant at 1% level

15.Length of peduncle

16.Inflorescence per plant

17.Pods per inflorescence

18.Pod per kg

19.Pods per plant

20.Pod yield per plant (kg)

21.100 seed weight (g)

22.Fibre content of pods (%)

23.Protein content of pods (%)

24.Keeping quality of pods (days)

The analysis of variance is presented in table 4.

4.2 Mean performance of the genotypes

The mean values of the thirty yard long bean genotypes for the 24 characters studied are presented in table 5.

The genotype VS-6 recorded the maximum mean vine length (476.8 cm) and the least was for VS-16 (249 cm). The maximum number of primary branches was observed for VS-21 (4.53) and it was minimum for VS-18 (1.93). The character petiole length was maximum for VS-5 (12.23 cm) and minimum for VS-10 (7.83 cm). The genotype VS-18 had the maximum length of terminal leaflet (16.21 cm), whereas it was lowest for VS-15 (12.04).

The genotype VS-13 was the earliest to flower (45.43 days) and VS-1, the latest (53.74 days). The genotype VS-19 took minimum days to first harvest (52.57) whereas VS-14 took the maximum number of days to first harvest (68.42).

Table 4 : Analysis of variance for 24 characters in 30 yard long bean genotypes (Mean squares are given)

Source	df	1	2	3	4	5	6	7	8
Replication	2	250.0	5.7986	0.8714	0.2344	0.0010	0.1084	0.1201	0.4063
Genotype	29	8044.3110**	1.2650**	3.5975**	2.8998**	1.7539**	3.5268**	1.9134**	16.5151**
Error	58	254.9483	0.3750	0.3279	0.2794	0.1111	0.3050	0.1287	0.6765

Source	df	9	10	11	12	13	14	15	16
Replication	2	0.2188	0.0272	0.9375	1.1445	4.6465	0.4932	0.5771	1.2422
Genotype	29	44.1272**	0.2467**	67.5436**	14.6599**	100.3194**	9.5503**	17.5557**	304.9812**
Error	58	0.8761	0.022	1.2724	0.2971	1.4203	0.3984	1.2469	6.5434

Source	df	17	18	19	20	21	22	23	24
Replication	2	1.0315	0.500	37.4219	0.0395	1.8457	0.0012	0.0122	0.0172
Genotype	29	4.7879**	422.4828**	58.1326**	0.8957**	15.3926**	0.2151**	0.2685**	1.0917**
Error	58	0.2243	0.4111	27.5140	0.0214	0.1013	0.0126	0.0170	0.0254

** Significant at 1% level

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Table 5 - Mean values for 24 biometric characters for 30 yard long bean genotypes

Genotypes	Vine length (cm)	Primary branches	Petiole length (cm)	Length of terminal leaflet (cm)	Breadth of lateral leaflet (cm)	Length of lateral leaflet (cm)	Breadth of lateral leaflet (cm)	Days to flowering	Days to first harvest	Harvesting interval (days)	Pod length (cm)	Pod girth (mm)
1	2	3	4	5	6	7	8	9	10	11	12	13
VS-1	362.67	2.86	11.46	14.22	7.21	12.70	7.44	53.74	67.07	3.42	41.38	24.96
VS-2	330.00	2.93	10.29	15.29	7.49	13.24	6.98	49.47	61.13	3.92	44.42	25.70
VS-3	445.00	3.63	9.29	14.72	7.87	12.34	7.48	47.07	59.83	3.38	51.44	26.70
VS-4	373.00	3.80	11.24	15.79	9.14	13.73	8.99	53.70	68.40	3.57	35.50	26.88
VS-5	411.67	3.53	12.23	15.13	8.61	12.93	7.82	53.07	64.37	3.97	52.22	24.84
VS-6	476.68	3.70	9.91	13.99	6.65	12.05	6.51	53.12	65.73	3.64	46.25	23.64
VS-7	406.00	4.13	9.02	12.37	6.95	10.72	6.37	48.67	58.53	3.42	41.41	25.74
VS-8	354.00	2.80	9.88	14.17	6.97	12.70	7.73	48.42	66.77	3.53	48.71	24.94
VS-9	383.33	4.33	12.17	13.48	7.46	12.33	7.22	46.27	58.23	3.48	48.53	23.89
VS-10	292.67	3.40	07.83	13.18	7.16	13.18	7.13	50.07	63.27	3.44	39.38	25.43
VS-11	453.66	3.20	10.38	13.87	7.55	13.03	7.25	49.72	60.13	3.69	41.31	26.33
VS-13	361.33	4.00	10.74	14.04	7.24	12.13	7.30	45.43	61.37	4.10	46.73	23.28
VS-14	386.33	3.13	12.04	14.01	7.40	13.02	7.39	52.03	68.42	4.45	43.06	31.62
VS-15	433.00	3.70	09.08	12.04	7.22	11.14	6.87	47.35	61.27	3.57	51.08	26.89
VS-16	249.00	4.07	10.28	13.47	6.62	13.47	6.62	48.50	62.67	3.03	48.49	28.98

Table 5 Continued

1	2	3	4	5	6	7	8	9	10	11	12	13
VS-17	364.66	2.93	10.33	13.62	7.72	11.75	7.41	50.67	68.03	3.83	37.45	24.22
VS-18	427.00	1.93	10.32	16.21	9.11	14.46	8.52	50.71	62.97	3.20	44.49	21.24
VS-19	456.00	4.40	11.32	15.76	8.57	14.51	8.60	48.01	52.57	3.35	39.37	25.66
VS-20	401.33	3.40	10.72	13.08	6.54	11.06	6.18	50.09	58.97	3.66	49.45	27.74
VS-21	378.33	4.53	9.11	14.02	8.16	12.98	8.59	47.88	66.77	3.95	54.29	27.69
VS-22	352.67	2.27	9.79	14.58	7.54	13.05	7.40	46.17	62.87	3.55	50.75	29.01
VS-23	370.66	3.33	9.93	12.64	6.76	10.58	6.91	45.90	61.00	3.68	40.98	25.60
VS-24	328.67	2.33	10.57	14.15	7.98	12.09	7.83	48.47	63.23	3.87	44.90	27.65
VS-25	360.33	4.00	11.95	13.46	7.63	12.45	7.98	50.06	63.23	3.37	50.16	26.58
VS-26	313.00	3.90	9.99	15.86	8.46	14.08	9.52	47.40	58.50	3.69	44.11	25.58
VS-27	371.68	4.23	9.62	12.79	6.22	10.77	6.62	46.47	60.27	3.38	46.70	22.43
VS-28	432.33	3.13	8.91	13.94	7.69	12.93	7.21	46.66	54.33	3.54	46.35	23.64
VS-29	425.67	3.06	8.71	13.79	7.09	12.03	7.43	49.39	61.33	3.59	39.29	21.98
VS-30	336.67	3.80	9.42	14.44	6.67	11.01	6.28	49.27	64.37	3.62	47.97	23.85
VS-31	337.00	3.53	10.57	13.30	6.85	11.33	7.07	49.48	61.33	3.29	46.13	26.27
CD (5%)	26.05	1.00	0.94	0.86	0.54	0.90	0.59	1.34	1.53	0.24	1.84	0.89
CD (1%)	34.66	1.33	1.24	1.15	0.72	1.19	0.78	1.79	2.03	0.32	2.44	1.18

Genotypes	Pod weight (g)	Beans per pod	Length of peduncle (cm)	Inflorescence per plant	Pods per inflorescence	Pods per kg	Pods per plant	Pod yield per plant (kg)	100 seed weight (g)	Fibre content of pods (%)	Protein content of pods (%)	Keeping quality of pods (days)
1	14	15	16	17	18	19	20	21	22	23	24	25
VS-1	19.80	17.90	16.20	30.00	5.40	50.23	49.00	0.94	17.99	2.05	5.33	3.59
VS-2	27.52	19.11	17.80	33.67	8.23	35.74	67.67	1.84	20.60	1.69	5.43	3.88
VS-3	29.22	18.97	20.97	27.33	6.00	33.63	84.33	2.46	19.05	2.11	5.27	3.00
VS-4	19.51	15.59	14.60	42.33	8.90	50.03	97.67	2.02	17.67	1.88	5.60	2.35
VS-5	32.98	20.66	15.20	41.00	7.23	30.20	71.00	2.47	22.17	1.95	4.93	2.17
VS-6	27.62	19.99	19.03	34.67	6.53	37.67	85.00	2.06	17.83	1.55	4.76	3.42
VS-7	24.72	18.75	15.17	50.33	4.80	42.95	81.33	1.88	15.76	2.21	5.45	3.03
VS-8	29.77	17.95	18.97	36.00	8.06	33.25	55.33	1.70	15.53	1.71	5.02	2.60
VS-9	26.07	18.26	19.00	50.00	7.70	37.67	96.33	2.59	16.65	1.59	5.44	2.71
VS-10	17.85	17.71	12.47	50.33	5.30	60.15	65.33	1.05	16.69	1.93	5.09	2.19
VS-11	15.30	18.14	18.00	43.83	4.70	74.88	72.67	1.05	19.55	1.49	4.75	2.47
VS-13	25.46	18.00	12.93	43.00	4.23	37.81	78.33	2.01	14.99	2.16	5.20	3.68
VS-14	21.44	15.95	15.80	37.67	5.17	50.04	89.00	1.87	17.13	2.81	5.49	2.19
VS-15	34.30	18.96	17.13	69.30	6.87	28.81	87.67	2.96	15.94	1.86	4.81	2.46
VS-16	25.84	19.87	19.23	40.67	6.73	39.50	92.00	2.31	17.63	1.95	4.92	3.04

Table 5 continued

1	14	15	16	17	18	19	20	21	22	23	24	25
VS-17	17.67	18.09	21.70	29.33	4.87	55.51	42.67	0.77	16.79	2.14	4.96	3.26
VS-18	17.81	20.94	18.73	25.67	4.30	60.04	80.33	1.36	14.01	1.75	4.84	2.49
VS-19	17.30	17.02	15.57	10.00	5.20	60.27	80.00	1.39	14.86	2.19	5.29	2.20
VS-20	37.14	13.36	18.90	34.33	5.16	27.99	66.33	2.34	16.62	1.84	4.87	3.01
VS-21	30.35	20.64	15.30	29.30	7.00	33.17	53.00	1.66	21.21	2.23	5.24	3.12
VS-22	30.86	20.96	14.23	30.67	6.90	32.82	58.00	1.80	16.39	1.87	5.90	2.26
VS-23	16.34	19.01	19.13	48.30	5.67	59.69	58.33	2.08	20.61	1.85	5.23	3.85
VS-24	26.13	17.06	17.17	29.33	7.00	39.55	81.67	2.06	19.73	2.34	4.85	3.73
VS-25	19.05	18.84	13.33	32.00	8.43	52.93	63.33	1.21	19.41	1.86	4.78	2.63
VS-26	20.81	17.15	16.13	39.00	5.40	49.80	81.67	1.72	14.48	2.22	4.85	2.15
VS-27	24.17	19.15	16.47	46.30	6.63	42.79	65.33	1.48	14.52	2.11	5.05	3.59
VS-28	20.94	15.48	19.83	34.00	6.70	49.84	79.67	1.59	13.83	1.87	5.03	2.69
VS-29	1.70	17.06	19.90	41.67	5.51	59.35	97.33	1.64	16.44	2.11	4.99	3.17
VS-30	24.00	15.84	18.57	45.00	5.87	42.85	71.66	1.67	17.45	1.83	4.95	3.39
VS-31	29.27	19.65	15.16	44.67	6.90	33.38	88.33	2.83	14.47	1.84	5.59	4.06
CD (5%)	1.95	1.03	1.82	4.18	0.77	1.05	8.57	0.24	0.52	0.18	0.21	0.26
CD (1%)	2.59	1.37	2.42	5.55	1.03	1.39	11.39	0.32	0.69	0.24	0.28	0.34

Length of pods was maximum in VS-21 (54.29 cm) and minimum in VS-4 (35.5 cm). VS-14 had the maximum pod girth (31.62 mm) and the minimum for VS-18 (21.24 mm). Maximum mean weight of pods was recorded by VS-20 (37.14 g) and minimum pod weight was for VS-11 (15.3 g).

Genotype VS-4 recorded the maximum number of pods/inflorescence (8.9) and the minimum was for VS-13 (4.29).

The number of pods to make one kg was least for VS-20 (27.99) and maximum for VS-11 (74.88). The genotype VS-4 recorded the maximum number of pods/plant (97.67) whereas the pod yield/plant was maximum for VS-15 (2.96 kg). The minimum number of pods/plant was observed for VS-17 (42.67) and the pod yield/plant was also minimum (0.77) for this genotype.

Genotype VS-5 recorded the highest 100 seed weight (22.17 g) whereas it was lowest for VS-28 (13.83 g). Maximum fibre content was recorded for VS-14 (2.81%) and protein content for VS-22 (5.9%). The lowest fibre content (1.49%) and protein content (4.75%) was recorded for VS-11. Shelf life was maximum for VS-31 (4.06 days) and least for VS-26 (2.15 days).

4.3 Genetic variability, heritability and genetic advance

The population mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) heritability, genetic advance, and genetic gain (as percentage of mean) for all the 24 characters studied are presented in table 6.

