GERMPLASM EVALUATION IN HORSE GRAM (*Dolichos biflorus.* L.)

BY

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THESIS

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DECLARATION

I hereby declare that this thesis, entitled **Germplasm Evaluation in Horse gram (Dolichos biflorus L.)** is a bonafide record of research work done by me during the course of research and that this 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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Introduction

INTRODUCTION

Pulses occupy a pivotal position, in the predominantly vegetarian diet of the Indian population. They are excellent source of proteins, supplementing the staple cereal based diet. They also form a good source of energy, minerals and vitamins and aid in correcting the protein malnutrition, which is prevalent in our country. They enhance the soil fertility through nitrogen fixation. Pulses, with their deep growing tap root, can thrive well under drought conditions. In spite of all these, the cultivation of pulses has not received due attention. The production and productivity lag woefully behind the increasing demand, consequent to the growth of population and per-capita income.

Horse gram is a pulse crop, common in the southern states of India. Its hardy nature and adaptability to a variety of soils make it an outstanding crop among the pulses. It can fix atmospheric nitrogen. Being extremely drought tolerant, its cultivation assumes great significance, in the present situation of water scarcity, prevailing all over the country. Horse gram is a short duration crop, of about 90 days duration and hence can be grown in rice fallows during summer. Thus it can be an excellent fit to the cropping systems, prevalent in some

pockets of Kerala. The cost of cultivation is very low and hence it is also designated as the "poor man's pulse". Thus this is a crop of great potential value.

Even then, the cultivation of horse gram is found to be confined to some pockets of Karnataka, Tamil Nadu, Andhra Pradesh and a few boarder areas of Kerala. The yield per unit area is also low, when compared to other crops. Due to the season-bound nature of the crop, its cultivation is restricted to the period of September-January. Lack of high yielding strains is another drawback. Due to the reasons, in the face of increasing competition from other pulses, the crop has lost more area to other crops like black gram and green gram. Not much has been done, regarding the improvement of production and productivity of this crop.

If high yielding varieties, suited to be grown in summer rice fallows of Kerala can be evolved, it will surely help in the popularisation of this valuable crop, thereby providing an increased consumption, which in turn, will help a lot in overcoming the wide spread protein malnutrition in our state.

The primary objective of the breeder is, the improvement in yield of the crop. For any crop improvement

programme the first and foremost requirement is a proper assessment of the variability present in the genetic stock. In the present situation, of genetic erosion becoming a serious threat, the conservation of the genetic resources and the efficient utilisation of existing variability assumes great significance.

The present study aims at assessing the genetic diversity among the given population of fifty genotypes of horse gram and clustering them into homogeneous groups, estimating the variability, finding out the correlation of yield and yield components and relating the productivity of the crop to the photosynthetic efficiency, by estimating certain physiological parameters.

The genetic diversity within a given population can be measured at the intra-cluster and inter-cluster levels, using the D^2 statistic proposed by Mahalanobis (1936). Using this, the selection of genetically divergent parents for maximum exploitation in hybridization is possible. The relative contribution of each character towards total divergence can also be computed.

Simple measures of variability, like variance, co-efficient of variation, heritability and genetic advance will help to find out the extent of variability among the genotypes for different characters.

Yield itself, being a complex character, is the combined effect of a number of interacting components. The interrelations between yield and the various components and also among the component characters can be measured using correlation co-efficients. This is helpful in understanding the traits upon which, selection is to be based.

The productivity of a crop can also be related to the photosynthetic efficiency, which, in turn, can be assessed, using the physiological parameters, like net assimilation rate and leaf area index. These will also help in evolving an ideal plant type.

Not many workers have attempted to study the above mentioned aspects in horse gram which, will provide valuable informations for any further breeding programme. With this view in mind, the present investigation has been undertaken with the following objectives:

1. To study the genetic variability in the expression of economic characters, in selected genotypes of horse gram.

2. To estimate heritability and genetic advance for the different characters.

3. To estimate genotypic, phenotypic and environmental correlations between the different characters and yield and also the interrelations among themselves.

4. To classify the different genotypes of horse gram based on genetic diversity.

5. To study the pattern of crop growth in horse gram and to identify the yield components for utilisation in further breeding programme.

Review of Literature

REVIEW OF LITERATURE

Extensive studies have been carried out regarding the clustering and variability measurements in pulses. Only a few works are there in horse gram, when compared to that in other pulses. A review of the works conducted so far will be of much use fc ırther studies.

2.1 Variability studies

A number of workers have studied the phenotypic and genotypic variations, genetic advance and heritability of yield and related characters in pulses. Such investigations have revealed the importance of these parameters in pulse improvement programmes.

2.1.1 In horse gram

Ganeshiah (1980) studied 100 horse gram varieties, which showed significant variation in the 18 characters analysed. Genotypic and phenotypic variation was greatest in number of secondary branches, high heritability estimates were found for number of days to flowering and to maturity. In general, variability was more in characters associated with post-flowering period. In 50 cultivars of horse gram, studied by Patil and Deshmukh (1982) seed yield, number of primary and secondary branches and pods per plant showed high heritability and genetic advance, indicating the

effectiveness of selection for these characters. Kabir and Sen (1987) concluded that, significant genetic differences existed for days to flowering and 6 yield components. Genotypic and phenotypic co-efficients of variation were highest for pod yield per plant. Heritability in the broad sense was high, for all the characters. Pods per plant, plant height, days to 50 per cent flowering and days to maturity showed the highest and 100 seed weight showed the lowest genotypic variance in horse gram, according to Suraiya et al. (1988). In their studies, all these characters, except 100 seed weight, exhibited high heritability and genetic advance, while seed yield per pod and pods per plant showed low heritability and genetic advance. Singh (1990) provided information on genetic variability, from data, on 9 characters in 40 horse gram varieties.

2.1.2 In other pulses

Primary and secondary branch number, pod number per plant, 100 seed weight and yield per plot gave high estimates of phenotypic and genotypic co-efficient of variation, heritability and expected genetic advance, in pigeonpea, according to Balyan and Sudhakar (1985). This is an indication of the predominance of additive gene effects. In a study by Angadi et al. (1988), in 11 hybrids and 9

varieties of pigeonpea, varietal differences were significant for all the quantitative characters studied. Konwar and Hazarika (1988) reported high heritability and high genetic advance, for days to maturity, days to flowering and plant height in pigeonpea. Patil et al. (1989) derived information on heritability, from data on 8 characters, in 22 cultivars of pigeonpea. Singh and Yadav (1991) studied genetic variability and heritability from data on 5 yield related traits, in pure line pigeonpeas, of diverse phenotypes.

Estimates of genotypic co-efficient of variation ranged from 15.8 per cent for days to flowering, to 40.26 per cent for seed yield per plant, in variability studies conducted by Maloo and Sharma (1987), in chickpea. They also recorded high expected genetic advance, combined with high heritability for seed yield, pods per plant and primary branches per plant. Genetic variability estimates carried out in chickpea, by Jivani and Yadavendra (1988), showed that, both the coefficients of variation were high for pods per plant and 100-seed weight. Plant height and harvest index had high heritability estimates. The greatest genetic gain was expected for 100 seed weight, pods per plant and days to flowering. Mishra et al. (1988) reported high heritability coupled with high genetic advance, for number of secondary branches per plant, number of pods per plant,

seed yield per plant, biological yield per plant and harvest index. Sharma and Maloo (1988) also derived informations on heritability and genetic variance, in 21 diverse varieties of chickpea, differing in dates of sowing. Singh and Singh (1989) observed high genotypic variability for 100 seed-weight, pods per plant, seed yield per plant and harvest index in chickpea, indicating scope for improvement by selection. Significant variability due to environmental differences were also noted. Samal and Jagadev (1989) also conducted genetic variability studies in chickpea. Sharma et al. (1990) reported highest genotypic and phenotypic variation and genetic advance for secondary branches per plant, followed by 100 seed weignt, in chickpea. Heritability was highest for 100 seed weight and days to maturity. Arora (1991) in his studies, observed that, sufficient genetic variability was present to allow selection for individual traits, for growth and other related characters, in chickpea. He obtained high co-efficient of variation for pods per plant, 100 seed weight and seed yield per plant and moderately high values for height, canopy spread, length of pod bearing branches and primary and secondary branches.

A study of 25 strains of blackgram by Patil and Narkhede (1987) indicated high heritability for yield per plant, pod length and plant height. Also, these showed high

genetic advance. Information on heritability derived by Lakshmiah et al. (1989) showed that heritability values ranged from 77 to 99 per cent, the highest being for days to 50 per cent maturity, in blackgram.

Patil et al. (1987) revealed that, in mungbean, variability for the 7 yield related traits studied were significant. Heritability was highest for days to flowering followed by 100 seed weight, plant height and seeds per pod. Additive gene effects were detected for plant height, days to flowering, days to maturity, pods per plant, seeds per pod, pod length, 100 seed weight and seed-yield. Ramana and Singh (1987) observed relatively high heritability and genotypic co-efficient of variation for number of pods and clusters per plant, in greengram. Pandey et al. (1988) reported pods per plant to be the most variable character, followed by seed yield per plant and flower per plant. High heritability coupled with moderate to high genetic advance and genotypic co-efficient of variation was found for seed yield per plant, internodal length, pods per plant, branches per plant and plant height. Studies by Ilhamuddin et al. (1989) in mungbean, showed significant differences for 8 quantitative characters. High genotypic and phenotypic variances were recorded for plant height and 1000 seed weight. Genotypic and phenotypic co-efficients of variation

were highest for yield per plant. Similar studies were also conducted by Singh et al. (1990).

Apte et al. (1987) reported high heritability for 100 seed weight, seeds per pod and days to maturity, in cowpea. The percentage genetic gain was high for 100 seed weight, plant height, branches per plant and seeds per pod. Patil and Baviskar (1987) observed maximum variation for seed yield per plant followed by pods per plant, pod clusters per plant and days to maturity. The genotypic co-efficient of variation and phenotypic coefficient of variation were highest for pods per plant, pod clusters per plant, seed yield and 100 seed weight. Heritability was highest for 100 seed weight, followed by days to maturity and pod length. Sharma et al. (1988), in cowpea, observed maximum genotypic variation for dry matter yield, followed by plant height, green forage yield, pods per plant, seed weight and green pod yield. Heritability ranged from 46.9 per cent for green pod yield, to 98 per cent for days to 50 per cent maturity. Heritability estimates and variability studies in parents and their F_1S in cowpea by Thiagarajan (1989), showed that, heritability and genetic advance were high for plant height, number of seeds per pod and 100 seed weight. In nigerian cowpea, Thiagarajan et al. (1989) observed high heritability and genetic advance for height, number of clusters per plant, number of pods per plant, number of

seeds per pod and seed yield per plant. High heritability was reported for plant height, seed number per plant, pods per primary branch, pod length and breadth, days to 50 per cent flowering, and maturity and seed yield, in cow pea by Roquib and Patnaik (1990). Most of these traits had high estimates of genetic advance.

Chen et al. (1986) reported low heritability, but high co-efficient of genetic variation, for 8 yield components in annual and wild soyabean. Rajput et al. (1987) observed considerable genetic variability in soyabean for pods per plant, plant height and grain yield per plant. High heritability and genetic advance were seen for pods per plant and branches per plant. Momirovic (1987), in a study of heritability and genetic variance, in 12 varieties of soyabean and their hybrids observed high broad sense heritability estimates for 1000 seed weight number of nodes per plant and also for seed number, seed yield and pc number. Yao et al. (1987) observed high heritabilit estimates for growth period, number of pods on the mai stem, 100-seed weight, height, number of single seeded pods and number of seeds per pod. Sharma and Abraham (1988) presented information on heritability and genetic advance of 31 indigenous genotypes of soyabeans.

Estimation of variability in lentil by Baidya et al. (1988) showed that seed weight per plot had the highest

phenotypic, genotypic and environmental co-efficients of variability. Heritability was highest for days to flowering but its genetic advance was low. Zaman et al. (1989) in his studies in lentil observed the highest co-efficient of variation for seed yield per plant, from the data on 8 yield components, in 190 accessions. Similar studies were conducted by Biswas and Das (1990).

Shah et al. (1986), in a study of 25 varieties of french bean, observed that, genetic advance was high for height and yield per plant but was low for other 6 .eld components. Vaid and Singh (1986) identified different groups of characters as promising, for improvement through breeding, the only consistently unpromising character being pod length. Among 11 genotypes of french bean studied by Mishra and Dash (1991) in two seasons, variability was greater for plant height yield and pod length, than that for days to maturity and pod girth. Very high heritability was estimated for yield and pod girth, and these two characters also showed high genetic advance as did for pod length.

Singh et al. (1991) reported that, additive genetic variance was higher than the non additive genetic variance, in all yield-traits, in large seeded common beans.

A high level of phenotypic variability was recorded for pods per plant, pod size and primary branches per plant in

pea, by Solanki et al. (1988). Association of high heritability with genetic advance, for fruit size and pod yield per plant was also noted. Prasad and Karmakar (1989) worked on variability and heritability.

Singh et al. (1988) observed highest variation in 100 seed weight, from studies on faba bean. Days to 50 per cent flowering and branches per plant exhibited highest heritability and genetic advance.

Lokesha and Shivashankar (1990) in their analysis of genetic variability in cluster beans, showed that the highest heritability estimates were obtained for seed-to-pod ratio, number of leaves and peduncle length.

Analysis of variance for 16 varieties of dolichos bean by Das (1987), indicated that, 100-seed weight and green pod yield per plant had high heritabilities.

Birari and Ghanekar (1991) also derived information on genetic variation and heritability, in 36 genotypes of field bean.

2.2 Correlation studies

An understanding of the correlation of different characters with yield and also among themselves is important

to carry out selection. A number of studies have been conducted in this regard.

2.2.1 In horse gram

Das (1972) reported positive correlation of number of branches per plant and number of pods per plant with seed yield per plant. Ganeshiah (1980), in his multivariate analysis for yield and its contributing characters gave the correlation between yield components. Patil and Deshmukh (1983) showed that seed yield was positively correlated with number of pods per plant, number of secondary branches and 100 seed weight. Birari et al. (1987) revealed a strong positive correlation of yield with number of days to first pod maturity, number of pods per plant and number of seeds per pod. A negative correlation was found between seed weight and yield. Singh (1990), in his correlation studies in horse gram derived information on 9 characters and their correlations.

2.2.2 In other pulses

Of the 12 characters recorded for 80 pigeonpea genotypes, plant height, number of branches per plant, number of pods per plant, pod weight and number of seeds per pod were positively correlated with each other and significantly correlated with yield, according to Bhongale

and Raut (1987). Malik et al. (1987) through their correlation studies revealed that, yield was positively and significantly correlated with plant height, primary branches per plant, pods per plant, clusters per plant and biological yield in pigeonpea. Angadi et al. (1988), through their studies in pigeonpea, brought out the importance of pods per plant, branches per plant and plant height in determining yield. They noticed non significant correlation of seeds per pod and 100 seed weight with seed yield, but significant positive correlation with pod length. Branches per plant showed significant negative correlation. In pigeonpea, in a trial involving determinate habits, by Chaudhary et al. (1988), high yield was associated with increased branching and plant spread, more clusters and pods and bolder seeds. In another trial, high yield was correlated with stand density, pod number, branches per plant, seeds per pod and smaller seeds. Earliness was negatively correlated with plant height, branch number and number of clusters per plant. In 64 diverse genotypes of pigeonpea derived from intervarietal crosses, Patel et al. (1988) showed that, seed yield was strongly correlated with plant height, branches per plant and pods per plant, at the genotypic level. Days to maturi-, was moderately correlated with seed yield. Balakrishnan and Natarajan (1989) in their association studies in pigeonpea, showed that, seed yield

per plant was positively correlated with number of pods per plant and percentage pod set, and was negatively correlated with dry matter efficiency and harvest index. Pod set percentage and dry matter efficiency were positively correlated with harvest index and number of pods per plant was negatively correlated with percentage pod set.

Khorgade (1986) reported positive and significant correlation of yield with 100 seed weight, number of branches and pods per plant, and negatively correlated with days to 50 per cent flowering and number of seeds per pod. Correlation analysis by Salimath and Bahl (1986) in chickpea revealed that seed yield was positively correlated with primary and secondary branches per plant, pods per plant and 100 seed weight. The ideal plant type is considered to be one in which maximum expression was given for total number of fruiting branches and pods.

Singh et al. (1986) revealed that seed size, pods per plant and primary branches per plant were the main yield component traits. Correlation analysis in chickpea by Paliwal et al. (1987) reported that, seed yield per plant was positively correlated (at phenotypic level) with plant height, days to 95 per cent maturity, days to 50 per cent flowering, pods per plant and seeds per plant. Sindhu and Prasad (1987) obtained positive correlation of yield with

days to maturity, 100 seed weight, pods per plant, seeds per plant and harvest index. Secondary branch number was negatively correlated with yield at genotypic level. Correlation studies in chickpea by Jivani and Yadavendra (1988) showed that, yield was positively and significantly correlated with branches per plant, pods per plant, 100 seed weight and harvest index. Mishra et al. (1988) reported positive correlation of seed yield, with plant spread, number of primary and secondary branches per plant, pod bearing length, number of pods per plant, biological yield per plant and harvest index. A positive and significant association of seed yield was reported by Sandhu et al. (1988) with pods per plant, secondary branches per plant, primary branches per plant and seeds per pod. Selection for secondary branches per plant and seeds per pod is recommended to improve yield. Results of correlation studies in chickpea by Malik et al. (1988) revealed that, pods per plant, seeds per pod and 100 seed weight were positively correlated with yield. Zade and Waryari (1988) showed significant positive correlation of yield, with pod weight per plant and 100-seed weight, and negative correlation with crop duration and duration of reproductive phase. The author suggested selecting for increased pod weight per plant, 100-seed weight and earliness, to improve yield. Significant positive correlations were found between

seed yield and number of pods per plant, and number of primary and secondary branches per plant, by Singh et al. (1989) also. Sharma et al. (1989) reported a highly significant positive correlation of yield, with number of pods per plant, primary branches per plant, secondary branches per plant and plant height. Singh and Singh (1989) showed that, pods per plant and seed yield were highly correlated genotypically. Studies conducted by Mani and Bahl (1990), in desi and kabuli types of chickpea indicated that, most associations in yield components were similar, in the two groups. Grain yield was positively correlated with primary and secondary branches, pod number, biological yield and harvest index. Chhinna et al. (1991) showed that, seed yield had a high positive correlation with pods per plant and number of secondary branches, in chickpea. Pods per plant was significantly correlated with number of secondary branches. In another study by Kumar and Arora (1991), correlation with seed yield was significant for biological yield, pods per plant, 100 seed mass and plant height, in chickpea.

Singh et al. (1986) concluded that, seed yield in blackgram was correlated with pods per cluster and pods per plant and was negatively correlated with days to flowering. Patil and Narkhade (1987) showed that, seed yield was positively and significantly correlated with pods per plant,

100 seed weight, pod length and seeds per pod, in blackgram. Waryari (1988) reported that, pod number, pod length, cluster number per plant and 100 seed weight, in blackgram were positively associated with yield. Khan (1988) could observe positive correlation of pod length and negative association of number per cluster with seed yield, in black gram.

Raut et al. (1988), in green gram, reported positive correlation of seed yield, with number of seeds per pod, number of branches per plant and clusters per plant. Association studies by Patil and Narkhede (1989) in mungbean, suggested that 100 seed weight, pod length, pods per plant and plant height should be used for selection programme. According to Satyan et al. (1989), seed yield in green gram, was positively and significantly correlated with plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, pod length, days to maturity and plant area.

Jindal and Gupta (1984) observed that, plant height, pods per plant, pod length and seeds per pod were significantly and positively correlated with seed yield, in cowpea. For days to maturity, the correlation was significant and negative. Similar results were obtained by

Patil and Bhapkar (1987), with regard to seed yield and the characters pods per plant and seeds per pod; but these two characters were negatively correlated with each other. Positive and significant correlation of pods per plant, seeds per pod, days to first flowering and days to 50 per cent maturity with seed yield was observed by Sharma et al. (1988). Tyagi and Koranne (1988) also noted positive and significant correlation of yield with number of branches per plant and seeds per pod, in cowpea. Similar results were obtained by Patil et al. (1989).

Song et al. (1987) reported significant positive correlation of yield, with number of seeds per pod, but not with days to flowering, days to maturity, 100 seed weight and protein and oil content, in soyabean. Momirovic (1987) observed that, seed yield was mainly influenced by node number per plant, followed by 1000 seed weight. Das et al. (1989) stated that, in soyabean, seed yield was significantly correlated with plant height and number of pods, nodules per plant and seeds per pod. Zaman (1989) from his studies in soyabean indicated that profusely branching plants, with high pod number had high yield potential. Amaranatha et al. (1990) observed that, in soyabean, seed yield per plant showed significant positive correlation, with number of seeds, pods and branches per plant,100 seed weight, days to maturity, days to 50 per cent

flowering and plant height. Deshmukh et al. (1991) derived information on yield correlations from data on yield and 8 related traits. Bhattacharya and Ram (1992) reported that, for determinate soyabean genotypes, plant height, pods per main stem, pods per branch and pods per plant were significant yield components. Feng et al. (1991) considered that, improvement in soyabean could be brought about by increasing the number of seeds per pod and number of pods per plant.