Vine length

Vine length ranged from 229 to 478 cm with a mean of 379.16cm. This character had a GCV of 13.44 and PCV of 14.08. The heritability was 0.91 (fig.1) and genetic advance as percent of mean was 26.42. (fig.2)

Heritability of 9 characters in yard long bean

X_1 - Number of primary branches

X_2 - Days to flowering

X_3 - Harvesting interval

X_4 - Pod length

X_5 - Pod weight

X_6 - Pods per plant

X_7 - Pods per kg

X_8 - Pod yield per plant

X_9 - Protein content of pods
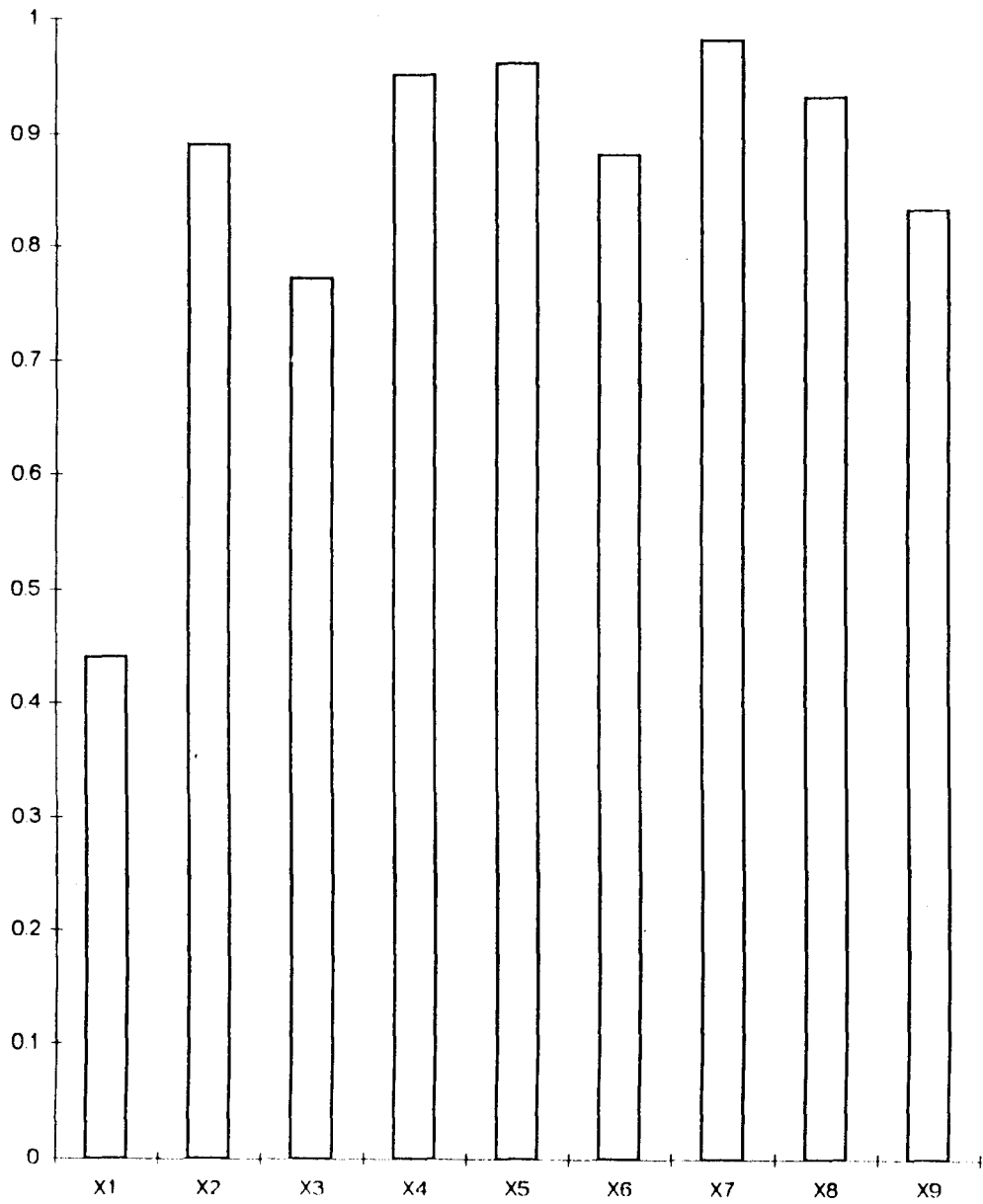
Fig I   Heritability of 9 characters in yard long bean

Genetic advance (as percentage of mean) for 9 characters in yard long bean

X_1 - Number of primary branches

X_2 - Days to flowering

X_3 - Harvesting interval

X_4 - Pod length

X_5 - Pod weight

X_6 - Pods per plant

X_7 - Pods per kg

X_8 - Pod yield per plant

X_9 - Protein content of pods
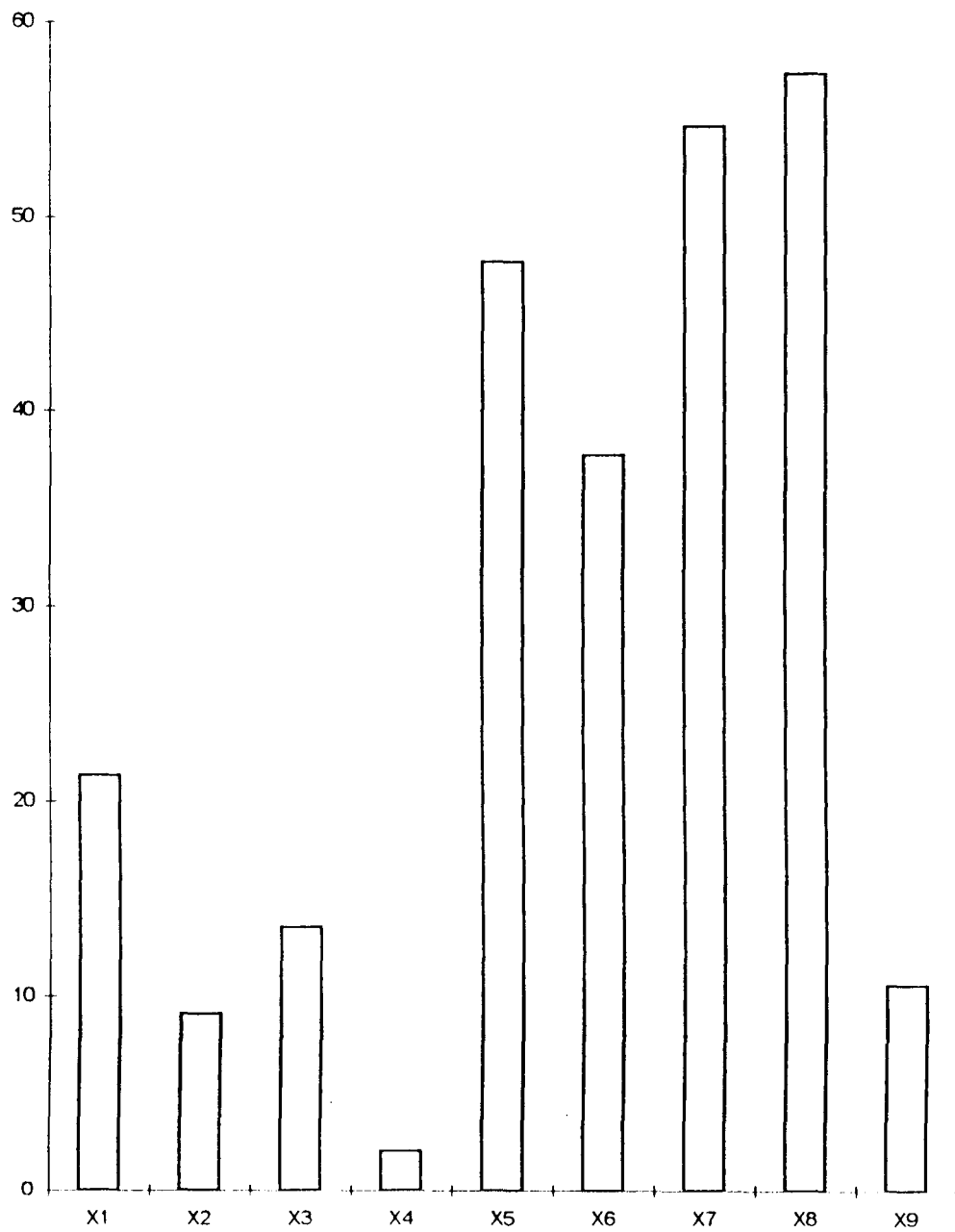
Fig 2   Genetic advance (as percentage of mean) for 9 characters in yard long bean

Table 6 Range, mean, PCV, GCV, heritability, genetic advance and genetic gain as percent of mean for 24 characters in yard long bean

Characters	Range	Mean ± SE	GCV	PCV	Heritability	Genetic advance	Genetic gain (as % of mean)
1. Vine length (cm)	229 - 498	379.145 ± 9.21	13.44	14.08	0.91	100.17	26.42
2. No. of primary branches	1.4 - 5.1	3.49 ± 0.35	15.69	23.63	0.44	0.74	21.30
3. Petiole length (cm)	7.26 - 12.92	10.24 ± 0.33	10.19	11.63	0.77	1.89	18.46
4. Length of terminal leaflet (cm)	11.97 - 17.6	14.07 ± 0.31	6.65	7.64	0.76	1.68	11.90
5. Breadth of terminal leaflet (cm)	6.0 - 9.96	7.48± 0.19	9.88	10.83	0.83	1.39	18.58
6. Length of lateral leaflet (cm)	9.77 - 15.24	12.49 ± 0.32	8.32	9.42	0.78	1.88	15.05
7. Breadth of lateral leaflet (cm)	5.97 - 9.91	7.42 ± 0.21	10.41	11.49	0.82	1.44	19.41
8. Days to first flowering	45 - 54.33	49.13 ± 0.47	4.68	4.96	0.89	4.46	9.07
9. Days to first harvest	51.90 - 69.1	62.23 ± 0.54	6.10	6.28	0.94	7.59	12.20
10. Harvesting interval	3.0 - 4.6	3.61 ± 0.09	7.59	8.63	0.77	0.49	13.57
11. Pod length (cm)	34.18 - 54.18	45.41 ± 0.65	10.35	10.64	0.95	0.94	2.07
12. Pod girth (mm)	20.79 - 32.5	25.63 ± 0.32	8.53	8.79	0.94	9.41	36.71

Table 6 continued

Characters	Range	Mean ± SE	GCV	PCV	Heritability	Genetic advance	Genetic gain (as % of mean)
13. Pod weight (g)	13.93 - 38.00	24.33 ± 0.69	23.57	24.08	0.96	11.58	47.59
14. Beans per pod	12.69 - 21.90	18.22 ± 0.36	9.58	10.19	0.88	3.38	18.55
15. Length of peduncle (cm)	11.90 - 23.00	18.23 ± 0.64	13.65	15.14	0.81	4.33	23.99
16. Inflorescence per plant	25.00 - 71.00	39.29 ± 1.48	24.37	25.16	0.94	19.90	50.65
17. Pos per inflorescence	3.90 - 9.10	6.25 ± 0.27	19.76	21.17	0.87	2.37	37.92
18. Pods per kg	27.25 - 75.02	44.75 ± 0.37	26.50	26.54	0.98	24.40	54.53
19. Pods per plant	39.00 - 110.00	74.68 ± 3.02	19.41	20.64	0.88	28.09	37.61
20. Pod yield per plant (kg)	0.69 - 3.09	1.87 ± 0.08	29.50	30.56	0.93	1.07	57.22
21. 100 seed weight (g)	13.61 - 22.32	17.11 ± 0.18	13.13	13.26	0.98	4.61	26.94
22. Fibre content of pods (%)	1.44 - 2.96	1.97 ± 0.06	13.21	14.39	0.84	0.49	24.87
23. Protein content of pods (%)	4.61 - 5.94	5.13 ± 0.08	5.64	6.19	0.83	0.54	10.53
24. Keeping quality (days)	2.00 - 4.22	2.83 ± 0.09	20.18	20.89	0.93	1.19	42.05

Number of primary branches

Significant variation was observed for this character among the genotypes. It ranged from 1.4 to 5.1 with an overall mean of 3.49. It recorded a PCV of 23.63 and the GCV was only 15.69. Heritability was very low (0.44). Genetic gain as percentage of mean was also low (21.3).

Petiole length

This character had a general mean of 10.24 cm and the range was 7.26 to 12.92 PCV was 11.63 and GCV was 10.19. It had a heritability of 0.77 and genetic gain of 18.46.

Length of terminal leaflet

It ranged from 11.97 to 17.6 cm with a mean of 14.07 cm. It had a heritability of 0.76 and genetic gain was 11.9. The PCV was 7.64 and GCV was 6.65.

Breadth of terminal leaflet

The range was 6.0-9.96, 7.48 cm being the overall mean. PCV was 10.83 and GCV was 9.88. Comparatively high heritability (0.83) but low genetic gain (18.58) was recorded.

Length of lateral leaflet

It ranged from 9.77 to 15.24 cm with a mean of 12.49 cm. PCV was 9.42 and GCV was 8.32. Heritability of 0.78 and genetic gain of 15.05 was recorded.

Breadth of lateral leaflet

This character had a mean of 7.42 cm and the range was 5.97 to 9.91. PCV was 11.49 and GCV was 10.41. Comparitively high heritability (0.82) and low genetic gain (19.41) was recorded.

Days to first flowering

It ranged from 45 to 54.33days. The general mean was 49.13 days. It recorded a PCV of 4.96 and GCV of 4.68. High heritability of 0.89 was observed for this character. But the genetic gain was low (9.07).

Days to first harvest

It had a mean of 62.23 days and ranged from 51.9 to 69.1 days. Very high heritability of 0.94 was observed for this character though the genetic gain was low (12.2). The PCV was 6.28 and GCV was 6.1.

Harvesting interval

It ranged from 3.0 to 4.6 with a mean of 3.61 days. The PCV and GCV were 8.63 and 7.59 respectively. Heritability was 0.77 and genetic gain was 13.57.

Pod length

The overall mean for the character was 45.4 cm and ranged from 34.18 to 54.18 cm. It had very high heritability of 0.95 and low genetic gain of 2.07. The PCV was 10.64 and GCV was 10.35.

Pod girth

It ranged from 20.79 to 32.55 mm with a mean of 25.63 mm. The PCV was 8.79 and GCV was 8.53. Very high heritability of 0.94 and moderately high genetic gain of 36.71 was recorded.

Pod weight

Pod weight widely ranged from 13.33g to 38.0g, the mean being 24.33g. Very high heritability of 0.96 and moderately high genetic gain of 47.59 was observed. The PCV was 24.08 and GCV was 23.57.

Beans per pod

It ranged from 12.69 to 21.9 with a mean of 18.22. PCV was 10.19 and GCV was 9.58. Moderately high heritability (0.88) and low genetic gain (18.55) was observed.

Length of peduncle

The range was 11.9 to 23.0 cm with a mean of 18.05 cm. Moderately high estimates of heritability (0.81) and genetic gain (23.99) was noticed. This trait recorded a PCV of 15.14 and GCV of 13.65.

Iinflorescence per plant

A very high range of 25 to 71.0 was observed with a mean of 39.29. Very high estimates of heritability (0.94) and high genetic gain of 50.65 was also recorded. PCV was 25.16 and GCV was 24.37.

Pods per inflorescence

This character had a mean of 6.25 and ranged from 3.9 to 9.1. The PCV was 21.7 and GCV 19.76. Moderately high heritability was shown (0.87) genetic gain as percentage of mean was also moderate (37.92).

Pods per kg

This character exhibited a mean of 44.75 and ranged from 27.25 to 75.02. The PCV and GCV were 26.54 and 26.5 respectively. Very high heritability was shown by this trait (0.98) and genetic gain was also high (54.53).

Pods per plant

This trait ranged considerably from 29.0 to 110.0, with a mean of 74.68. The PCV was 20.64 and GCV was 19.41. High heritability of 0.88 and moderate genetic gain of 37.61 was observed.

Pod yield per plant

A very high range of 0.691 to 3.09 kg was observed with a mean of 1.87kg. The PCV was 30.56 and GCV was 29.5. Very high heritability of 0.93 and very high genetic gain of 57.22 was observed.

100 seed weight

This character had an overall mean of 17.11g with a range of 13.61 to 22.32 g. The PCV was 13.26 and GCV was 13.13. Very high heritability of 0.98 was observed for this trait. Genetic gain was moderate (26.94).

Fibre content of pods

It ranged from 1.44 to 2.96% with a mean of 1.97%. The PCV was 14.39 and GCV was 13.21. Moderately high heritability of 0.84 was recorded. The genetic gain was 24.87.

Protein content of pods

This trait showed a range of 4.61 to 5.94%, the mean being 5.13%. The PCV was 6.19 and GCV was 5.64. Moderately high heritability (0.83) and low genetic gain (10.53) was shown by this trait.

Keeping quality of pods

The general mean was 2.83 and the range was 2.0 to 4.22 days. The PCV was 20.89 and GCV was 20.18. High heritability and moderately high genetic advance of 0.93 and 42.05 respectively was recorded.

4.4 Correlation Studies

The phenotypic, genotypic and environmental correlations among the traits is worked out and presented in tables 7, 8 and 9. The traits were numbered from 1 to 24 as listed in section 4.1.

Table 7 Phenotypic Correlation Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
1	1.0000																							
2	0.0185	1.0000																						
3	0.0081	0.0620	1.0000																					
4	0.0511	-0.2048	0.2522	1.0000																				
5	0.1655	-0.1411	0.2819	0.7158	1.0000																			
6	-0.0698	-0.0877	0.2371	0.7719	0.6853	1.0000																		
7	-0.0186	-0.0104	0.2377	0.6398	0.7856	0.6770	1.0000																	
8	0.1108	-0.1826	0.2921	0.2318	0.2066	0.1960	0.1014	1.0000																
9	-0.2628	-0.1990	0.1420	0.0309	0.0428	0.0174	0.0902	0.5570	1.0000															
10	0.0612	-0.0875	0.2135	0.0452	0.0931	0.0559	0.0666	0.0824	0.2918	1.0000														
11		0.1478	0.0016	-0.0601	-0.1268	-0.1126	-0.1425	-0.3777	-0.0370	0.0229	1.0000													
12	-0.2523	0.0151	0.1718	-0.0909	0.0015	0.1177	0.0266	0.0557	0.1887	0.2152	0.1773	1.0000												
13	-0.0582	0.0822	-0.0417	-0.1799	-0.2362	-0.2637	-0.3053	-0.1246	0.0406	0.1025	0.7116	0.2801	1.0000											
14	-0.0051	-0.0143	-0.0732	0.0311	0.0981	0.1013	0.0675	-0.0852	0.1474	-0.2001	0.3313	-0.1156	0.1100	1.0000										
15	0.2413	-0.2132	-0.1471	-0.0223	-0.1389	-0.1473	-0.2393	-0.0615	-0.0840	-0.0977	-0.0355	-0.2222	-0.0506	-0.0936	1.0000									
16	-0.0678	0.2258	-0.0646	-0.3758	-0.3184	-0.3088	-0.3043	-0.0006	-0.0641	-0.1137	-0.1488	-0.0852	0.0121	-0.0536	-0.2450	1.0000								
17	-0.2031	0.1234	0.1716	0.0016	0.0240	0.0367	0.1029	0.0396	0.1941	-0.0934	0.3039	0.1728	0.3193	0.1132	-0.1128	-0.0458	1.0000							
18	0.1310	-0.1280	-0.0315	0.1112	0.2197	0.2742	0.2496	0.1461	-0.0987	0.0960	-0.7186	-0.2327	-0.9241	-0.1499	0.0310	0.0133	-0.4221	1.0000						
19	0.1687	0.1662	0.0812	0.0769	0.1247	0.1076	0.0172	0.0058	-0.2907	-0.1149	-0.0842	0.0331	0.0089	-0.1039	0.0243	0.0899	0.0749	-0.0354	1.0000					
20	0.0378	0.7835	0.1176	-0.1470	-0.1254	-0.2619	-0.2201	-0.1895	-0.1663	0.0207	0.4646	0.2505	0.6601	0.1086	0.0452	0.1486	0.3150	-0.6890	0.5692	1.0000				
21	-0.0312	-0.0017	0.1974	-0.0117	0.0843	-0.0443	-0.0005	0.2648	0.3694	0.3288	0.1901	0.3092	0.1201	0.2184	0.0018	-0.1088	0.3086	-0.0853	-0.2443	0.0600	1.0000			
22	-0.1294	0.0782	0.0610	-0.0189	0.1209	-0.0102	0.2240	-0.0089	0.1063	0.3972	-0.1214	0.3347	-0.0809	-0.1964	-0.2107	-0.0632	-0.2834	0.0128	0.0250	-0.0967	-0.0528	1.0000		
23	-0.1296	-0.0231	0.1157	0.0383	0.0304	0.0364	0.0340	-0.0898	0.0297	0.0881	-0.1212	0.2977	0.0847	0.0706	-0.2789	0.0733	0.1444	-0.1868	0.0417	0.1569	-0.0566	0.1593	1.0000	
24	-0.1910	0.0230	-0.0820	-0.2955	-0.4779	-0.5109	-0.4016	-0.1335	0.0576	0.0286	-0.0006	-0.2328	0.0764	0.0849	0.2103	0.0541	0.0212	-0.2092	-0.1528	0.1094	0.1480	-0.0544	0.0597	1.0000

Table 8 Genotypic Correlation Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
1	1.0000																							
2	0.0090	1.0000																						
3	0.0304	0.0490	1.0000																					
4	0.1039	-0.2909	0.3127	1.0000																				
5	0.2127	-0.1766	0.3066	0.8116	1.0000																			
6	-0.0345	-0.2171	0.2438	0.8055	0.7561	1.0000																		
7	0.0048	-0.0701	0.2534	0.7545	0.9060	0.7613	1.0000																	
8	0.1134	-0.2287	0.9860	0.2583	0.2319	0.2397	0.1355	1.0000																
9	-0.2708	-0.3308	0.1529	0.0351	0.0253	-0.0072	0.1131	0.6091	1.0000															
10	0.0811	-0.0966	0.2280	0.0859	0.0971	-0.0494	0.0843	0.1250	0.3537	1.0000														
11	0.0009	0.1875	0.0351	-0.0943	-0.1541	-0.1595	-0.1711	-0.3278	-0.0370	0.0031	1.0000													
12	-0.2737	0.0305	0.2226	-0.1263	-0.0175	0.0987	0.0277	0.0507	0.1863	0.2812	0.1929	1.0000												
13	-0.0540	0.1232	-0.0720	-0.1892	-0.2709	-0.3031	-0.3427	-0.1156	0.0490	0.1101	0.7604	0.3023	1.0000											
14	-0.0066	-0.0701	-0.0723	0.0383	0.0744	0.0828	0.0613	-0.1123	0.1687	-0.2275	0.3504	-0.1443	0.1298	1.0000										
15	0.2799	-0.2745	-0.1831	-0.0487	-0.1949	-0.2147	-0.3125	-0.0923	-0.0927	-0.1434	-0.0002	0.2575	-0.0605	-0.1048	1.0000									
16	-0.0751	0.3974	-0.0697	-0.4388	-0.3677	-0.3405	-0.3023	0.0011	-0.0756	-0.1366	-0.1577	-0.0943	0.0144	-0.0598	-0.2388	1.0000								
17	-0.2234	0.1460	0.2174	0.0632	0.0895	0.0760	0.1435	0.0799	0.2163	-0.0818	0.3488	0.2115	0.3450	0.1401	-0.1052	-0.0636	1.0000							
18	0.1378	-0.1738	-0.0420	0.1249	0.2340	0.3118	0.2764	0.1541	-0.1034	-0.1149	-0.7385	-0.2388	-0.9451	-0.1560	0.0297	0.0144	-0.4493	1.0000						
19	0.1797	0.2820	0.0783	0.1252	0.1342	0.1486	0.0152	-0.0103	-0.3011	-0.1348	-0.0837	0.0245	-0.0052	-0.1638	0.0372	0.0826	0.0815	-0.0379	1.0000					
20	0.0516	0.2856	0.1049	-0.1765	-0.1438	-0.3127	-0.2717	-0.2112	-0.1573	0.0214	0.5011	0.2526	0.6918	0.0899	0.0721	0.1484	0.3425	-0.7147	0.5521	1.0000				
21	-0.0455	0.0304	0.2263	-0.0013	0.0925	-0.0392	0.0150	0.2728	0.3784	0.3721	0.2012	0.3187	0.1222	0.2441	0.0031	-0.1181	0.3325	0.0867	-0.2682	0.0670	1.0000			
22	-0.1584	0.0990	-0.0716	0.0474	0.1351	0.0637	0.2708	-0.0312	0.1251	0.4434	-0.1402	0.3940	-0.1013	-0.2106	-0.2479	-0.0678	-0.3110	0.0090	0.0488	-0.0850	-0.0679	1.0000		
23	-0.1563	0.0558	0.1251	0.0710	0.0725	0.0686	0.0677	-0.1237	0.0445	0.0695	-0.1185	0.3387	0.0970	0.0958	0.3711	0.0727	0.1950	-0.2045	0.0392	0.1668	-0.0587	0.2307	1.0000	
24	-0.2012	-0.0514	-0.1235	-0.3598	-0.5271	-0.6104	-0.4716	-0.1248	0.0743	0.0189	-0.0104	-0.2300	0.0713	0.1129	0.2386	0.0661	0.0142	-0.2143	-0.1611	0.1183	0.1670	-0.0682	0.0524	1.0000

Table 9 Error Correlation Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
1	1.0000																							
2	0.0571	1.0000																						
3	-0.1203	0.0933	1.0000																					
4	-0.2387	-0.0995	0.0572	1.0000																				
5	-0.1592	-0.1112	0.1862	0.3546	1.0000																			
6	-0.2898	0.1126	0.2141	0.6616	0.3983	1.0000																		
7	-0.1805	0.1008	0.1788	0.2136	0.2108	0.3417	1.0000																	
8	0.0883	-0.1571	-0.2281	0.1213	0.0546	-0.0199	-0.0997	1.0000																
9	-0.1670	0.0800	0.1032	0.0098	0.2071	0.2090	-0.0923	0.0028	1.0000															
10	-0.0483	-0.0872	0.1622	-0.0875	0.0777	-0.0782	-0.0033	-0.1312	-0.0893	1.0000														
11	-0.0123	0.1531	-0.2523	0.1720	0.1026	0.2206	0.0845	-0.0970	0.0365	0.1824	1.0000													
12	0.0160	-0.0253	-0.1564	0.1331	0.1705	0.2916	0.0217	0.1151	0.2276	-0.2153	-0.0837	1.0000												
13	-0.1268	0.0139	0.2059	-0.1865	0.0675	-0.0183	-0.0124	-0.2634	-0.1239	0.0794	-0.2602	-0.1448	1.0000											
14	0.0088	0.1160	-0.0834	-0.0039	0.2458	0.2038	0.1086	0.1245	-0.0809	0.0735	0.1366	0.1959	-0.1377	1.0000										
15	0.0031	-0.1510	-0.0108	0.0734	0.1204	0.1159	0.0893	0.1172	-0.0271	0.0779	-0.0329	0.0303	0.0331	-0.0317	1.0000									
16	0.0225	-0.1609	-0.0454	-0.0474	0.0616	-0.1512	-0.3703	-0.0187	0.1172	-0.0271	0.0779	-0.0329	0.0303	0.0331	-0.0317	1.0000								
17	-0.0378	0.1225	0.0792	-0.2819	-0.1303	-0.1514	0.1226	-0.2534	-0.0222	-0.1539	-0.1516	-0.2161	0.0546	-0.0802	-0.1564	0.1321	1.0000							
18	-0.0162	-0.3173	0.2009	0.1004	0.3028	-0.0200	-0.3290	0.0675	0.1212	6.1873	-0.1181	-0.1021	-0.0028	-0.1860	0.1832	0.1698	-0.1663	1.0000						
19	0.0734	-0.0392	0.1016	-0.1528	0.0702	-0.0979	0.0398	0.1306	-0.1945	-0.0215	-0.0964	0.1304	0.4981	0.3535	-0.0496	0.1740	0.0272	0.0111	1.0000					
20	-0.1234	-0.0490	0.2294	0.0102	0.0110	0.0364	0.1607	0.0277	-0.3020	0.0199	-0.1446	0.2196	0.1191	0.3045	-0.1556	0.1517	0.0676	-0.0069	0.7655	1.0000				
21	0.2824	-0.2081	0.0142	-0.1547	0.0127	-0.1523	-0.2381	0.2233	0.1686	0.0716	-0.1118	0.0914	0.0549	-0.1890	-0.0165	0.1308	0.0243	0.0557	0.1160	-0.1092	1.0000			
22	0.0792	0.0604	0.0177	-0.2904	0.0484	-0.3311	-0.0081	0.1351	-0.0543	0.2078	0.0403	-0.1698	0.1257	-0.1085	-0.3220	-0.0300	-0.1183	0.2116	-0.1270	-0.2062	0.1613	1.0000		
23	0.0527	-0.1855	0.0996	-0.0693	-0.1776	-0.0974	-0.1271	0.1189	-0.0989	0.1660	-0.1683	-0.0209	-0.0228	-0.0828	0.1483	0.0891	-0.1475	-0.0230	0.0575	0.1187	-0.0636	-0.2076	1.0000	
24	-0.0722	0.2897	0.1818	0.0552	-0.1278	0.0782	0.1050	-0.2304	-0.1851	0.1024	0.1525	-0.2766	0.1709	-0.2011	0.0217	-0.1211	0.0907	-0.1760	-0.0728	-0.0132	-0.3260	0.0588	0.1275	1.0000

4.4.1 Phenotypic Correlation Coefficients

In general the phenotypic correlation coefficients were found to be lower than genotypic correlation coefficients.

Pod yield per plant was positively and highly correlated with pod length (0.4616), pod weight (0.6601) and pods per plant (0.5692). Strong negative association was obtained between pods per kg and pod length (-0.7186), pod weight b (-0.9241) and pods per inflorescence (-0.4221).

Days to first harvest was associated with days to first flowering (0.5570). Strong association between pod length and pod weight was noticed (0.7116).

Fibre content of pods had positive association with harvesting interval (0.3972).

Keeping quality of pods were negatively associated with breadth of terminal leaflet (-0.4779), length of lateral leaflet (-0.5109) and breadth of lateral leaflet (-0.4016).

4.4.2 Genotypic Correlation Coefficients

High positive correlation was obtained between pod yield per plant with pod length (0.5011), pod weight (0.6918) and pods per plant (0.5521). Strong negative correlation was obtained between pod yield per plant and pods per kg. (-0.7147).

Number of primary branches was positively associated with number of inflorescence per plant (0.3974). Very high negative correlation was obtained for pods per kg with pod weight (-0.9451) and pod length (-0.7385). This character had negative association with number of pods per inflorescence (-0.4493). Days to first harvest was associated with days to first flowering (0.6091).