Correlation studies in french bean by Shele and Kale (1988) indicated that, green pod yield and seed yield were mainly determined by plant height, earliness, leaf number and duration of harvest for green pod and plant height.

Lokesha and Shivasankar (1990), observed strong association of pod and seed yield, with plant dry weight, number of leaves at 60 days and number of single-podded clusters, in cluster bean.

In peas, days to 50 per cent flowering, days to maturity, plant height, pods and primary branches were positively associated with grain yield, according to Singh (1985). Srivastava and Sinch (1989) observed highly significant positive correlations of yield, with number of pods per plant and number of primary branches, seed weight, with pod length and pod breadth, in peas.

In broad bean, Naidu et al. (1985) reported significant negative correlation of yield with flowering time, maturity and height, and positive correlation with internodal length, branches per plant, clusters per plant, pods per plant and seeds per pod. They suggested that, pod and seed number should be given priority, during selection.

2.3 Genetic divergence

The importance of genetic diversity for successful selection and hybridisation had been recognised by several workers. A quantitative assessment of genetic divergence among various genotypes, the relative contribution of the different characters towards total divergence and association between genetic divergence and geographic divergence have proved to be essential informations in genetic improvement programme.

2.3.1 In horse gram

Genetic divergence studies were conducted in horse gram by Ramakrishnan et al. (1979) using Mahalanobis-D^2 statistic. They studied 8 yield components among 11 genetically diverse varieties, representing different geographical areas of the world and found no association between geographical and genetic diversity. According to them, 100-seed weight and dry weight of nodular tissues formed the chief contributors to total divergence.

Geneshiah et al. (1984) studied genetic variability for yield and other characters in 100 genotypes of horse gram from six countries. The entries could be grouped into 3 to 5 clusters depending on the variability of each trait.

2.3.2 In other pulses

Malik et al. (1985) used D^2 analysis to group 35 Indian cultivars of pigeonpea into 8 clusters. In a study conducted by Hazarika and Singh (1986), using 12 parental lines and their 32 hybrids of pigeonpea, determinate lines and hybrids were grouped in one of the two clusters. Sixteen of the hybrids were grouped in different clusters from their parents. Patel et al. (1988) suggested that the main discriminating traits between the clusters formed by D^2 analysis in pigeonpea were, number of secondary branches, pods per plants and clusters per plant. Nine clusters could be formed from 40 genetic stocks. Gartan et al. (1989) grouped 58 determinate and indeterminate genotypes of pigeonpea into fifteen clusters. Shoran (1989) could not find any relationship between clustering of genotypes and geographic diversity in pigeonpea. D^2 analysis by Murthy and Dorairaj (1990) allowed 40 early maturing genotypes of pigeonpea to be grouped into three clusters. Genetic divergence was independent of geographic origin. High heritability for earliness, seed yield and protein content was obtained in crosses of genotypes from distant clusters.

Divergence analysis of 22 varieties of chickpea by Dasgupta et al. (1987) gave 5 clusters, with 100-seed weight giving the maximum contribution to divergence. Again, it reflected the difference between desi and kabuli types, with no relationship with geographical divergence. Similar results were obtained by Lal et al. (1989). In a study involving 7 parents and 21 F_1 hybrids of chickpea by Mian and Bahl (1989), the parents with moderate D^2 values (26.6 to 35.8) were seen to give hybrids with highest heterosis. Samal et al. (1989) grouped 23 cultivars of chickpea into 6 clusters and suggested that, crosses involving cultivars from clusters with greatest cluster distance exhibited high heterosis. Singh et al. (1990) showed that, composition of the clusters was influenced by environment, while studying 60 chickpea types in two environments. Sandhu and Gumber (1991) grouped 59 strains of chickpea into 12 clusters. Intracluster D^2-values ranged from 0.0 to 13.6 and inter cluster distance, from 15.0 to 156.5.

In raymash, Vaid et al. (1988) showed that, days to flowering days to maturity, plant height and 100-gram weight were the most important characters determining divergence. The 9 groups were clearly demarcated into late maturing tall and early maturing dwarf groups.

Sindhu et al. (1989) conducted multivariate analysis of data, on 10 yield components, using 20 genotypes of

blackgram. Similar works were conducted by Perraju and Singh (1990), in which 50 blackgram genotypes were formed into 11 clusters. Dasgupta and Das (1991) concluded that, days to flowering, pods per plant, and pod length made the greatest contribution to genetic distance, among the 9 clusters formed from 38 blackgram varieties of India and Nepal.

Genetic diversity for quantitative characters was studied by Misra (1986) in green gram. The analysis suggested the formation of 16 clusters, with the clustering not relating to geographical origin. Ramana and Singh (1987), through their D^2 analysis in spring and kharif greengram, studied the effect of genotypes on cluster distance, cluster divergence and genotypic divergence. Days to flowering and 100 seed-weight contributed most to genetic divergence in kharif and spring respectively. Genetic divergence was determined in 20 genotypes of mungbean by Singh and Pathak (1987) for seed yield per plant and 10 yield related characters. The genotypes were grouped into 6 clusters, the members of each cluster being geographically unrelated.

Marangappanavar (1986) concluded that, inter cluster spatial patterns were not consistent with varietal geographic distribution, following his clustering studies in cowpea. D^2 statistic and Euclidean distance co-efficient

were used as measures of genetic divergence in Vigna sublobata by Sharma et al. (1986). Patil and Bhapkar (1987) did not obtain any relationship between clustering and geographical distribution. According to Thiagarajan et al. (1988), days to 50 per cent flowering, 100 seed weight and plant height contributed most to genetic divergence in cowpea. Of the 12 hybrids and their parents, the parents fell into 5 clusters and the hybrids into another 5 clusters. Wide genetic diversity was exhibited among the 13 clusters, formed from 40 genotypes of cowpea, in the studies of Dharmalingam and Kadambavanasundaram (1989). Genotypes belonging to the 2 most divergent clusters were recommended as suitable for inclusion in heterosis breeding programmes. On the basis of analysis of data on 30 geographically diverse cowpea accessions, 4 clusters were formed by Thiagarajan and Natarajan (1989). Number of pods per plant, number of seeds per pod and seed yield per plant made the largest contribution to genetic divergence. No parallelism existed between geographic and genetic diversity.

[illegible]a et al. (1987) grouped 75 genotypes of soyabean into 5 clusters, based on yield and 11 yield related characters. Sichkar et al. (1988) suggested that the degree of expression of economic characters was also as important as the genetic distance of the parents involved in the crosses. Sharma and Luthra (1987) in their divergence

studies in soyabean using 56 genotypes, concluded that, the composition of clusters formed using D^2 statistic differed between groups, due to environmental variations.

Henry and Krishna (1990) compared cluster bean cultivars from various parts of India and formed 10 groups. The clustering did not reliably reflect geographic diversity, suggesting that, cultivars from the same area may have different genetic backgrounds. Breeding using the members from the most divergent clusters, was considered as the basis for producing best cultivars.

Data on 9 quantitative characters in 36 indigenous and foreign french bean types, on analysis, gave 11 clusters with varieties from the same eco-geographical region being assigned to the same cluster. Seven characters accounted for 90 per cent of the total diversity according to this study by Shele and Kale (1988).

Dobhal and Ram (1985), using D^2 analysis grouped 32 indigenous and foreign lines of pea into 11 clusters. No relationship with geographical diversity was indicated by clustering. Similar results were revealed by Saxena et al. (1985) and Singh and Tripathi (1985). Varlakhov et al. (1985) suggested that, when genetic distance of the parents involved in the crosses was large, one of the parents had low gea effects and heterosis was absent. According to

Singh (1987), in pea, plant height, nodule number per plant and harvest index contributed most to the total divergence.

In a study conducted in faba bean, Sindhu (1985) could observe positive relationship between geographical and genetic diversity. The twenty-four strains from 9 countries were grouped into 11 clusters, on the basis of seed yield per plant, 8 yield related characters and protein contents. Chhabra et al. (1988) classified 93 faba bean genotypes into 6 clusters. Katiyar and Singh (1990) assigned 40 indigenous and exotic faba bean genotypes to 12 clusters. No geographic pattern was detected in clustering. The greatest divergence was noted for pod number per plant and 100 seed weight. Another work by Khare and Singh (1990) on 25 genotypes of faba bean revealed 3 clusters, which were unrelated in terms of geographical distribution.

Henry and Krishna (1986), on analysing 53 moth bean genotypes, formed 15 clusters, with early and late maturing ones belonging to 4 clusters and mid season ones to 7 clusters. Genetic distance was best measured by the traits, days to flowering, days to maturity, pods per plant and yield per plant. Deokar et al. (1991) could group 40 lines from different parts of India into 6 clusters.

Days to flowering and number of pods per bunch contributed most to genetic divergence in hyacinth bean,

according to Singh (1991). The 48 strains from 8 Indian states could be grouped into 10 clusters.

2.4 Growth analysis

The technique of growth analysis had been applied, to account for the variation of yield in terms of growth and development of the plants in a number of crops. In pulses also, several such studies have been undertaken. An overall view of the works done so far will be of help for pursuing the studies.

2.4.1 In horse gram

Manian et al. (1989) investigated the dry-matter partitioning in 200 genotypes of horse gram and isolated an ideotype with high dry matter production and high partitioning efficiency at the time of early pod formation, coupled with high yield. They also concluded that, a higher dry matter production at grain-filling stage was probably playing a significant role in the productivity of the crop. Manian et al. (1990) estimated leaf area in two cultivars of horse gram by non-destructive leaf measurements. A standard equation of, leaf area = 1.72 x length x breadth of terminal leaflets, could be used.

2.4.2 In other pulses

Balakrishnan et al. (1987) found that, in pigeonpea, average leaf area index (LAI) reached a peak at 50 per cent flowering, crop growth rate (CGR) was highest between 50 days after sowing (DAS) and first flowering, while net assimilation rate (NAR) was at its peak at 50 DAS. The critical LAI was estimated as 5.3. Consi erable variability was found among the cultivars for different physiological parameters, in pigeonpea, by Mehra et al. (1987). It was concluded that, a desirable plant type should have a reproductive sink, more competitive at the time of flower flushes, but at the same time a higher LAI was desirable during reproductive phase. Sharma et al. (1987) showed that, leaf area could be estimated from the product of leaf length x leaf width x 0.7489, in pigeonpea. This estimated value showed significant correlation ($r = 0.996$) with actual leaf area. Studies with four short and two medium duration pigeonpea varieties, by Vanangamudi et al. (1987) revealed that, there was a marked difference in dry matter accumulation in seed yield and harvest index, among cultivars. The higher harvest index of medium duration cultivars resulted from both increased seed yield and total dry matter accumulation.

Padalia and Patel (1980) found out a linear relationship between actual leaf area and that estimated

using the length-width method in groundnut. Murty et al. (1983) studied the pattern of variation in physiological parameters in three groundnut varieties and concluded that it differed with varieties. Leaf and stem photosynthesis contributed to dry matter yield upto 60 DAS and thereafter stem photosynthesis was more important. Significant varietal difference was observed by Hiremath et al. (1984) for leaf photosynthetic rate, leaf traits, total dry matter and harvest index , in groundnut. Varietal variations studied in morphology and growth of 3 semi-spreading and 3 spreading varieties of groundnut by Velu and Gopalakrishnan (1987), showed a decreasing trend over time for NAR and relative growth rate (RGR), for most cases. Changes in CGR and LAI appeared to be closely interrelated, and showed considerable variation, between and within the same group. Shelke et al. (1988) estimated leaf area constants for two groundnut cultivars, based on linear measurements of intact leaves and 2 weighted regression co-efficient models (0.8298 for ICGS-11 and 0.8720 for JL-24). Analysis of dry matter production and yield potential in groundnut genotypes by Kumari and Singh (1990) revealed that, dry matter accumulation was greater in vegetative parts upto 90 days and thereafter it was more in pods. Assimilate partitioning had the greatest effect on pod yield. Dry matter partitioning to pod ranged from 48 per cent in K-2 to 90 per cent in TG-17. Davis and Mack (1991) showed that, in peanut, most of the growth

characters measured increased with time, and showed significant correlation with LAI, for each cultivar.

Growth analysis of urd-bean by Pandey et al. (1980) revealed an inverse relationship between leaf area and NAR. The leaf area increased till 70 DAS in all cultivars. The increase in CGR at 60-70 DAS was attributed to the increase in LAR and leaf area. They ascribed the increase in NAR partly to a response of photosynthetic apparatus, on increased demand for assimilates by the growing seed fraction, and partly, to the photosynthetic contribution made by the growing pods. In greengram, leaf area constants were determined for estimating leaf areas in two cultivars (0.7198 for J-81 and 0.7095 for T.44) by Potdar et al. (1980). Singh and Singh (1981) discussed the association of seed yield with different physiological characters. In mungbean grown in summer and Kharif, yield was positively influenced, directly and indirectly respectively by NAR, RGR and specific leaf weight but not by leaf weight ratio and specific leaf area. Sequential analysis of plant growth, treating some of the traditional indices of plant growth as yield components was carried out by Joliffe et al. (1982) in greengram. Variability studies by Singh et al. (1985) in 4 mung-bean cultivars indicated that CGR, RGR, NAR, LAI leaf area ratio, leaf-weight ratio, specific leaf weight and harvest index were higher in all cultivars during summer.

Photosynthetic rate, total dry matter, pod yield and harvest index measured for 20 cultivars of green gram were studied at different growth stages by Srinivasan et al. (1985). He observed significant cultivar differences in all the parameters studied. At the early pod development stage, a positive and significant correlation existed between leaf photosynthesis, total dry matter, pod yield and harvest index. Leaf photosynthesis increased with age and the higher photosynthetic rates at the early pod developmental stage could increase seed yield, if high dry matter and harvest index were ensured at this stage. Significant genotypic variation was found between 25 varieties of mung-bean studied by Nijhavan (1988), at four growth stages, for leaf area, specific leaf weight, T-O value (a measurement of total green area) and LAR, at one or more stages of growth. Highest yielding varieties had the highest leaf area and T-O value and LAR at maturity. Seed yield was positively correlated with leaf area and T-O value, at all but the first stage. LAR was negatively correlated with specific leaf weight. Manian et al. (1987) showed that, the area of a trifoliate leaf could be accurately estimated from a regression equation, incorporating the product of length and width of a terminal leaflet.

Rani and Rao (1981) concluded that, mid-season and late varieties of blackgram were superior to early cultivars, in

efficient partitioning of dry matter during reproductive stage. Dry matter depletion of leaves was higher than that f stem; it was higher in mid season and late cultivars than n early cultivars. Balakrishnan et al. (1987) estimated eaf area in blackgram, using a regression equation based on he relationship A =K (L x B) where A = leaf area. L x B in he length x breadth of the leaf. The regression equation is =a+bx+K (y = leaf area a, b and K are constants and x is the product of length and breadth).

Leaf area of cowpea was estimated from linear measurements and was shown to be 2.325 L.W. (L = Length of leaf and W = maximum leaf width) by Yeboah et al. (1983). Plant growth analysis conducted by Fernandez and Miller (1987) in 5 indeterminate and one determinate cultivars of cowpea revealed that, dry matter accumulation and leaf area per plant reached maximum at 56 DAP in all indeterminate cultivars and one week later in the determinate one. RGR declined linearly with time. He also reported that, NAR of the determinate cultivar was at is peak at 4 weeks, and became negative in the determinate type and LAR declined curvilinearly with time in all cultivars. Sharma et al. (1987) reported that, in cowpea, leaf area could be estimated from the formula A = LxBx0.6654.

Uprety (1981), from his evaluation of growth and yield characters in soyabean, found that yield was determined

differently among cultivars. The difference in seed yield was also attributable to the duration of the period from flowering to yield formation. Positive correlation of NAR and specific leaf weight with seed yield, fruit number and harvest index was observed. Hudge et al. (1982) also reported significant differences in total dry matter accumulation among cultivars of soyabean. In 16 cultivars and lines of soyabean, Sharma et al. (1982) reported positive and highly significant correlation of seed yield per plant, with NAR from pod development to maturity. LAI differed between genotypes at pod maturity and physiological maturity, but was similar at flowering. Studies by Zhang and Liu (1982) in soyabean showed that, a negative correlation existed between LAI and yield, at all stages. The NAR at all stages was positively correlated with yield, LAI was negatively correlated with NAR. Beaver et al. (1985) reported significant variation in dry matter accumulation and seed yield, in determinate and indeterminate soyabeans, studied. Pedro et al. (1985) could also find variation in growth among soyabean cultivars. Spaeth and Sinclair (1985) reported a linear increase in harvest index, during seed-filling in all but the early cultivars of soyabean, whereas in early cultivars, it increased curvilinearly. This could be used to calculate the length of seed filling period. Bhardwaj and Bhagsari (1990) observed significant variation

for all traits (harvest index, yield, LAI, biomass and height) among small and large seeded genotypes of soyabean. Small and medium seeded types had a higher HI and lower LAI than the other groups. Yield was positively correlated with harvest index, in large and small seeded types. You et al. (1991) used data from 12 soyabean cultivars and showed that, a close correlation existed between leaf area and the product of leaf width and leaf length.

Pandey and Singh (1980) reported that, CGR, NAR and RGR varied with the stage of development and genotype in field pea. Studies by Nath and Bhardwaj (1983) in field peas showed that, dry matter accumulation during the pre-flowering period varied between the two cultivars but during the post-flowering period, it was more or less similar in both the cultivars.

Fletcher (1986) indicated that, in garden peas, the main components of biomass variability were, stem length, average leaf area and inverse leaf weight ratio.

Rhoden and Cray (1988) observed that, in southern pea, leaf area (LA) and dry matter content (DM) were closely correlated as were leaf area and plant dry matter. The leaf area-leaf dry matter content ratio were consistent in all cultivars throughout the vegetative growth period.

cotyledons, when the main stem had 15-18 nodes. At 35 node stage, 15 per cent of the nodes bore pods. In a growth analysis conducted in faba bean, Singh et al. (1988) recorded a higher LAR during 35-70 DAS and 75-105 DAS. LAI and CGR increased, whereas RGR, NAR and relative growth rate decreased with increasing plant density, at both stages of crop growth.

Tsai (1982) reported that, in rice bean accumulation of dry matter was controlled by leaf area duration. Both NAR and RGR decreased as growth progressed. Most dry matter was accumulated in leaf and main stem, during early growth.

In field bean, Balakrishnan et al. (1985) reported that, leaf area could be predicted using a regression equation $y = 3.09 + 1.63x$ (y = leaf area of a trifoliate leaf; x=length X breadth of terminal leaflet of the trifoliate leaf), or by using the formula. $A = 1.685$ (LXB) (L = Length and B = Breadth of the terminal leaflet). Actual leaf area was significantly correlated with the two methods ($r=0.9647$ and $r = 0.9630$ respectively).

Pandey (1980) concluded that, in lentil a relatively small portion of the total dry matter was produced before flower initiation, and the bulk of it was produced after anthesis. The maximum CGR and NAR was observed during pod filling stage in all genotype. The sharp rise in NAR during pod filling was probably due to an increased demand on assimilates, by the growing seed fraction, and partly to the photosynthetic contribution, by green pods.

Analysis of growth in faba bean by Solarzano et al. (1982) revealed that, maximum production of active leaf area was between nodal stages 30 and 35 of the main stem. LAI increased rapidly after nodal stage 18, reaching a maximum of 306 at 30 nodal stage. NAR decreased rapidly between nodal stage 5 and 21 and showed a minor increase after flowering, but decreased at the start of seed filling. The first flower appeared between 12th and 18th node above the

Materials and Methods

MATERIALS AND METHODS

The studies reported herein, were carried out in the research plot of the Department of Agricultural Botany, College of Horticulture, Vellanikkara, from October, 1992 to February, 1993.

3.1 Materials

Fifty genotypes of horse gram (Dolichos biflorus L.), representing the indigenous types from different States were selected, from the germplasm collection at National Bureau of Plant Genetic Resources, Regional Station, Thrissur, for this study. The particulars of these genotypes are given in Table 1.

3.2 Methods

The experiment, consisting of fifty treatments with two replications, was laid out in Randomised Block Design in an area of 43 x 25 m^2 with a plot size of 3.8 m x 2.1 m. The spacing adopted was 30 cm x 25 cm (Fig. 1).

Seeds were sown @ 3 seeds per hole, which was later thinned to one seedling per hole. The crop received timely management and care as per recommendations given in "Package of Practices Recommendations - Crops 1989". No plant protection measures were needed.

Table 1. Particulars of fifty genotypes of horse gram (*Dolichos biflorus* L.) used for the study.