Days to first flowering had positive association with petiole length (0.3986). Fibre content of pods was positively associated with harvesting interval (0.4434) and pod girth (0.3940). Weight of pods was strongly associated with pod length (0.7604).

Leaf dimensions were found to have negative association with number of inflorescence per plant as well as keeping quality of pods. Correlation between number of inflorescence per plant with length of terminal leaflet was -0.4388 and that with breadth of terminal leaflet was -0.3677. Similarly keeping quality or shelf life of pods had negative associations with leaf dimensions - with length of terminal leaflet: -0.5271, with length of lateral leaflet: -0.6104 and with breadth of lateral leaflet: -0.4716.

4.4.3 Error Correlation Coefficients

These were found to be very low indicating that the influence of environment is negligible in the expression of characters. But few error coefficients like pods per plant and pod yield per plant had a positive and strong association (0.7655). The correlation between length of lateral leaflet with length of terminal leaflet (0.6616) and breadth of terminal leaflet (0.3983) was also found to be high.

Based on the phenotypic and genotypic correlations, it was observed that the characters which highly contributed to pod yield per plant were pod length, pod weight, pods per kg and pods per plant. Pod weight exhibited high and strong positive association with pod yield. This was followed by pods per plant and pod length. The character, pods per kg had high negative correlation with yield.

4.5 Path coefficient analysis

In path coefficient analysis the genotypic correlations among yield and its component characters were partitioned into different components to find put the direct

or indirect contribution of each character on pod yield (Table 10). The following characters which act independently on yield, viz., petiole length (x_1), length of lateral leaflet (x_2) breadth of lateral leaflet (x_3), pod length (x_4), pod girth (x_5), pod weight (x_6), pods per inflorescence (x_7), pods per kg (x_8), pods per plant (x_9) and days to first flowering (x_{10}) were selected for path coefficient analysis. These components had comparatively high genotypic correlation to yield (fig. 3).

The path analysis revealed that the number of pods per plant exerted the maximum positive direct effect on pod yield (0.5655) followed by pod weight (0.4690). Petiole length also had direct positive effect (0.1780) on pod yield.

Though the direct effect of petiole length on pod yield is 0.1780, the total correlation is only 0.1049 due to negative indirect effects of length of lateral leaflet (-0.7770), days to first flowering (-0.0637) and weight of pods (-0.0388).

The total correlation of length of lateral leaflet on yield is -0.3127 and its direct effect is also -0.3158. The negative and positive indirect effects through other traits got nullified.

The direct effect of breadth of lateral leaflet is 0.1390 and the total correlation with yield is -0.2717. The positive direct effect was nullified by the negative indirect effects through breadth of lateral leaflet (-0.2404) and pod weight (-0.1607). Pods per kg (-0.0595) also contributes indirectly to total correlation. Length of pods exerted a positive indirect effect through pod weight (0.3566), pods per kg (0.1591) and days to flowering (0.0524) on total yield (0.5011), though its direct effect is low and negative (-0.0711).

The positive but low direct effect of pod girth (0.0368) along with its indirect effects through pod weight (0.1418), pods per kg (0.0514), petiole length (0.0396) and pods per plant (0.0252) contribute to the total yield (0.2526).

Table 10. Direct and indirect effects of yield components on pod yield in yard long bean

Characters	Petiole length	Length of lateral leaflet	Breadth of lateral leaflet	Length of pods	Pod girth	Weight of pads	Pods per inflorescence	Pods per kg	Pods per plant	Days to first flowering	Genotypic correlation with yield
Petiole length	0.1780	-0.0770	0.052	-0025	0.0082	-0.0338	0.0072	0.0090	0.0443	-0.0637	0.1049
Length of lateral leaflet	0.0434	-0.3158	0.1059	0.0113	0.0036	-0.1421	0.0025	-0.0672	0.0840	-0.0387	-0.3127
Breadth of lateral leaflet	0.0451	-0.2404	0.1390	0.0122	0.0010	-0.1607	0.0047	-0.-595	0.0086	-0.0217	-0.2717
Pod length	0.0062	0.0504	-0.0238	-0.0711	0.0071	0.3566	0.0115	0.1591	-0.0473	0.0524	0.5011
Pod girth	0.0396	-0.0312	0.0039	-0.0137	0.0368	0.1418	0.0070	0.0514	0.0252	-0.0081	0.2526
Wt. of pods	-0.0128	0.0957	-0.0476	-0.0540	0.0111	0.4690	0.0114	0.2036	-0.0029	0.0185	0.6918
Pods per inflorescence	0.0387	-0.0240	0.0200	-0.0248	0.0078	0.1618	0.0330	0.0968	0.0461	-0.0128	0.3425
Pods per kg	-0.0075	-0.0985	0.0384	0.0525	-0.0078	-0.4432	0.0145	-0.2154	-0.0224	-0.0246	-0.7147
Pods per Plant	0.0139	-0.0469	0.0021	0.0059	0.0009	-0.0024	0.0029	0.0086	0.5655	0.0016	0.5521
Days to flowering	0.0709	-0.0757	0.0188	0.0233	0.0019	-0.0542	0.0026	-0.0332	-0.0058	-0.1598	-0.2112

Residue = 0.1110

Underlined figures are the direct effects.

Figure 3

Path Diagram

X_1 - Petiole length

X_2 - Length of lateral leaflet

X_3 - Breadth of lateral leaflet

X_4 - Length of pods

X_5 - Pod girth

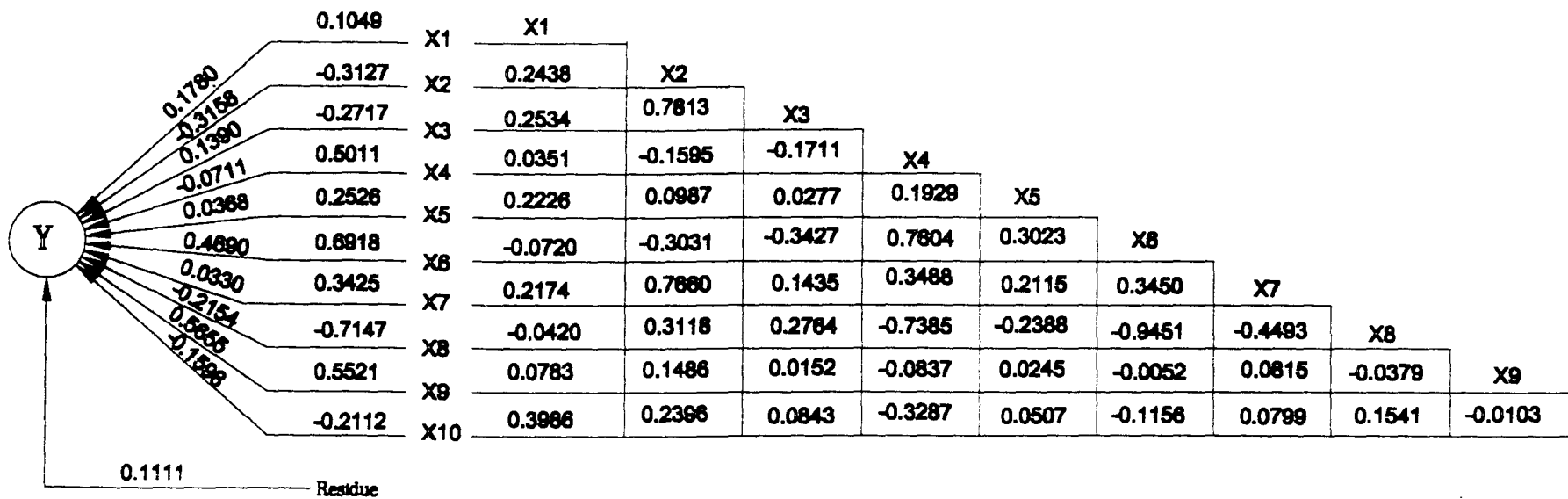X_6 - Weight of pods

X_7 - Pods/inflorescence

X_8 - Pods/kg

X_9 - Pods/plant

X_{10} - Days to first flowering

Y - Genotypic correlation with yield

Fig. 3 Path diagram - Showing direct and indirect effects of the components on yield

Pod weight exerted a strong and positive direct effect (0.4690) on total yield (0.6918) along with its indirect effect through pods per kg (0.2036), days to first flowering (0.0185), length of lateral leaflet (0.0957) and pods per inflorescence (0.0114).

The direct effect of pods per inflorescence to total correlation (0.3425) is low (0.0330). But its indirect inflorescence through weight of pods (0.1618), pods per kg (0.0968), pods per plant (0.0461), pods per inflorescence (0.0387) and breadth of lateral leaflet (0.02) contribute to the correlation of 0.3425.

The total correlation of yield with pods per kg is -0.7147, though its direct effect is only -0.2154. The high negative indirect effect through pod weight (-0.4432) length of lateral leaflet (-0.0985), days to first flowering (-0.0246) and pods per plant (-0.0224) contribute to the high total correlation.

The direct effect of pods per plant on total correlation is high (0.5655) and the total correlation is 0.5521. The positive and negative indirect effects got nullified.

The total correlation between yield and days to flowering is -0.2112, the direct effect is -0.1598 only. The total correlation is also contributed by the indirect effects via length of lateral leaflet (-0.0757), pod weight (-0.0542) and pods per kg (-0.0332).

The residue obtained is 0.1111 indicating that eighty nine percent of the variation was attributed to direct and indirect effect of the component characters taken for path analysis.

4.6 Selection Index

Selection index is used to discriminate the varieties based on major components of yield, viz., length of vine(x_1), number of primary branches(x_2), petiole length(x_3), length of lateral leaflet(x_4), breadth of lateral leaflet(x_5), days to first flowering(x_6),

length of pods(x_7), pod girth(x_8), pod weight(x_9), pods per inflorescence (x_{10}), pods per kg(x_{11}), pods per plant(x_{12}) and pod yield per plant(x_{13}). The selection index worked out is given below.

$$I = 0.9185x_1 + -0.2801x_2 + 0.7612x_3 + 3.9548x_4 + 0.5196x_5 + 1.2612x_6 + 1.0015x_7 + -0.2161x_8 + 1.1333x_9 + 0.5493x_{10} + 1.2458x_{11} + 0.6933x_{12} + 11.2579x_{13}$$

The selection index values are worked out and presented in table 11. The highest index score was recorded by the variety VS-6 (2333.66) followed by VS-11 (2258.58), VS-19 (2253.56), VS-3 (2211.32) and VS-18 (2198.074). The lowest sores were recorded by VS-16 (1702.63), VS-10 (1761.09), VS-2 (1846.03) and VS-26 (1852.99). If 20% selection is adopted, the varieties VS-6, VS-11, VS-19, VS-3, VS-18 and VS-15 are identified as superior varieties.

4.7 Genetic divergence among the genotypes, D^2 analysis

The thirty yard long bean genotypes were grouped into four clusters based on the D^2 analysis. The clustering pattern is given in table 12. The characters chosen for D^2 analysis were vine length, number of primary branches, petiole length, length of lateral leaflet, breadth of lateral leaflet, days to first flowering, pod length, pod girth, pod weight, pods per inflorescence, pods per kg, pods per plant and pod yield per plant.

Cluster IV was the largest with 18 genotypes followed by cluster III with 9 genotype. Cluster II had two and cluster I had one genotype (fig.4)

The inter and intra cluster D^2 values are presented in table 13. The inter cluster distance was maximum between clusters I and III (224.89) followed by cluster II and III (156.48). The inter cluster distance between cluster I and IV was also high (150.51). The least distance was between clusters I and II (80.55).

Table 11 Selection Index

Selection indices arranged in descending order

SL. No.	Genotype	Selection index values
1	VS - 6	2333.66
2	VS - 11	2258.58
3	VS - 19	2253.56
4	VS - 3	2211.32
5	VS - 18	2198.074
6	VS - 15	2186.666
7	VS - 29	2183.861
8	VS - 28	2161.972
9	VS - 5	2136.189
10	VS - 14	2078.016
11	VS - 9	2072.942
12	VS - 4	2058.808
13	VS - 7	2049.851
14	VS - 20	2044.801
15	VS - 21	1958.288
16	VS - 25	1948.257
17	VS - 23	1937.345
18	VS - 13	1934.872
19	VS - 31	1922.825
20	VS - 27	1921.428
21	VS - 1	1894.585
22	VS - 22	1886.853
23	VS - 8	1883.187
24	VS - 24	1871.415
25	VS - 30	1858.317
26	VS - 17	1855.992
27	VS - 26	1852.99
28	VS - 2	1846.034
29	VS - 10	1761.089
30	VS - 16	1702.629

Table 12 Clustering pattern in 30 yard long bean genotypes

Cluster Number	Number of genotypes in each cluster	Genotypes
I	1	VS - 16
II	2	VS - 10, VS - 26
III	9	VS - 3, VS - 6, VS - 7, VS - 11, VS - 15, VS - 18, VS - 19, VS - 28, VS - 29
IV	18	VS - 1, VS - 2, VS - 4, VS - 5, VS - 8, VS - 9, VS - 13, VS - 14, VS - 17, VS - 20 VS - 21, VS - 22, VS - 23, VS - 24, VS - 25, VS - 27, VS - 30, VS - 31

Table 13. Average Inter and Intra D^2 values among four clusters of genotypes in yard long bean

Cluster	I	II	III	IV
I	0.00	6487.54	50575.81	22652.38
		(80.55)	(224.89)	(150.51)
II		1202.34	24486.45	7261.73
		(34.67)	(156.48)	(85.21)
III			2311.05	9786.768
			(48.07)	(98.93)
IV				3306.75
				(57.50)

(D values in parenthesis)

Fig. 4 Cluster diagram
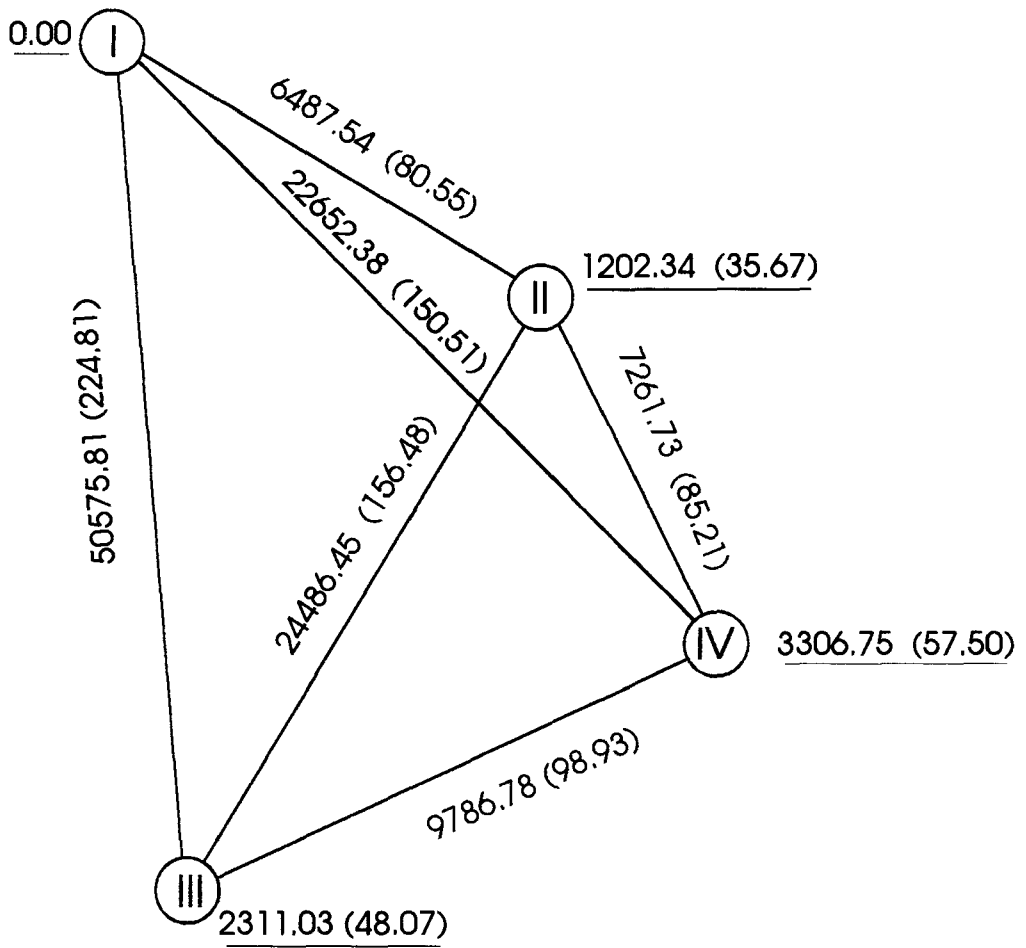
D values in paranthesis

Underlined figures indicate intra cluster distance

The intra cluster distance was on the increase for increasing cluster size. Cluster I had the lowest intra cluster distance. The cluster II had an intra cluster distance of 34.76 followed by cluster III (48.07) and cluster IV (57.50).