Genotypes (Acc. No.)	Source	Treatment Number
IC 22765	Delhi	V_1
IC 26128	Ernakulam, Kerala	V_2
IC 45733	Dindigal, Tamil Nadu	V_3
IC 45748	Dindigal, Tamil Nadu	V_4
IC 50714	Karnataka	V_5
IC 44014	Unknown, From NBPG HQ	V_6
PLKU 187	Unknown, From HQ	V_7
IC 68587	Kasargode, Kerala	V_8
IC 88999	Idukki, Kerala	V_9
IC 71723	Thirunelveli, Tamil Nadu	V_{10}
IC 71764	Thirunelveli, Tamil Nadu	V_{11}
IC 71766	Delhi	V_{12}
IC 1978	Delhi	V_{13}
IC 22800	Delhi	V_{14}
IC 32835	Delhi	V_{15}

IC 33353	Delhi	V_{16}
IC 44013	Idukki, Kerala	V_{17}
IC 44018	Madurai, Tamil Nadu	V_{18}
IC 45719	Madurai	V_{19}
IC 50728	Madurai	V_{20}
PLKU 168	Unknown	V_{21}
IC 68591	Kasargode, Kerala	V_{22}
IC 45702	Thirunelveli	V_{23}
IC 5078	Dindigal, Tamil Nadu	V_{24}
PLKU 358	Unknown	V_{25}
IC 71733	Thirunelveli	V_{26}
IC 71742	Thirunelveli	V_{27}
IC 71749	Tamil Nadu	V_{28}
IC 71775	Madurai, Tamil Nadu	V_{29}
IC 71785	Madurai, Tamil Nadu	V_{30}
IC 71812	Madurai, Tamil Nadu	V_{31}
IC 23448	Delhi	V_{32}

IC 45756	Dindigal, Tamil Nadu	V_{33}
IC 241	Avinashi, Tamil Nadu	V_{34}
IC 33050	Delhi	V_{35}
IC 50726	Madurai, Tamil Nadu	V_{36}
R_5	Unknown	V_{37}
IC 22787	Delhi	V_{38}
IC 23508	Delhi	V_{39}
IC 24	Unknown	V_{40}
IC 71823	Madurai, Tamil Nadu	V_{41}
PLKU 159	Unknown	V_{42}
TCR 558	Madurai, Tamil Nadu	V_{43}
IC 45734	Dindigal, Tamil Nadu	V_{44}
IC 26132	Delhi	V_{45}
IC 71726	Thirunelveli, Tamil Nadu	V_{46}
IC 71730	Thirunelveli, Tamil Nadu	V_{47}
T 58/14	Delhi	V_{48}
IC 22804	Delhi	V_{49}
IC 32861	Delhi	V_{50}

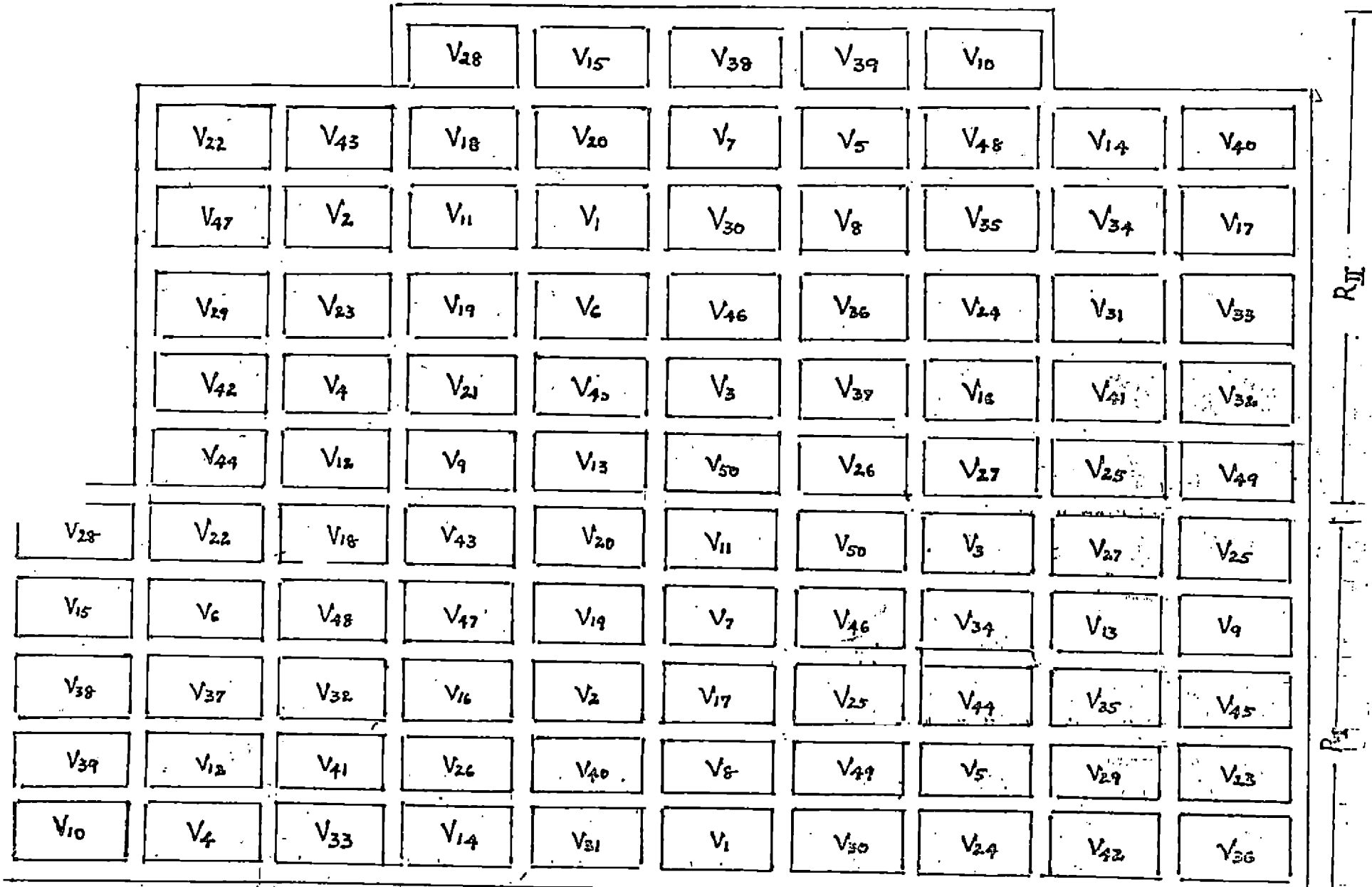

V28 V15 V38 V39 V10
V22 V43 V18 V20 V7 V5 V48 V14 V40
V47 V2 V11 V1 V30 V8 V35 V34 V17
V29 V23 V19 V6 V46 V36 V24 V31 V33
V42 V4 V21 V45 V3 V37 V16 V41 V32
V44 V12 V9 V13 V50 V26 V27 V25 V49
V28 V22 V18 V43 V20 V11 V50 V3 V27 V25
V15 V6 V48 V47 V19 V7 V46 V34 V13 V9
V38 V37 V32 V16 V2 V17 V25 V44 V35 V45
V39 V12 V41 V26 V40 V8 V49 V5 V29 V23
V10 V4 V33 V14 V31 V1 V50 V24 V42 V36
R11
R21

Plate 1. Overall view of the experimental plot

The experiment consisted of two aspects of studies, viz. genetic analysis and physiological studies, which included growth analysis.

3.2.1 Genetic analysis

Leaving a border row on all sides, a total of twenty five plants were selected at random and labelled in each plot, for taking observations. Morphological observations on nine economically important characters were taken and statistically analysed.

3.2.1.1 Observations

i. Height of the plant (x_1)

The height of the plants were measured at maturity and expressed in centimeters.

ii. Number of primary branches (x_2)

All the primary branches were counted and recorded, after full maturity of the plants.

iii. Days to 50 per cent flowering (x_3)

Flowering of 50 per cent plants in the plot was taken. For this, the two central rows of each plot were taken and daily count was made on the number of plants having opened flowers. The period between sowing date and the date on which 50 per cent of the plants flowered, was taken as days to 50 per cent flowering.

iv. Number of pods per plant (x_4)

All the pods, having seeds were counted, for each plant.

v. Length of pods (x_5)

Ten pods per plant were taken randomly and their length was measured in centimeters

vi. Number of seeds per pod (x_6)

All the pods from each plant were shelled and the number of seeds per pod was noted.

vii. 100 seed weight (x_7)

Hundred seeds were randomly taken from each plot and the weight was noted.

viii. Days to maturity (x_8)

The number of days taken for harvest was noted, starting from the date of sowing. This was done on per plot basis. All the sample plants of each plot, were harvested on the same day.

ix. Seed yield per plant (y)

Yield of seeds from each plant was weighed after normal drying and the weight was expressed in grams.

3.2.1.2 Statistical analysis

The data collected at maturity were tabulated and subjected to statistical analysis as follows:

i. Analysis of variance

Analysis of variance was worked out for all the nine characters studied, to test the significance of treatments, according to the procedure of Panse and Sukhatme (1957).