4.8 Genetic Cataloguing of the yard long bean accessions

Since a specific list of descriptors is not available for yard long bean, a descriptor was developed using the IBPGR and NBPGR descriptors for cowpea. A 0-9 scoring scale is adopted. The morphological characters are broadly classified into 1. Plant data during vegetative stage 2. Inflorescence and fruit data and 3. Plant duration data. The cataloguing is presented in table 14.

Based on the descriptor developed for yard long bean, the accessions were scored for morphological characters on a 0-9 scale (Table 14).

All the accessions had climbing habit with indeterminate growth pattern. They were all vigorous and leafy. Leaf shape and size exhibited variation among the genotypes (plates 1 and 2). Plant pigmentation varied among the genotypes. Genotypes VS-2, VS-3, VS-9, VS-14, VS-16, VS-23, VS-26 and VS-30 had plain green stem without any pigmentation. Genotype VS-- 5 had extensive dark red pigmentation through out the stem, petioles, calyx etc. Intermediate stem pigmentation was observed for VS-4, VS-8, VS-11, VS-18 and VS-28. Rest of the genotypes had moderate coloration at the base and tip of petioles.

Flower pigment pattern also showed marked variation (plate 3). The flowers were completely pigmented in VS-5 and VS-10. Genotypes VS-6, VS-20, VS-22, VS-24 and VS-29 had pigmented wings and lightly pigmented standards. White flowers were found in VS-3, VS-9, VS-13, VS-16, VS-17, VS-18, VS-24, VS-27 and

Table 14 Genetic cataloguing of yard long bean using descriptors

Descriptor	VS-1	VS-2	VS-3	VS-4	VS-5	VS-6	VS-7	VS-8	VS-9	VS-10	VS-11	VS-13	VS-14	VS-15	VS-16
1. Plant Data-vegetative															
1.1 Growth habit	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
1.2 Growth pattern	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
1.3 Plant vigour	7	7	7	7	7	7	7	4	7	7	7	7	7	7	7
1.4 Leafiness	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
1.5 Plant pigmentation	3	0	0	5	7	3	3	5	0	1	5	3	0	1	0
2. Inflorescence and Fruit Data															
2.1 Flower pigment pattern	2	2	0	2	5	3	2	2	0	5	2	0	2	2	0
2.2 Calyx colour	3	5	0	0	5	5	3	5	3	5	0	0	0	3	0
2.3 Calyx lobing	3	7	3	3	7	7	3	7	7	7	5	5	3	5	7
2.4 Days to 50% flowering	3	2	2	3	3	3	2	2	2	3	2	2	3	2	2
2.5 Duration of flowering	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
2.6 Raceme position	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
2.7 Number of clusters per plant	1	1	1	2	2	1	2	1	2	2	2	2	1	3	2
2.8 Days to first mature pods	3	2	2	3	3	3	2	3	2	3	2	2	3	2	2
2.9 Pod attachment to peduncle	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3

Descriptor	VS-1	VS-2	VS-3	VS-4	VS-5	VS-6	VS-7	VS-8	VS-9	VS-10	VS-11	VS-13	VS-14	VS-15	VS-16
2.10 Immature pod pigmentation	0	1	0	0	5	1	0	0	1	0	0	0	0	0	0
2.11 Pod length	3	3	1	3	1	1	3	1	1	3	3	1	3	1	1
2.12 Pod curvature	3	3	3	3	0	3	5	3	0	3	3	0	3	3	5
2.13 Pod fibrousness	2	1	2	1	1	1	2	1	1	1	1	2	2	1	1
2.14 Locules per pod	2	3	3	2	3	3	3	2	3	2	3	2	2	3	3
2.15 Hundred seed weight	2	3	3	2	3	3	1	1	2	2	3	1	2	1	2
2.16 Seed colour	7	9	6	7	3	9	3	9	6	9	5	6	3	2	6
3. Plant duration															
3.1 Senescence	1	3	2	1	1	2	3	1	4	2	2	3	1	4	4
3.2 Perenniality	2	2	2	2	2	2	3	3	3	3	2	3	3	1	0

Table 14 continued ....

Descriptor	VS-17	VS-18	VS-19	VS-20	VS-21	VS-22	VS-23	VS-24	VS-25	VS-26	VS-27	VS-28	VS-29	VS-30	VS-31
1. Plant Data-vegetative															
1.1 Growth habit	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
1.2 Growth pattern	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
1.3 Plant vigour	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
1.4 Leafiness	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
1.5 Plant pigmentation	1	5	1	3	1	3	0	3	3	0	3	5	3	0	3
2. Inflorescence and Fruit Data															
2.1 Flower pigment pattern	0	0	2	2	2	2	3	0	2	2	0	2	2	3	0
2.2 Calyx colour	3	3	2	3	2	2	2	2	3	2	2	2	2	2	2
2.3 Calyx lobing	0	0	3	3	3	3	5	0	5	3	3	3	0	0	0
2.4 Days to 50% flowering	5	7	5	7	7	5	3	3	7	3	5	5	7	5	5
2.5 Duration of flowering	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
2.6 Raceme position	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
2.7 Number of clusters per plant	1	1	1	1	1	1	2	1	1	1	2	1	2	2	2
2.8 Days to first mature pods	3	2	1	2	3	2	2	2	2	2	2	1	2	2	2
2.9 Pod attachment to peduncle	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3

Table 14 continued ...

Descriptor	VS-17	VS-18	VS-19	VS-20	VS-21	VS-22	VS-23	VS-24	VS-25	VS-26	VS-27	VS-28	VS-29	VS-30	VS-31
2.10Immature pod pigmentation	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0
2.11 Pod length	3	3	3	1	1	1	3	3	3	3	1	1	3	1	1
2.12 Pod curvature	3	0	0	0	0	5	3	3	3	3	3	5	3	3	3
2.13 Pod fibrousness	2	1	2	1	2	1	1	2	2	2	2	1	2	1	1
2.14 Locules per pod	3	3	2	1	3	3	3	2	2	2	3	2	2	2	3
2.15 Hundred seed weight	2	1	1	2	3	2	3	3	3	1	1	1	2	2	1
2.16 Seed colour	7	8	3	1	4	9	9	4	4	3	2	3	3	6	2
3. Plant duration															
3.1 Senescence	2	2	2	4	2	2	1	2	2	2	3	3	2	4	4
3.2 Perenniality	3	3	3	3	2	3	3	1	1	3	3	3	3	3	3

VS-31. Rest of the accessions had flowers with pigmented margins on wing and standard.

Calyx colouration and lobing exhibited striking variation among the accessions (plate 4). Plain green calyx were observed for genotypes VS-3, VS-4, VS-11, VS-13, VS-14, VS-16, VS-17, VS-18, VS-24, VS-29, VS-30 and VS-31 where as solid purple pigmentation were observed in the calyx of VS-2, VS-5, VS-6, VS-8, VS-10, VS-23 and VS-25. Similarly prominent lobing of calyx, resulting in long pointed tooth were noticed only in VS-2, VS-4, VS-5, VS-7, VS-8, VS-9, VS-16, VS-18, VS-20, VS-21, VS-25 and VS-29. Very small teeth resulting in lightly lobed calyx were observed in VS-1, VS-3, VS-4, VS-6, VS-13, VS-23, VS-24 and VS-26. Rest had calyces with medium lobing.

Immature pod colour belonged to the following categories - plain green, green with red tip and dark purple (plates 5,6,7). Most of the genotypes had plain green pods. Dark purple pigmented pods were the peculiarity of VS-5. Plain green pods with purple tips were noticed in VS-2, VS-6, VS-8, VS-9, VS-10, VS-18, VS-23 and VS-25.

The genotypes also exhibited predominant variability for seed colouration (plates 8 and 9). Black seeds were observed in genotypes VS-2, VS-6, VS-8, VS-10, VS-22, VS-23 and VS-25. Genotypes VS-5, VS-7, VS-14, VS-19, VS-21, VS-24, VS-26, VS-28 and VS-29 had brown seeds. Light brown seeds were noticed only in VS-20 and brown seeds with white tip in VS-11. A brown and white combination was seen in the seeds of VS- VS-3, VS-9, VS-13, VS-15, VS-16, VS-18, VS-27, VS-30 and VS-31. Dark brown seeds were noticed in VS-1, VS-4 and VS-17.

Scoring for perenniality and plant senescence was done at full maturity stage when the peak bearing stage was over. At this stage, majority of the plants were green

GB

and new flowers were found emerging genotypes VS-1, VS-4, VS-5, VS-14, VS-23 and VS-25 were fully green even and flowering. While VS-2, VS-7, VS-13, VS-27 and VS-28 had 40% plants green. They were found to produce new leaves and flowers. Only 10-25% plants were green in genotypes VS-9, VS-15, VS-16, VS-20, VS-30 and VS-31 at full maturity, but still capable of producing new flowers and pods.

4.9 Pest and Disease scoring

The yard long bean accessions were scored for major pests and diseases occurred during the season using a 0-9 scale (table 15). The incidence of the following diseases and pests were noticed.

Disease	Causal Organism
1. Cowpea Rust	*Uromyces appendiculatus*
2. Cercospora leaf spot	*Cercospora canascens*
3. Anthracnose (Colletotrichum leaf spot)	*Colletotrichum lindemuthianum*
4. Fusarium wilt	*Fusarium oxysporum*
5. Cowpea mosaic	*Cowpea mosaic virus*

Pest	Scientific name
1. American serpentine leaf miner	*Lyriomyza trifolii*
2. Pod bug	*Riptortus pedestris*
3. Cowpea Aphid	*Aphis craccivora*

Scoring for the incidence of diseases and pests

The genotypes were scored on a 0-9 scale for the incidence of diseases namely cowpea just, mosaic, cercospoa leaf spot, anthracnose, and fusarium with and pests

Table 15

Scoring for Major Diseases and Pests of Yard long bean

Name of disease	VS-1	VS-2	VS-3	VS-4	VS-5	VS-6	VS-7	VS-8	VS-9	VS-10	VS-11	VS-13	VS-14	VS-15	VS-16
Cowpea Rust	0	9	5	5	5	5	0	7	0	9	0	0	0	0	0
Mosaic	5	5	0	3	5	5	5	7	3	5	7	7	5	7	7
Cercospora leaf spot	5	5	5	3	5	5	7	3	7	3	7	5	5	5	5
Colletotrichum leaf spot	3	0	3	0	0	3	0	0	7	5	0	0	0	9	7
Fisarium wilt	0	3	0	3	0	3	0	0	0	0	0	3	7	3	7
INSECT PESTS															
Serpentine leaf miner	7	5	7	7	7	7	7	9	7	7	9	7	7	7	9
Pod Bug	5	3	5	3	3	0	5	3	5	3	5	0	5	0	0
Cowpea Aphid	7	5	0	3	5	3	3	5	3	5	3	5	7	0	0

Table 15 continued....

Name of disease	VS-17	VS-18	VS-19	VS-20	VS-21	VS-22	VS-23	VS-24	VS-25	VS-26	VS-27	VS-28	VS-29	VS-30	VS-31
Cowpea Rust	0	0	9	0	9	7	3	5	3	7	5	7	7	0	0
Mosaic	5	5	3	5	5	5	3	5	3	5	3	5	9	3	7
Cercospora leaf spot	7	7	7	3	3	7	5	3	3	7	5	7	7	3	7
Colletotrichum leaf spot	5	5	0	7	0	0	0	5	0	0	7	0	0	7	9
Fisarium wilt	3	7	3	5	3	0	0	0	0	3	0	0	0	0	3
INSECT PESTS															
Serpentine leaf miner	7	9	9	7	9	5	9	7	5	5	9	9	9	7	9
Pod Bug	3	3	3	0	0	0	3	0	3	3	0	3	0	5	0
Cowpea Aphid	3	3	9	0	0	3	3	0	5	0	3	5	3	3	0

Plate 1. Variation in leaf characters – 1

Plate 2. Variation in leaf characters – 2

Plate 3. Variation in flower colour

Plate 4. Variation in calyx characters
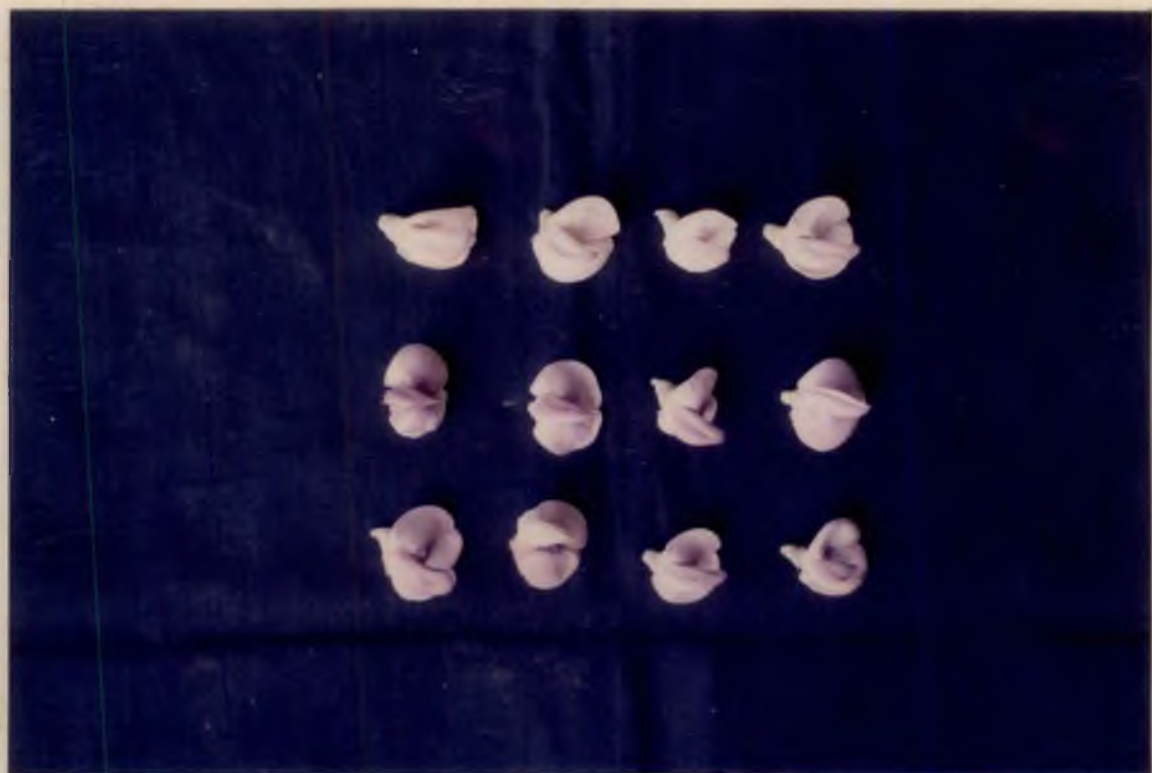
Plate 5. Variation in fruit characters – 1

Plate 6. Variation in fruit characters – 2

VS 1 VS 2 VS 3 VS 4 VS 5 VS 6 VS 7 VS 8 VS 9 VS 10

VS 11 VS 13 VS 14 VS 15 VS 16 VS 17 VS 18 VS 19 VS 20 VS 21
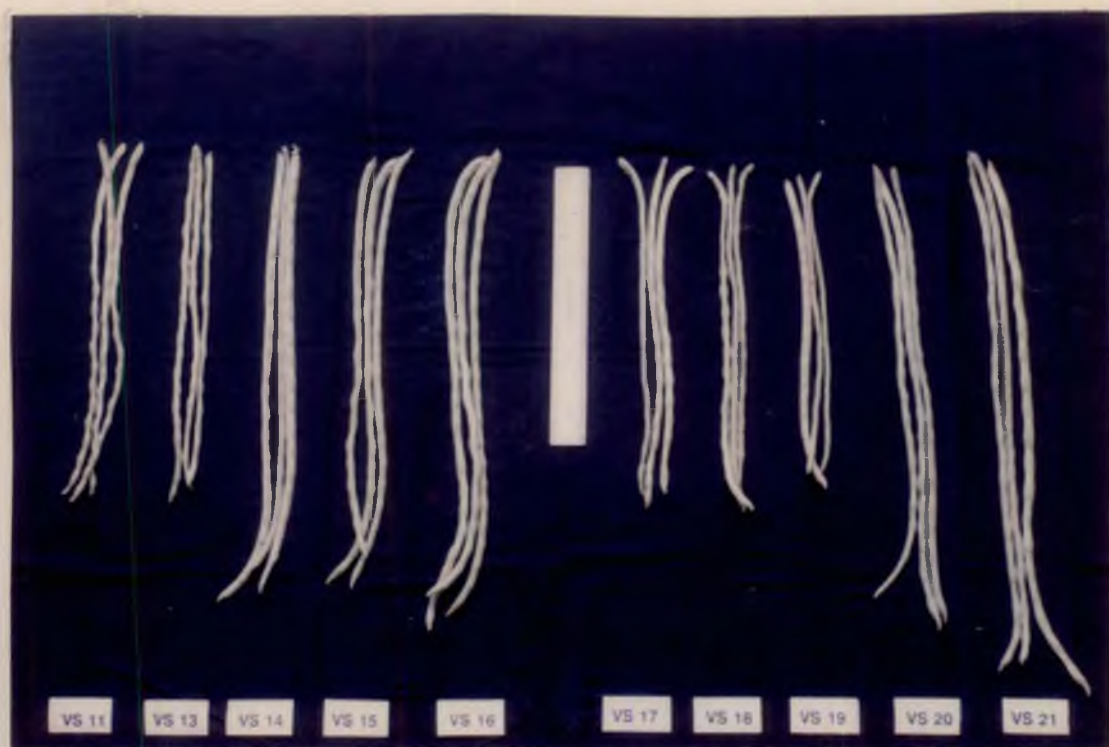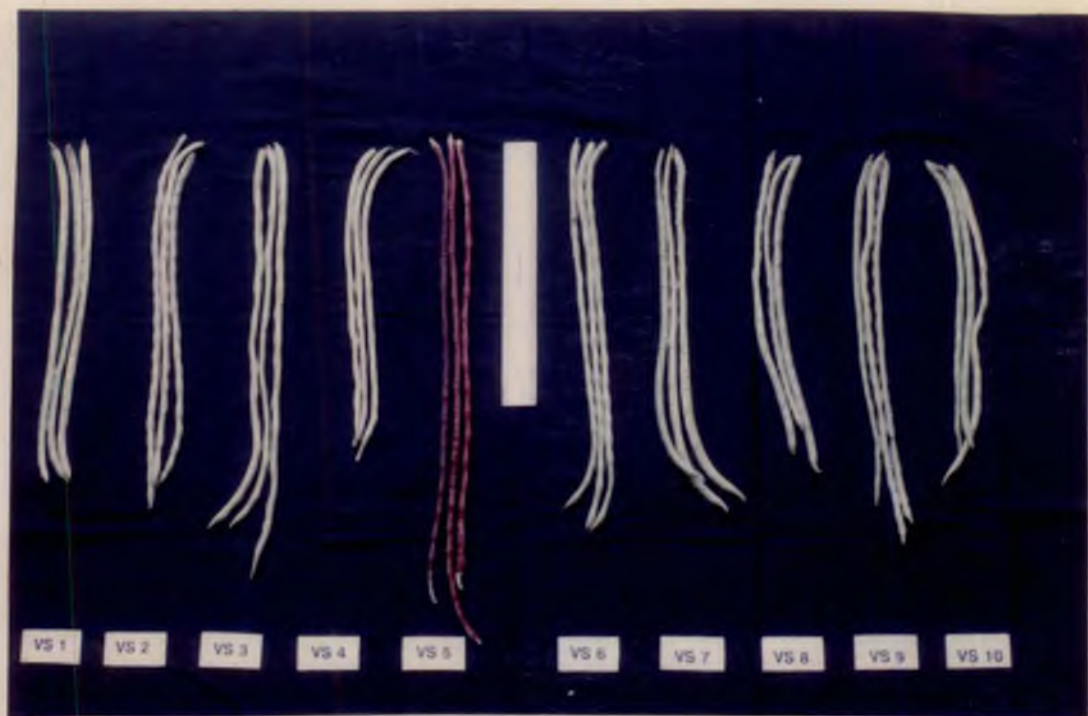
Plate 7. Variation in fruit characters – 3

Plate 8. Variation in seed colour – 1

VS 22   VS 23   VS 24   VS 25   VS 26   VS 27   VS 28   VS 29   VS 30   VS 31

VS 1   VS 2   VS 3   VS 4
VS 5   VS 6   VS 7   VS 8
VS 9   Sarika   Malika   VS 13
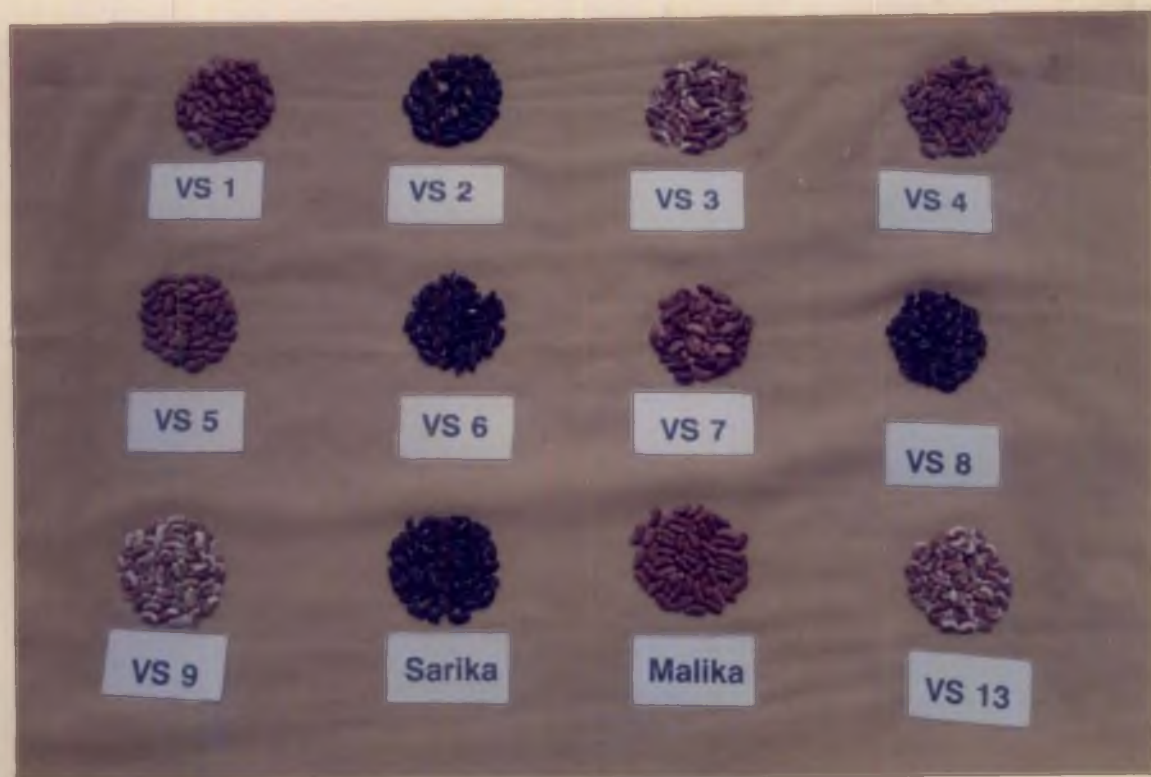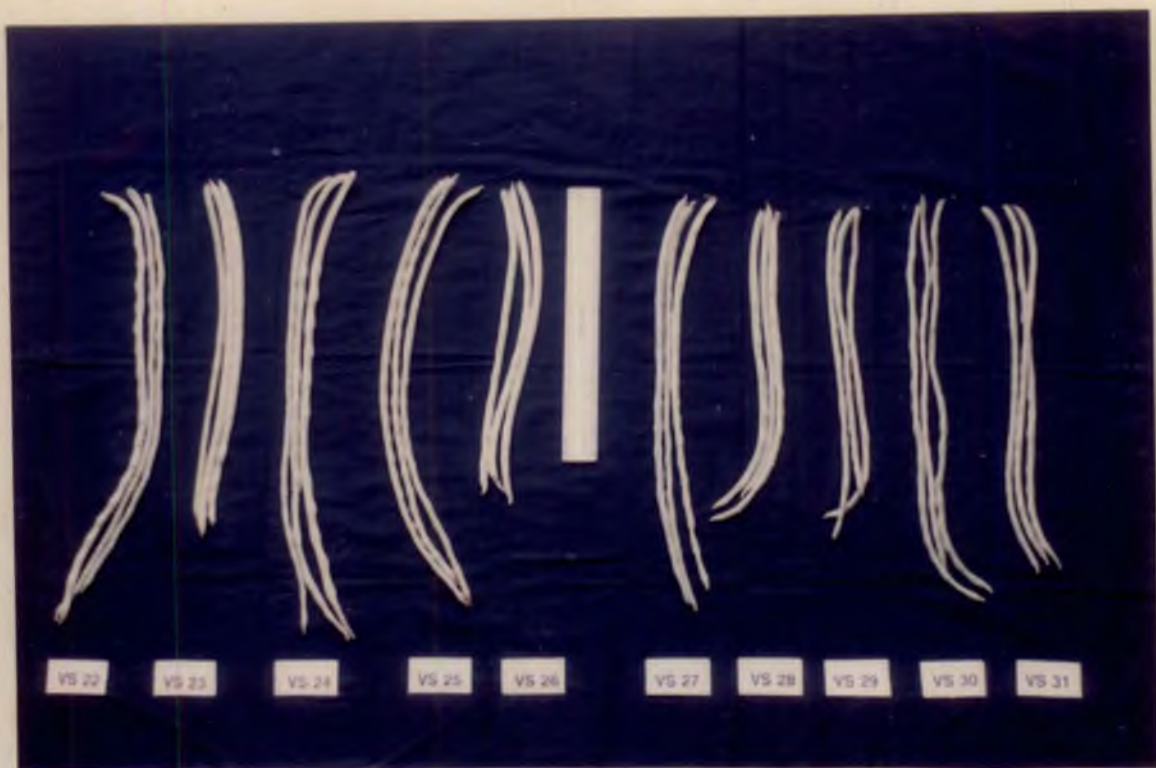
Plate 9. Variation in seed colour – 2

Plate 10. Cercospora leaf spot – symptoms
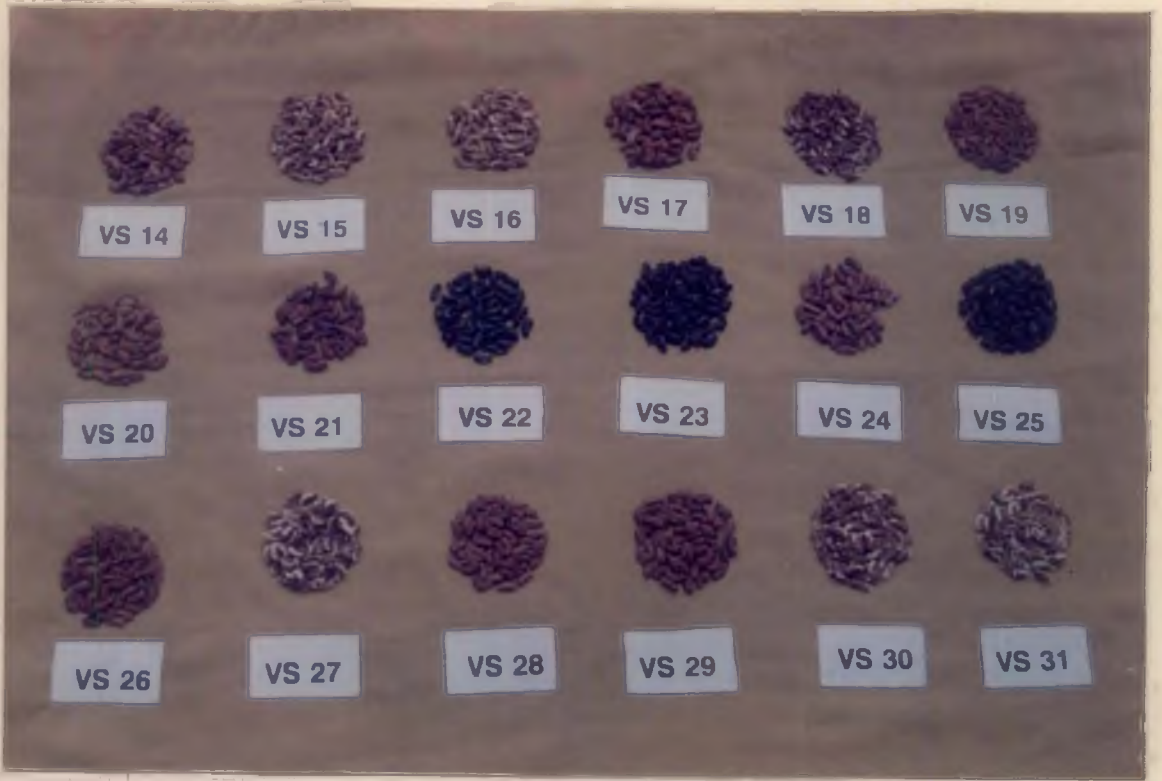
Plate 11. Anthracnose – symptoms

Plate 12. American serpentine leaf miner - symptoms

namely American serpentine leaf miner, pod bug and cowpea aphid, which occurred during the crop season.