ANOVA

Source of variation	Degrees of freedom	Sum of squares	Mean squares	Variance Ratio (F)
Replication	(r-1)	SSR	S^2R	S^2R/S^2E
Treatment	(v-1)	SSv	S^2V	S^2V/S^2E
Error	(r-1) (v-1)	SSE	S^2E	

r = No. of replications

V = No. of varieties

SSR = Replication sum of squares

SSV = Varietal sum of squares

SSE = Error sum of squares

S^2R = Replication mean square

S^2V = Varietal mean square

S^2E = Error mean square

The significance of the computed values for 'F' was tested with reference to the 'F' table (Panse and Sukhatme, 1957).

ii. Variance

Genotypic, environmental and phenotypic variance, co-efficient of variation and correlation co-efficients were computed. Variability and genetic advance were also calculated.

a) Genotypic variance (Johnson et al., 1955).

$$Vg = \frac{MST - MSE}{r}$$

MST = Mean square for treatment

MSE = Mean square for error

r = Number of replications

b) Error (environmental) variance

$$Ve = MSE$$

where Ve = Error variance

MSE = Mean square for error

c) Phenotypic variance

$$Vp = Vg + Ve$$

where Vp = Phenotypic variance

Vg = Genotypic variance

Ve = Error variance

iii. Co-efficient of variation

a) Genotypic co-efficient of variation (Burton, 1952)

$$CVg = \frac{Vg}{Mean} \times 100$$

CVg = Genotypic co-efficient of variation

Vg = Genotypic variance

b) Environmental co-efficient of variation

$$CVe = \frac{Ve}{Mean} \times 100$$

where CVe = Environmental co-efficient of variation

Ve = Error (Environmental) variance

c) Phenotypic co-efficient of variation (Burton, 1952)

$$CVp = \frac{Vp}{Mean} \times 100$$

where CVp = Phenotypic co-efficient of variation

Vp = Phenotypic variance

iv. Heritability in the broad sense (Burton and Devane, 1953)

$$h^2 = \frac{Vg}{Vp} \times 100$$

where h^2 = Heritability expressed in percentage

Vg = Genotypic variance

Vp = Phenotypic variance

v. Expected genetic advance under selection (Lush, 1949 and Johnson *et al.*, 1955).

$$GA = \frac{ih^2 Vp}{Mean} \times 100$$

where GA = Genetic advance

i = Selection differential expressed in phenotypic standard deviation (2.060 in the case of 5% selection in large sample (Miller *et al.*, 1958 and Allard, 1960).

h^2 = Heritability in the broad sense

Vp = Phenotypic variance

vi. Co-variance

a) Genotypic covariance

$$Cov_g = \frac{MSPT - MSPE}{r}$$

where Cov_g = Genotypic covariance

MSPT = Mean sum of products for treatments

MSPE = Mean sum of products for error

r = The number of replications

b) Error (Environmental) covariance

$$Cov_e = MSPE$$

where Cov_e = error (Environmental covariance)

c) Phenotypic covariance

$$Cov_p = Cov_g + Cov_e$$

where Cov_p = Phenotypic covariance

Cov_g = Genotypic covariance

Cov_e = Error (Environmental) covariance

vii. Correlation co-efficient

a) Genotypic correlation co-efficient

$$r_g = \frac{Cov_{g1.2}}{V_{g1} x V_{g2}}$$

where r_g = genotypic correlation co-efficient

$Cov_{g1.2}$ = Genotypic covariance of variables 1 and 2

V_{g1} = Genotypic variance of variable 1

V_{g2} = Genotypic variance of variable 2

b) Environmental correlation co-efficient

$$r_e = \frac{Cov_{e1.2}}{V_{e1} x V_{e2}}$$

where r_e = Environmental correlation co-efficient

$Cov_{e1.2}$ = Environmental covariance of variables 1 and 2

V_{e1} = Environmental variance of variable 1

V_{e2} = Environmental variance of variable 2

) Phenotypic correlation co-efficient

$$r_p = \frac{Cov_{p.1.2}}{V_{p.1} x V_{p.2}}$$

where r_p = Phenotypic correlation co-efficient

$Cov_{p.1.2}$ = Phenotypic covariance of variable 1 and 2

$V_{p.1}$ = Phenotypic variance of variable 1

$V_{p.2}$ = Phenotypic variance of variable 2

viii) D^2 analysis

Mahalanobis D^2 analysis was carried out, to study the divergence of the genotypes. The D^2 values were calculated for the differ... ...notypes as suggested by Rao, 1952.

The genotypes were then grouped into different clusters, using the non-heirarchial Euclidean clustering method (Spark, 1958)

3.2.2 Growth analysis

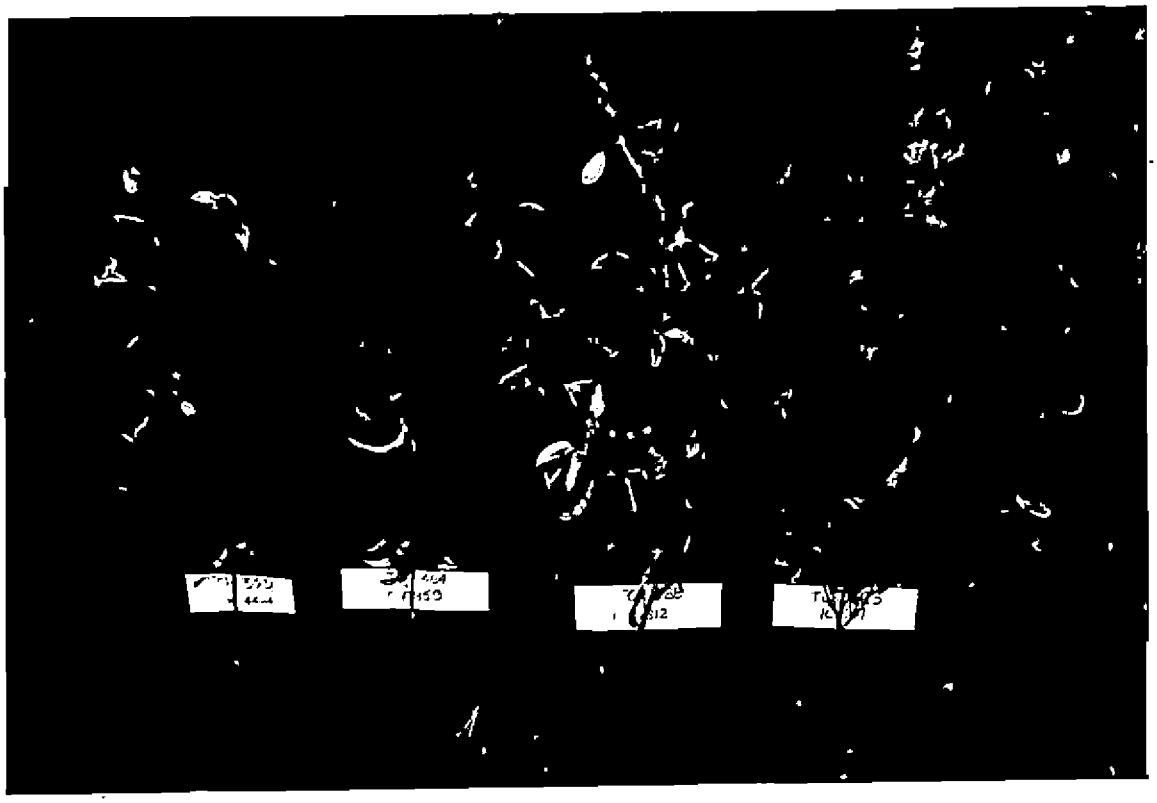
Growth analysis was
representative morphotypes. Fo
of three representative plants,
ten days interval. The plants
from 10th day onwards. Stems, leaves and reproductive parts were separated and dried at 60°C in the oven at 48 hours and then weighed. Leaf area of the sampled plants was also measured using standard leaf area constants.

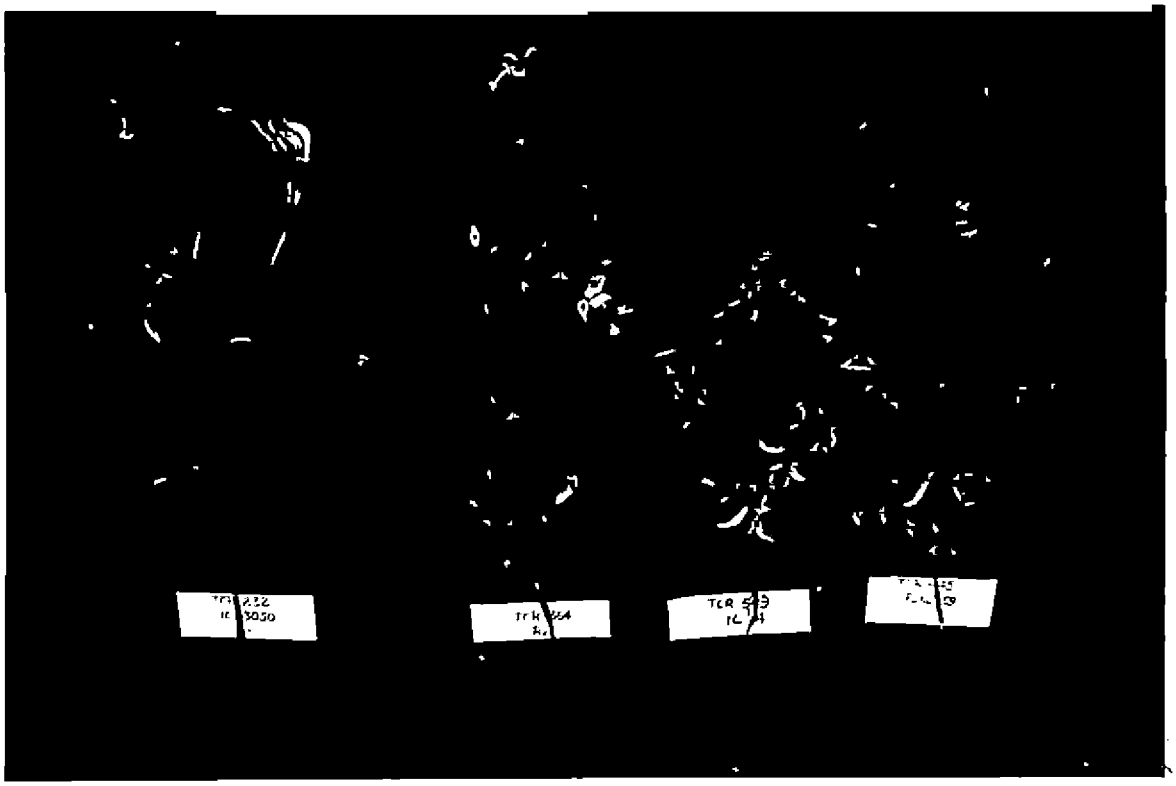
At each sampling date, observations were taken on the following morphological attributes:

1. Plant height in cm
2. Leaf number
3. Number of primary branches

Plate 2a. Genotypes used for growth analysis

Plate 2b. Genotypes used for growth analysis





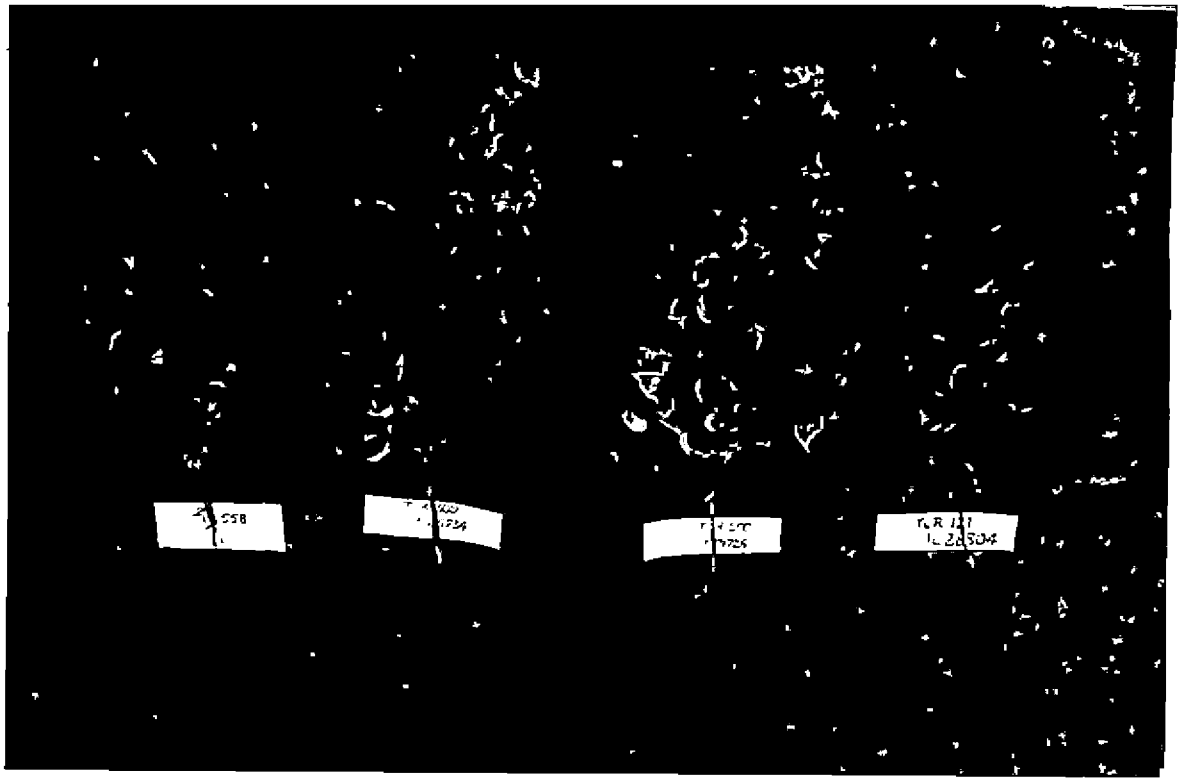


Plate 2c. Genotypes used for growth analysis

4. Number of secondary branches
5. Number of tertiary branches
6. Total number of branches
7. Number of pods on main stem
8. Number of pods on primary branches
9. Number of pods on secondary branches
10. Number of pods on tertiary branches
11. Total number of pods

From the observed data the values on per plant basis and unit area basis was calculated. The dry weight of different plant parts was found out. Leaf area was calculated using constants (Manian et al., 1990) (Leaf area = Length x width of terminal leaflet x 1.72). The data obtained on leaf area, dry weight and total plant dry weight, at different stages were used, to calculate the different morphological and physiological growth parameters, like total dry matter, leaf area index, relative growth rate, crop growth rate and harvest index as given below.

i. Total dry matter (TDM)

This was measured as the dry weight produced per plant or per unit area at each sampling.

ii. Leaf area Index (LAI)

It was measured in terms of total leaf area (m^2) per square meter of land area.

iii). Crop Growth Rate (CGR) (Watson, 1952).

It is the dry weight gain by unit area of crop in unit time.

$$CGR = \frac{W_2 - W_1}{t_2 - t_1} \; g.day^{-1} \; m^{-2}$$

where CGR = Crop growth rate

W_2 = Dry weight at time t_2 (in g)

W_1 = Dry weight at time t_1 (in g)

iv. Relative Growth Rate (RGR) (Friend et al., 1962)

It represents the increase in dry weight in time t_2-t_1, over dry weight at time t_1

$$RGR = \frac{InW_2 - InW_1}{t_2 - t_1} \; g.g^{-1} \; day^{-1}$$

v. Net Assimilation Rate (NAR) (Radford, 1967)

Dry weight gained in time $t_2 - t_1$ divided by average leaf area during $t_2 - t_1$.

$$NAR = \frac{W_2 - W_1}{t_2 - t_1} \times \frac{In\ A_2 - In\ A_1}{A_2 - A_1} \; g/m^2 \; day^{-2}$$

where W_1 and W_2 refer to dry weights of plant parts. A_1 and A_2 are leaf areas from unit field area of two consecutive samples at time t_1 and t_2 in days respectively.

vi. Harvest Index (HI)

The harvest index of each plot was obtained from the means of seed weight and total dry weight of plants per m^2 at final harvest.

These parameters were used to study the growth pattern of the genotypes.

RESULTS

The observations made on the 50 genotypes of horse gram during the experiment and the results obtained are presented below. The characters studied and the corresponding symbols are listed.

Characters	Symbols
1. Plant height	x_1
2. Number of primary branches	x_2
3. Days to 50% flowering	x_3
4. Number of pods per plant	x_4
5. Length of pods	x_5
6. Number of seeds per pod	x_6
7. 100 seed weight	x_7
8. Days to maturity	x_8
9. Seed yield per plant	y

4.1 Estimation of variability, heritability and genetic advance

The mean values of the nine characters studied for the fifty varieties of horse gram are presented in Table 2 and the analysis of variance is presented in Table 3. Significant difference was observed for all the nine characters, between all the fifty genotypes.

Table 2. Mean value of the nine characters

Genotypes	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	y
V_1	41.39	2.82	44.0	17.08	6.51	6.21	3.96	85.50	9.31
V_2	39.88	3.68	43.50	22.26	6.62	6.20	3.83	85.0	10.04
V_3	48.87	6.16	43.50	34.10	5.74	5.55	3.71	89.0	9.92
V_4	49.42	8.82	42.5	35.00	5.74	5.65	3.53	86.0	11.93
V_5	36.48	3.74	41.0	21.62	5.90	6.25	3.04	89.0	9.03
V_6	35.95	7.31	54.0	20.84	6.08	6.15	4.10	115.0	11.32
V_7	37.13	5.34	39.50	26.54	6.14	6.15	3.46	78.0	10.20
V_8	33.90	4.74	40.0	25.11	5.79	5.91	4.89	89.5	12.13
V_9	37.75	4.46	46.0	30.34	6.35	6.05	4.11	95.5	10.04
V_{10}	43.13	6.46	39.5	31.14	5.92	5.90	4.00	89.5	6.38
V_{11}	51.06	4.10	39.50	28.16	6.07	6.51	3.89	86.5	9.85
V_{12}	55.09	4.14	44.50	24.82	6.49	6.20	3.89	90.50	8.36
V_{13}	39.76	4.38	49.0	24.40	6.35	5.70	4.05	103.0	6.61
V_{14}	52.64	2.90	44.0	22.10	6.00	5.83	3.14	92.0	18.28
V_{15}	52.93	5.24	41.5	37.30	6.65	6.35	3.48	89.50	9.66
V_{16}	52.77	5.56	51.1	31.14	6.29	6.60	3.21	109.0	9.69

V_{17}	40.56	5.54	42.5	33.48	6.73	6.85	3.71	96.5	10.87
V_{18}	45.15	5.38	39.0	34.70	6.36	6.30	3.70	86.0	10.30
V_{19}	46.78	6.36	41.0	42.40	6.13	6.15	4.12	91.0	12.06
V_{20}	51.01	5.80	41.5	32.84	6.17	6.20	4.18	92.5	10.27
V_{21}	45.25	5.86	40.5	52.96	6.25	6.61	3.46	89.5	12.78
V_{22}	46.64	5.86	40.5	30.86	6.33	6.67	3.76	71.0	8.14
V_{23}	49.51	5.18	55.0	31.32	6.07	6.07	5.27	104.5	6.30
V_{24}	52.37	5.62	51.5	38.88	5.72	6.28	3.32	116.0	7.48
V_{25}	38.53	4.90	39.5	25.72	5.97	6.51	3.50	74.5	10.53
V_{26}	53.03	5.46	45.5	34.24	6.89	6.45	3.40	95.5	10.55
V_{27}	57.20	6.44	44.5	37.20	6.52	6.63	2.93	89.0	6.55
V_{28}	45.23	6.48	39.5	36.64	6.71	6.59	3.80	83.5	7.06
V_{29}	45.76	5.82	47.5	33.74	6.79	6.59	3.53	101.5	8.78
V_{30}	49.12	6.32	45.0	34.62	5.30	5.69	4.10	96.5	13.49
V_{31}	46.88	4.47	39.0	28.46	5.84	6.43	3.45	80.5	6.17
V_{32}	30.25	4.28	66.5	27.46	6.61	6.40	3.45	104.0	13.55
V_{33}	30.75	3.90	64.0	24.62	6.20	6.37	3.65	115.0	6.49

V_{34}	52.40	9.97	55.5	28.12	6.38	6.44	3.27	98.0	11.92
V_{35}	35.61	4.48	39.5	21.92	5.99	6.13	3.80	84.5	8.10
V_{36}	53.39	5.74	40.0	28.96	5.80	5.81	3.80	90.5	10.12
V_{37}	54.72	7.62	63.5	55.74	6.23	6.06	2.97	118.5	12.67
V_{38}	55.28	5.24	39.50	36.14	6.16	6.32	3.72	75.0	16.23
V_{39}	47.14	5.18	39.50	31.82	5.30	5.86	3.49	75.5	15.86
V_{40}	34.09	7.86	38.50	23.80	5.47	5.79	3.79	72.5	11.88
V_{41}	42.82	4.72	41.0	38.52	5.49	6.00	3.89	85.00	12.06
V_{42}	35.69	6.50	44.50	41.66	5.87	5.84	3.61	89.00	7.83
V_{43}	35.31	10.40	41.50	45.0	5.60	5.91	3.71	75.5	11.72
V_{44}	43.13	6.98	39.0	43.56	5.84	6.22	3.73	90.5	10.41
V_{45}	51.53	6.36	44.50	33.10	6.27	6.29	4.15	90.00	14.31
V_{46}	40.39	5.09	45.00	26.80	5.82	5.74	3.94	88.5	11.49
V_{47}	42.63	5.00	38.00	28.30	6.21	6.36	3.60	76.5	9.90
V_{48}	47.74	6.32	39.0	28.98	6.39	6.48	3.88	73.00	10.67
V_{49}	48.39	3.63	44.50	29.62	6.43	6.50	3.92	95.5	8.15
V_{50}	50.03	6.58	41.50	42.84	6.45	7.01	3.74	88.5	10.17

Table 3. ANOVA for yield and its components in horse gram

Source of variation	df	Mean square								
		x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	y
Block	1	1.9688	0.5884	40.9688	87.8516	0.1841	0.5955	0.00012	44.8750	0.1904
Treatment	49	102.6444**	3.5409**	99.8980**	107.9955**	0.7815**	0.1843**	0.7012**	270.0057**	13.8572**
Error	49	6.4853	0.5929	1.2047	13.6650	0.0059	0.0605	0.0036	1.4617	4.5428