Among the diseases cercospora leaf spot was found in all the genotype.Medium to high incidence was noticed for majority of the genotypes VS-4, VS-8, VS-10, VS-20, VS-21, VS-24, VS-25 and VS-30 had low incidence (plate 10).

Cowpea mosaic was also found attacking almost all the genotypes. Most of the genotypes were subjected to medium or high incidence of this sap transmitted virus disease. Low incidence was noticed in VS-4, VS-9, VS-19, VS-23, VS-25, VS-27 and VS-30. VS-29 showed very high incidence. However VS-3 was found free of mosaic.

Cowpea rust was found severe in genotypes VS-2, VS-10, VS-19 and VS-21. No incidence was observed in VS-1, VS-7, VS-9, VS-11, VS-13, VS-14, VS-15, VS-16, VS-17, VS-18, VS-20, VS-30 and VS-31. Anthracnose was found very high in the top yielders VS-15 and VS- 31(plate 11). Rest were either free of the disease or had only low incidence. Fusarium wilt which devastates the whole plant was high only in   VS-14, VS-16 and VS-18, VS-20 had medium incidence. The other genotypes were free of the disease or showed only very low incidence.

Among the insect pests, American serpentine leaf miner was found to attack all the genotypes at all stages of the crop to varying degrees (plate 12). Very high incidence was observed in VS-8, VS-11, VS-16, VS-18, VS-19, VS-21, VS-23, VS-27, VS-28, VS-29 and VS-31. All the others were subjected to medium or high incidence.

Low to medium incidence of pod bug was noticed at late stages of the crop. However VS-6, VS-13, VS-15, VS-16, VS-20, VS-21, VS-22, VS-24, VS-27, VS-29 and VS-31 were unattacked. Attack of cowpea aphid was found during early fruiting

stage. However, high incidence was noticed only in VS-19, VS-1 and VS-14, VS-3,

VS-15, VS-16, VS-20, VS-21, VS-24 and VS-31 were free from aphid attack.

Discussion

5. DISCUSSION

The improvement of any crop depends on altering the genetic make up of the existing varieties. Improvement of yield and its components through a suitable breeding method largely depends on the available variability, heritability of the character, genetic advance under selection and the association among characters. Vegetable cowpea or yard long bean, a crop of much demand in Kerala exhibits high variability with respect to vegetative and productive characters and the exploitation of this variability can help in future improvement of the crop. Hence the present study was undertaken to assess the genetic diversity and to investigate the genetic parameters, degrees and pattern of association among characters, to prepare a selection index based on major yield attributing characters in yard long bean. Based on a descriptor, the genotypes were described for morphological characters. They were also scored for the incidence of major diseases and pests of yard long bean. The results obtained from this study are discussed below.

5.1 Genetic variability, heritability and genetic advance

An insight into the magnitude of variability present in a crop species is of utmost importance as it provides a basis for effective selection. The observed variability in the population is the total variation that arise due to genotypic and environmental effects. Of the various estimates of quantitative variability, range and variation around mean are very basic ones. Heritability in conjunction with genetic advance would provide better information on the criteria of selection (Johnson *et al*, 1955).

In the present study, analysis of variance showed significant differences for all the twenty four characters, viz, vine length, number of primary branches, petiole length, length of terminal leaflet, breadth of terminal leaflet, length of lateral leaflet, breadth of lateral leaflet, days to first flowering, days to first harvest, harvesting interval, pod length, pod girth, pod weight, beans per pod, length of peduncle, inflorescence per plant, pods per inflorescence, pods per kg, pods per plant, pod yield per plant, hundred seed weight, fibre content of pods, protein content of pods and keeping quality of pods.

The genotype VS-15 was the top yielder of green pods followed by VS-31 and VS-9. Pod length and pod weight are direct contributors to yield per plant. The highest pod length was exhibited by VS-21 followed by VS-5 and VS-3. Genotype VS-20 recorded the maximum pod weight followed by VS-15 and VS-5. The poorest yielder was VS-17.

Existence of high variability was reported by Pandita *et al*, (1982) and Yap(1983) in cowpea for all the characters studied. De Mooy (1985) could obtain variability in flowering, number of pods per plant and seed characters in cowpea which is in conformity with the results of the present investigation. Similar results were also obtained by Patil and Baviskar (1987) for pods per plant, pod clusters per plant and days to maturity. Wide variation was observed for length of vine, days to first flowering, length of pods, pod girth, weight of pods, number of inflorescence per plant, number of pods per kg, 100 seed weight, protein content of pods etc in the present study. This finding agrees with the findings of Ram *et al* (1994), Sobha (1994), Sawant (1994) and Aghora *et al* (1994). Closer values of phenotypic and genotypic variances obtained in this study suggest the predominant influence of genetic component over the environmental effect on its phenotype.

Coefficient of variation - phenotypic (PCV) and genotypic (GCV) - are another means of expressing the amount of variability. It is a better index for comparison of characters with different units of measurement, than estimates of quantitative variation like range and variation around mean.

In the present study, PCV ranged from 4.96 to 30.56 (Table 6). Highest PCV was recorded for pod yield per plant followed by number of pods per kg and number of inflorescence per plant. This result is in agreement with the findings of Vaid and Singh (1983) and Patil and Baviskar (1987). Days to flowering had the lowest PCV as obtained by Sreekumar *et al* (1979).

Since phenotype constitute both genotypic effect and environmental influence, crop improvement programme cannot be undertaken solely on phenotypic performance. The GCV provides a more precise measure of genetic variability. It ranged from 4.68 (days to first flowering) to 29.5 (pod yield per plant). High values of GCV was also obtained for number of pods per kg, number of inflorescence per plant and weight of pods. The highest GCV was obtained for pod yield per plant. Similar results were obtained in cowpea by Ramachandran *et al* (1980), Jana *et al* (1982), Vaid and Singh (1983), Savithramma (1992), Sobha (1994) and Sreekumar *et al* (1996). The high magnitude of GCV for most of the characters revealed the great extent of variability for these characters, thereby suggesting good scope for improvement through selection. Further, the magnitude of genetic variation nearly approached the phenotypic variation in all the characters (Table 6) indicating that selection on phenotypic basis will hold good for genotypic basis also. (Fig 3)

The total variability existing in a population is the sum of heritable and non heritable components and it is necessary to portion these components, since the magnitude of heritable variability is an important aspect of genetic constitution of any

Coefficient of variation for 9 characters in yard long bean

X_1 - Vine length

X_2 - Days to flowering

X_3 - Harvesting interval

X_4 - Pod length

X_5 - Pod weight

X_6 - Pods per plant

X_7 - Pods per kg

X_8 - Pod yield per plant
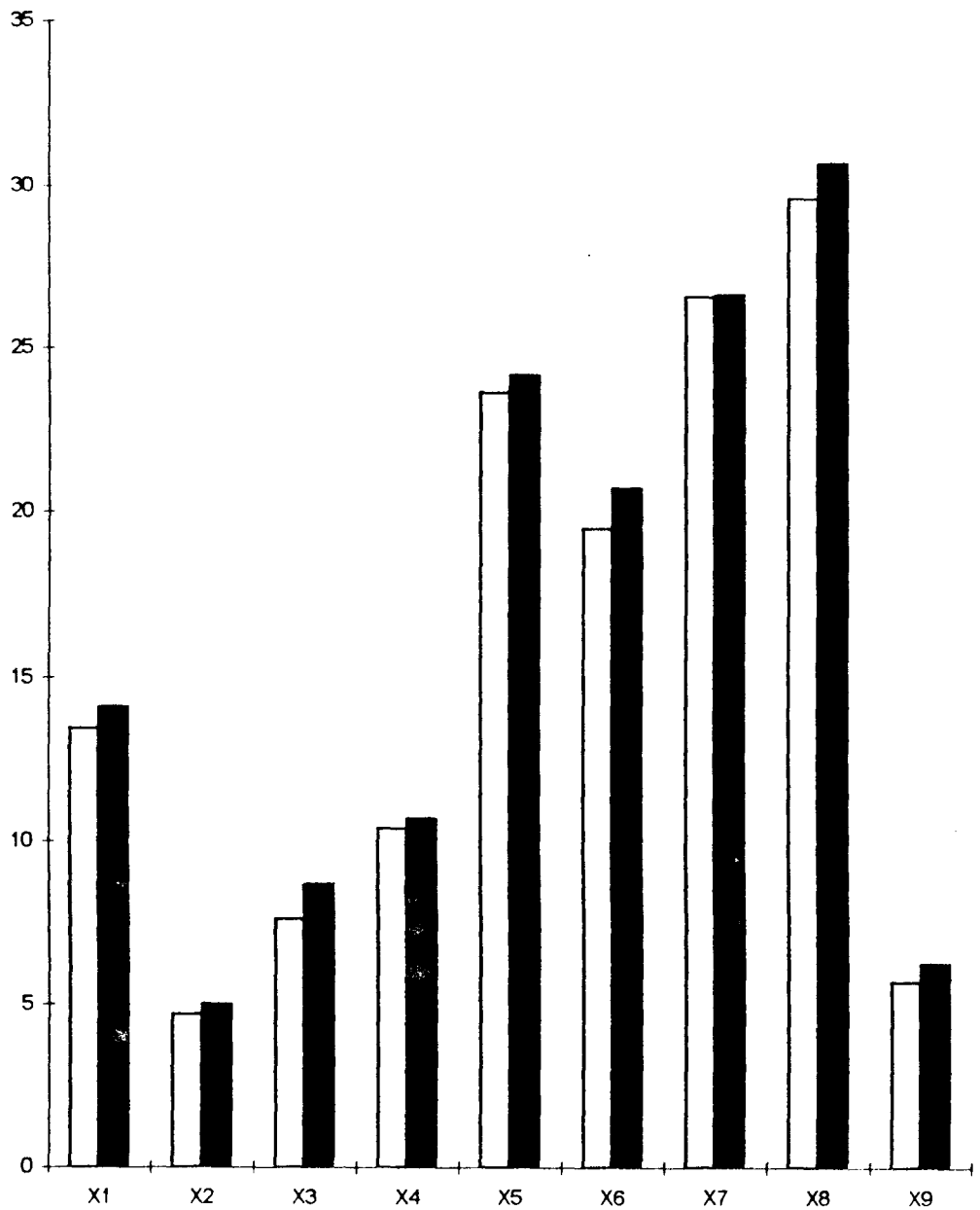
X_9 - Protein content of pods

Fig 5   Coefficient of variation for 9 characters in yard long bean

■   Phenotypic coefficient of variation

☐   Genotypic coefficient of variation

breeding material. The magnitude of heritability indicates the effectiveness with which the selection of genotype can be made based on phenotypic performance (Johnson *et al*, 1955). High value of heritability indicated that the phenotype of the trait strongly reflected the genotype and suggests the major role of genetic constitution in the expression of that character. Allard (1960) suggested that gain from selection for a particular character depends largely on the heritability of the character. Even though high heritability estimate gives indication of effectiveness of selection based on the phenotypic performance, it does not necessarily mean a high genetic advance for a particular character. Johnson *et al* (1955) in their study stated that heritability as well as genetic advance were more useful than heritability alone in predicting the resultant effect of selecting the best individuals. However, Hanson (1961) concluded that high heritability and genetic advance are complementary aspects. Estimates of genetic advances together with heritability would be helpful in assessing the nature of gene action.

High heritability along with high genetic gain was observed for pod yield per plant, number of pods per kg, number of inflorescence per plant, weight of pods and keeping quality of pods indicating that their variation is mainly due to action of additive genes and these traits can be improved by selection. This confirms the earlier findings of Pandita *et al* (1982), Vaid and Singh (1983) and Ram *et al* (1994).

High heritability and moderate genetic gain was observed for vine length, pod girth and 100 seed weight. Characters like days to first flowering, days to first harvest and length of pods exhibited high heritability, but low genetic gain indicating the action of non-additive genes for expression of these characters. Thus it implies that high heritability is not always an indication of high genetic gain (Johnson *et al*, 1955).

5.2 Correlation studies

Correlation provides information on the nature and extent of relationship between all pairs of characters. So when the breeder applies selection for a particular trait, the population under selection is not only improved for that trait, but also for the characters associated with it. Therefore analysis of yield in terms of genotypic (r_g), phenotypic (r_p) and error (r_e) correlation coefficient of component character lead to the understanding of characters that can form the basis of selection. The genotypic correlations provide a reliable measure of genetic association between the character and help to differentiate the vital association useful in breeding from non vital ones (Falconer, 1981).

In the present investigation, the characters which strongly contributed to pod yield per plant were pod length, pod weight, number of pods per kg and pods per plant. Weight of pods exhibited high and strong positive association with pod yield ($r_p = 0.6601$, $r_g = 0.6918$ and $r_e = 0.1191$). This was followed by number of pods per plant ($r_p = 0.5692$, $r_g = 0.5521$ and $r_e = 0.7655$) and length of pods. ($r_p = 0.4616$, $r_g = 0.5011$, $r_e = -0.1446$). The character, number of pods per kg had significant negative correlation with yield ($r_p = -0.6890$, $r_g = -0.7147$ and $r_e = -0.0069$). A similar trend was obtained in earlier investigations by Jana *et al* (1982), Sharma *et al* (1988), Samiullah *et al* (1993), Sobha (1994) and Sreekumar *et al* (1996).

Positive association was observed between number of primary branches and number of inflorescence per plant. Number of pods per kg exerted high and negative correlation with yield. Pod length had positive association with number of seeds per pod. Days to first flowering had positive and strong correlation with days to first

harvest. Similar findings were made by Perrino *et al* (1993) and Tamilselvam and Das (1994).

Length of pods and weight of pods were positively correlated with number of pods per inflorescence which in turn was associated with pod yield per plant. Also high correlation was noticed between length and weight of pods.

The negative correlation of leaf size with yield may be due to partitioning of energy to reproductive phase.

High positive phenotypic and genotypic correlation coefficients of pod yield with number of pods per plant, length of pods and weight of pods indicate that selection based on any one of the above characters may also result in improvement of pod yield in yard long bean.

A higher positive error correlation coefficient between pod yield per plant and number of pods per plant indicate the strong influence of environment on these characters. In general, the phenotypic correlations were smaller then genotypic correlations which indicated that environment had small effect on these characters.

5.3 Path Coefficient Analysis

Selection based on yield alone is not very efficient but that based on its components as well could be more efficient (Evans, 1978). Although correlation studies between yield and its components and relative contribution to yield will be of great use in planning and evaluating breeding programmes, it cannot give the exact position of the relative importance of direct and indirect effects of the various yield attributes. Path coefficient analysis helps in partitioning the genotypic correlation coefficients into direct and indirect effects of the component characters on yield. This helps to understand the contribution of these component characters to yield and on the

basis of which programmes can be devised so as to improve the desirable component characters which can cause a resultant increase in yield. This analysis also reveal whether the component characters under study were responsible for the variation in yield.

In the present study, the path analysis indicated that number of pods per plant exerted the maximum positive direct effect on pod yield followed by pod weight. (Fig.1). This finding is in conformity with that obtained by Murthy (1982), Jana et al (1983) and Obisesan (1985).

The length of pods exerted a positive indirect effect through weight of pods and number of pods/kg on pod yield. Weight of pods exerted a strong and positive direct effect on pod yield along with its indirect effect through number of pods/kg. Number of pods/kg had a negative direct effect on total yield along with its indirect effect through weight of pods, and length of lateral leaflet. Similar results were obtained by Biradar et al (1991) and Sobha (1994).

In the present study, the residual effect noticed was only 0.1111 indicating that the variation in pod yield was highly attributable to factors selected in the study.

5.4 Selection index - a discriminant function analysis

Discriminant function analysis is a method of selection of genotypes based on simultaneous analysis of observation on multiple characters. This analysis was first developed by Fisher (1936) and later applied by Smith (1937) for making selection on several characters simultaneously. According to Hazel (1943), a selection based on suitable selection index is more efficient than selection based on individual characters

Selection index was constructed using thirteen characters which showed high correlation with yield. viz., length of vine, number of primary branches, petiole length,

length of lateral leaflet, breadth of lateral leaflet, days to first flowering, pod length, pod girth, pod weight, pods per inflorescence, pods per kg, pods per plant and pod yield per plant. Based on the analysis, the genotype VS-6 attained the maximum selection index value, followed by VS-11, VS-19 and VS-3 and the least scores were obtained for VS-16, VS-10 and VS-2.

5.5 Genetic divergence analysis

Breeding of crop plants adopting hybridisation as a tool is one of the most important crop improvement methods. For this, choice of parents is of utmost importance. The success of the hybridisation programme largely depends on the genetic diversity of the parents. So the breeder is interested to know the genetic divergence among the different types available due to reasons that, crosses between genetically diverse parents are likely to produce high heterotic effects and that the crosses involving distantly related parents with in the same species produces a wide spectrum of variability. However, the maximum heterosis generally occurs at an optimal or intermediate level of diversity. One of the potent techniques in measuring genetic divergence, the D^2 statistic (Mahalanobis, 1928) which measures the force of differentiation at the inter cluster and intra cluster levels and thus provides a reasonable basis for selection of genetically divergent parents in breeding programmes. D^2 analysis is a means of studying the genetic divergence within a group of diverse genotypes. It permits precise comparsion among all possible pairs of genotypes in any population According to Endang *et al* (1971), the clustering pattern could be utilized in choosing parental combinations for prospective breeding programmes to generate the highest possible variability in the yield components.

The thirty cowpea genotypes were grouped into four clusters (Fig.2) using Tocher's method (Rao, 1952). Maximum inter cluster distance was shown between cluster I and III followed by clusters II and III. Intra cluster distance increased as the cluster size increased. It was minimum in cluster I followed by cluster II. The maximum intra cluster distance was exhibited by cluster IV, indicating the heterogeneity among the 18 members of the cluster. For hybridization works, maximum heterosis can be expected if parents are selected from cluster I and III followed by cluster II and III. Crossing of selected lines in a diallel fashion may generate useful segregants.

5.6 Genetic catalogueing of yard long bean accessions

Genetic catalogueing of genotypes based on standard descriptors, help to easily describe the morphological features of a genotype and thus helps international exchange of information about new accessions in a more clear way. The following relevant observations were made from the prepared catalogue.

All the genotypes were of climbing habit with indeterminate growth habit. During the vegetative stage, all of them were vigorous and leafy. Most of the genotypes had purple or red pigmentation on stem, branches and petioles. Those with intermediate stem pigmentation were found to posses flowers with purple pigmented margins, wing and standard petal. The pendant pods were found distributed throughout the canopy in all the genotypes.

Association between flower colour and immature pod pigmentation was noticed. All genotypes having white or cream flowers gave rise to plain green pods having seeds with brown and white patches. Plain green pods were also found to be produced from flowers with pigmented wings and standard with light v-shaped pattern

of pigment, in most cases. Violet flower colour and pigmented tipped pods were found related. Such pods had black coloured seeds.

Scoring for perenniality and senescence revealed that most of the genotypes were able to produce fruits even at late stages of the crop.

5.7 Scoring for major diseases and pests of yard long bean

Incidence of diseases and pests is a major biotic stress to which all the cultivated plant species are subjected to. Yard long bean is also no exception. However no devastating disease or pest is reported so far, compared to other vegetable crops of Kerala.

Among the diseases, cowpea mosaic was the most important affecting all the genotypes to varying degrees. However, genotype VS-3 was found comparatively free of this sap transmitted virus diseases. Low incidence was noticed in genotypes VS-4, VS-9, VS-19, VS-23, VS-25, VS-27 and VS-30 also. Very high mosaic incidence was noticed in case of VS-29.

Cercospora leaf spot caused by *Cercospora canascens* was found to affect all the genotypes. This disease reduces the photosynthetic area and can affect the yield. Incidence of cowpea rust, caused by *Uromyces appendiculatus* and anthracnose caused by *Colletotrichum lindemuthianum* were found serious only in a few genotypes. VS-2, VS-10, VS-19 and VS-21 were severely affected by cowpea rust where as anthracnose was found high only in VS-15 and VS-31 which are the top yielding genotypes.

Fusarium wilt caused by *Fusarium oxysporum* which can devastate the whole plant is a serious disease, affecting the crop in many cultivated areas. In this study among the genotypes, VS-14, VS-16 and VS-18 had comparatively high incidence of

Fusarium wilt. VS-20 had moderate incidence. Rest of the genotypes were either free or less susceptible to this fungal disease.

Among the insect pests, the most important was the American serpentine leaf miner, *Lyriomyza trifolii*. The larva of this pest tunnels the leaf while feeding the contents, making white or silvery markings on the leaf. This causes effective loss of photosynthetic area, indirectly contributing to reduction in yield. None of the genotypes were found free from the attack of this pest. Comparatively low incidence was noticed for genotypes VS-2, VS-22, VS-25 and VS-26.

Attack of pod bug (*Riptortus pedestris*) was found in the later stages of the crop. This pest sucks the juice from immature pods and causes its shrinkage and eventual drying. No serious incidence was noticed and genotypes VS-6, VS-13, VS-15, VS-16, VS-20, VS-21, VS-22, VS-24, VS-27, VS-29 and VS-31 were found unattacked.

At flowering stage, some of the genotypes were found attacked by cowpea aphid (*Aphis craccivora*). Their adults and nymphs aggregates and sucks sap from tender fruits and stem leading to yellowing, weakening and drying of pods and stem. High yielding genotypes like VS-15, VS-31, VS-3 and VS-9 were free of this pest. Rest had only low or moderate incidence.

In general, no genotype was found highly prone to all the major pests and diseases. Genotypes VS-3, VS-6, VS-24, VS-25 and VS-30 had comparatively low incidence for all pests and diseases. The genotype VS-15, the top yielder was prone to anthracnose, mosaic and serpentine leaf miner. It was free from rust and pod bug.

Summary

6. SUMMARY

The present study, "Genetic variability in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt)" was conducted in the Department of Horticulture, College of Agriculture, Vellayani, during the period 1996-97. This study envisaged the objective of assessing the variability existing in the germplasm of yard long bean in yield, yield attributes, morphological characters, pest and disease resistance and to identify suitable lines which can be utilised in further breeding programmes.

Thirty diverse genotypes of yard long bean collected from southern parts of Kerala were evaluated in a randomised block design with three replications. Observations were recorded on 24 characters viz., vine length, number of primary branches, petiole length, length of terminal leaflet, breadth of terminal leaflet, length of lateral leaflet, breadth of lateral leaflet, days to flowering, days to first harvest, harvesting interval, pod length, pod girth, pod weight, beans per pod, length of peduncle, inflorescence per plant, pods per inflorescence, pods per kg., pods per plant, pod yield per plant 100 seed weight, fibre content of pods, protein content of pods and keeping quality of pods.

Significant difference was observed among the genotypes for all the 24 characters studied. The genotype VS-15 was the top yielder of green pods (2.96 kg / plant) followed by VS-31 (2.83kg/plant). VS-17 was the poorest yielder (0.77 kg / plant). Highest pod length was exhibited by VS-21 (54.29cm), while the highest pod weight was shown by VS-20 (37.14 g).

The phenotypic coefficient of variation (PCV) ranged from 4.96 to 30.56 and the highest PCV was recorded for pod yield per plant followed by pods per kg. (26.54). The genotypic coefficient of variation (GCV) also followed a similar trend as that of PCV. It ranged from 4.68 to 29.5. The highest GCV was exhibited by pod yield per plant followed by pods per kg. (26.5).

Heritability estimates ranged from 0.44 for number of primary branches to 0.98 for pods per kg. High heritability along with high genetic gain was observed for pod yield per plant (0.93 and 57.22%), pods per kg. (0.98 and 54.33%), inflorescence per plant (0.94 and 50.65%), pod weight (0.96 and 47.59%) and keeping quality of pods (0.93 and 42.05%).

At genotypic level, pod yield per plant was positively correlated with pod weight, pod length, pods per kg. and pods per plant. Pod weight had the maximum genotypic association with yield. Genotypic correlation was found to be higher than phenotypic correlation for most of the characters.

Path coefficient analysis indicated that pods per plant exerted the maximum positive direct effect (0.5655) on yield followed by pod weight (0.4690). Length of lateral leaflet (-0.3158) and pods per kg. (-0.2154) exerted negative direct effect on yield. This indicates that for yard long bean, a selection model with increased number of pods and higher pod weight is needed for yield improvement.

A selection index was formulated using thirteen characters having correlation with yield. The maximum index score was recorded by VS-6, followed by VS-11. The least was recorded by VS-16, followed by VS-10.

The thirty yard long bean genotypes were grouped into four clusters using Mahalanobis D^2 statistic. Cluster I contained a single genotype followed by cluster II having two genotypes. Cluster III had nine and cluster IV had eighteen genotypes.

The maximum intercluster distance was exhibited between clusters I and III followed by clusters II and III. The largest cluster, cluster IV had the maximum intra cluster distance.

Scoring for morphological characters using standard descriptors was done using a 0-9 scale. Association was found between flower colour, with stem pigmentation, pod pigmentation and seed colour.

The genotypes were scored for the incidence of major diseases occurred during the season, viz., cowpea rust, Cercospora leaf spot, anthracnose, Fusarium wilt, cowpea mosaic and pests, American serpentine leaf miner, pod bug, and cowpea aphid. American serpentine leaf miner, cowpea mosaic and Cercospora leaf spot was found affecting almost all the genotypes to varying degrees.

Genotypes VS-15, VS-31, VS-9, VS-5 and VS-3 were identified as elite based on their superiority in yield and yield attributes and can be used for further crop improvement.

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GENETIC VARIABILITY IN YARD LONG BEAN

(*Vigna unguiculata* subsp. *sesquipedalis*

(L.) Verdcourt)

By

RESMI P.S.

ABSTRACT OF THE THESIS

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ABSTRACT

Thirty yard long bean genotypes varying in morphological traits collected from the southern parts of Kerala were evaluated in an RBD with three replications in the Department of Horticulture, College of Agriculture, Vellayani during 1996-97. The objective was to assess the variability existing in the germplasm in yield, yield attributes, morphological characters and pest and disease resistance and to identify suitable lines for further breeding programmes.

Variability analysis revealed significant difference among the genotypes for all the characters studied. GCV and PCV were highest for pod yield per plant followed by pods per kg.

High heritability coupled with high genetic gain was observed for pod yield per plant, pods per kg, inflorescence per plant, pod weight and keeping quality of pods.

Pod yield per plant was strongly associated with pod weight, pod length, pods per kg and pods per plant. Path analysis revealed that the primary yield contributors were pods per plant followed by pod weight owing to their high positive direct effects.

Genotypes VS-6 and VS-11 recorded the maximum selection index scores and the minimum was for VS-16 followed by VS-10.

Mahalanobis D^2 analysis could group the genotypes into four clusters, cluster IV being the largest with 18 genotypes with the highest intracluster D^2 value. Cluster I and III were the most distant clusters and the genotypes belonging to these clusters can be utilized in hybridisation breeding.

Genetic catalogueing of the genotypes were made using standard descriptors. Association between flower colour, stem colour, pod pigmentation and seed colour was noticed.

Scoring for major diseases and pests revealed that cowpea mosaic and American serpentine leaf miner was affecting almost all the yard long bean genotypes to varying degrees.

Genotypes VS-15, VS-31, VS-9, VS-5 and VS-3 were found elite and can be used for future breeding programmes.