** Indicates 'F' values significant at 1% level.

Table 4. Components of variance, PCV, GCV, ECV, heritability and genetic advance for yield and other characters in horse gram

riables	Variance			Co-efficient of variation			Herita-bility h^2 %	Genetic advance (at 5% intensity of selection)
	Geno-typic (V_g)	Environ-mental (V_e)	Pheno-typic (V_p)	Geno-typic (gcv)	Environ-mental (ecv)	Pheno-typic (pcv)		
Plant height	48.0796	6.4853	54.5649	15.3153	5.6248	16.3153	88.1145	
Number of primary branches	1.4741	0.5926	2.0667	22.2428	14.0991	26.3312	71.3309	
Days to 50% flowering	49.3466	1.2047	50.5513	15.8571	2.4802	18.3302	97.6214	
Number of pods per plant	47.1647	13.6650	60.8298	21.8594	11.7665	24.7183	77.5343	
Length of pods	0.3578	0.0059	0.3637	4.8934	3.8721	9.8654	97.7832	
Number of seeds per pod	0.0619	0.0605	0.1224	3.2871	4.5637	7.8593	52.4734	
100 seed weight	0.3488	0.0036	0.3524	15.9036	1.6356	15.9837	98.9824	
Days to maturity	134.5478	1.4617	136.0096	12.8326	1.3376	12.9022	98.9253	
Yield	4.6572	4.5428	9.2000	21.0345	20.7746	29.5641	50.6218	

Table 5. Estimates of genotypic variances and covariances for different characters in horse gram (components of variances in paranthesis)

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	y
x_1	(48.0796)	1.8595	-0.1805	13.2191	2.2769	0.4157	-0.5866	13.0230	1.7818
x_2	..	(1.4741)	-0.3883	2.6102	-0.0779	0.0110	-0.0533	-0.2635	1.3706
x_3	..	..	(49.3466)	0.8463	0.6113	0.1435	-1.8528	66.4920	0.1610
x_4	..	..	..	(47.1647)	-0.2716	0.2511	-0.3656	10.5501	5.6482
x_5	..	..	..	..	(0.3578)	0.2708	0.0806	0.4151	0.4075
x_6	..	..	..	..	..	(0.0619)	-0.0246	0.2427	0.2913
x_7	..	..	..	..	..	..	(0.3488)	0.4133	-0.1706
x_8	..	..	..	..	..	..	..	(134.5478)	-4.5494
Y	..	..	..	..	..	..	..	..	(4.6572)

Table 6. Estimates of environmental (error) variances and covariances for different characters in horse gram (components of variances in paranthesis)

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	y
x_1	(6.4853)	-0.1591	-0.5737	2.5175	0.0518	-0.0494	-0.1675	0.1677	0.1653
x_2	..	(0.5926)	0.0696	0.6417	-0.0027	-0.0159	0.0385	0.0858	-0.3783
x_3	..	..	(1.2047)	0.2659	0.0079	-0.1063	0.3380	-0.2124	-0.1449
x_4	..	..	..	(13.6650)	0.0943	0.1551	0.1137	0.2997	0.6048
x_5	..	..	..	..	(0.0059)	0.4434	0.0053	-0.0340	0.0034
x_6	..	..	..	..	..	(0.0805)	0.0066	0.0249	0.1378
x_7	..	..	..	..	..	..	(0.0488)	0.1191	0.3358
x_8	..	..	..	..	..	..	..	(1.4617)	-0.2127
Y	..	..	..	..	..	..	..	..	(4.5428)

Table 7. Estimates of phenotypic variances and covariances for different characters in horse gram (components of variances in paranthesis)

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	y
x_1	(54.5649)	1.7004	-0.7541	15.7366	2.3287	0.3663	0.7542	13.1907	1.9471
x_2	..	(2.0667)	-0.3187	3.2519	-0.0806	-0.	)	-0.1777	0.9923
x_3	..	..	(50.5513)	1.1122	0.6192	0.0372	-1.5148	66.2796	0.0161
x_4	..	..	..	(60.8298)	-0.1773	0.4162	-0.2519	10.8497	6.2536
x_5	..	..	..	..	(0.3637)	0.7142	-0.0859	0.3811	0.4109
x_6	..	..	..	..	..	(0.1224)	0.0182	0.2676	0.4291
x_7	..	..	..	..	..	..	(0.6976)	0.5324	-0.1652
x_8	..	..	..	..	..	..	..	(136.0096)	-4.7617
Y	..	..	..	..	..	..	..	..	(9.2000)

The variance due to genotype (V_g), environment (V_e) and phenotype (V_p), co-efficient of variation due to genotype (gcv), due to environment (ecv) and due to phenotype (pcv), heritability in the broad sense (h^2) and genetic advance (GA) for the nine characters were computed. The results are presented in the Table 4 to Table 7.

4.1.1 Plant height

Plant height ranged from 37.2 cm in V_{27} to 50.25 cm in V_{32} with a general mean of 45.28. The character showed a genotypic variance of 48.0796and a phenotypic variance of 54.5649 The gcv was 15.3153per cent with a high heritability of 88.1145 per cent and a genetic advance of 29.6174per cent.

4.1.2 Number of primary branches

V_{43} had the maximum number of primary branches (10.40) and V_1 the minimum (2.82), The mean value was 5.46 This character had a genotypic variance of1.4741 which was low and a phenotypic variance of 2.0667. The genotypic and phenotypic coefficients of variation were22.2428 and 26.3312 per cent respectively. Heritability for this character was 71.3309per cent, with a genetic advance of 38.6960per cent.

4.1.3 Days to 50% flowering

Days to 50% flowering was the highest for V_{32} (66.50) and the lowest for V_{47} (38.0). The mean of the character was 44.30 days. This character had a very high heritability of 97.6214 with Vg and Vp being 49.3466 and 50.5513 respectively. The environmental variance was very small. Genetic advance was 32.2714. GCV and PCV values were 15.8571 and 18.3302 per cent respectively.

4.1.4 Number of pods per plant

The maximum number of pods was for V_{37} (55.74) and the minimum was for V_1 (17.08) with a mean value of 31.42. A heritability of 77.5343 was exhibited with a genetic advance of 39.4803 per cent. V_g and V_p values were 47.1647 and 60.8297 per cent. The environmental component of variance was greatest in this case 13.6650. GCV amounted to 21.8594 per cent and PCV to 24.7183 respectively.

4.1.5 Length of pods

Length of pods ranged from 5.47 (V_{40}) to 6.17 (V_{20}) with a mean pod length of 6.12 cm. A genotypic variance of 0.3578 and phenotypic variance of 0.3637 accounted for a heritability of 97.7832. Genetic advance was 50.0236 per cent. GCV and PCV values were 4.8934 and 9.8654 per cent respectively. This showed the highest genetic advance.

4.1.6 Number of seeds per pod

V_3 had the lowest number of seeds per pod (5.55) and V_{50}, the highest number (7.01). The mean value was 6.22. This character showed a moderate heritability of 52.4734 per cent, Vg being 0.0619 and V_p being 0.1224. The genetic advance that could be obtained by selection was 6.0813. The environmental component was comparatively more in this case. This showed the lowest genetic advance.

4.1.7 100 seed weight

This character was lowest for V_{27} (2.93) and highest for V_{20} (4.18) the mean value was 3.71. This character showed the highest heritability of 98.9824 (Vg - 0.3488, Vp 0.3524), with lowest environmental influence (0.0369). The GCV and PCV values were 15.9036 and 15.9837 per cent respectively and genetic advance was 32.59 per cent.

4.1.8 Days to maturity

The genotype V_{37} had the longest duration (118.0 days) and V_{22} had the shortest duration (71.0 days). The mean duration was 90.39 days. In this case also, heritability was very high (98.9253 (Vg = 134.5478 Vp = 136.0096). Genetic advance was low (26.2047).

4.1.9 Yield per plant

Maximum yield was for V_{14} (18.28g per plant) and minimum was for V_{21} (6.17 per plant) with a mean yield of 10.26. The heritability was lowest in this case, the value being 50.6218 per cent (Vg = 4.6572 Vp = 9.2000). Genetic advance was 30.8296 per cent. GCV and PCV values were 21.0345 and 29.5641 respectively.

4.2 Correlation studies

The association between yield and other characters and inter correlations among the characters were also studied. The correlation coefficients (genotypic, environmental and phenotypic) were worked out. These are given in Tables 8 to 10 and Fig. 2.

The genotypic and phenotypic correlation coefficients followed the same kind of association, with the genotypic values slightly higher.

Number of primary branches, number of pods per plant, length of pods and number of seeds per pod showed significant positive correlation with yield, with the number of seeds per pod having the maximum correlation (0.5327) and number of pods per plant following closely behind (0.5231). The components plant height, days to 50% flowering and days

Table 8. Genotypic correlation among yield and eight components in horse gram.

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	y
x_1	..	0.2209	-0.0037	-0.0775	0.5497**	0.2409	-0.1432	0.1619	0.1191
x_2	..	..	-0.0455	0.3989*	-0.2141	0.0361	-0.0743	-0.0187	0.5031**
x_3	..	..	..	0.0175	0.1457	0.0342	-0.5466**	0.8160**	0.1060
x_4	..	..	..	..	-0.0662	0.1505	-0.0753	0.1324	0.5231**
x_5	..	..	..	..	..	0.5078**	0.2285	0.0599	0.5111**
x_6	..	..	..	..	..	..	-0.1644	0.0826	0.5327**
x_7	..	..	..	..	..	..	..	0.6030**	-0.2736
x_8	..	..	..	..	..	..	..	..	0.1817
Y	..	..	..	..	..	..	..	..	..

* Significant at 5% level
** Significant at 1% level

Table 9. Environmental correlation among yield and eight components in horsegram

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	y
x_1	..	-0.0812	-0.2502	0.2674	0.0860	-0.0684	-0.3424	-0.0553	0.0305
x_2	..	..	0.0884	0.2255	-0.0148	-0.0728	-0.2604	0.0922	0.2306
x_3	..	..	..	0.0655	0.0304	0.3413*	0.5393**	0.1601	-0.0619
x_4	..	..	..	..	0.1079	0.1439	0.1601	0.0671	0.0768
x_5	..	..	..	..	..	0.2401	0.1167	-0.1189	0.0067
x_6	..	..	..	..	..	..	0.1211	0.0726	0.2286
x_7	..	..	..	..	..	..	..	0.0129	0.2668
x_8	..	..	..	..	..	..	..	..	0.0825
Y	..	..	..	..	..	..	..	..	..

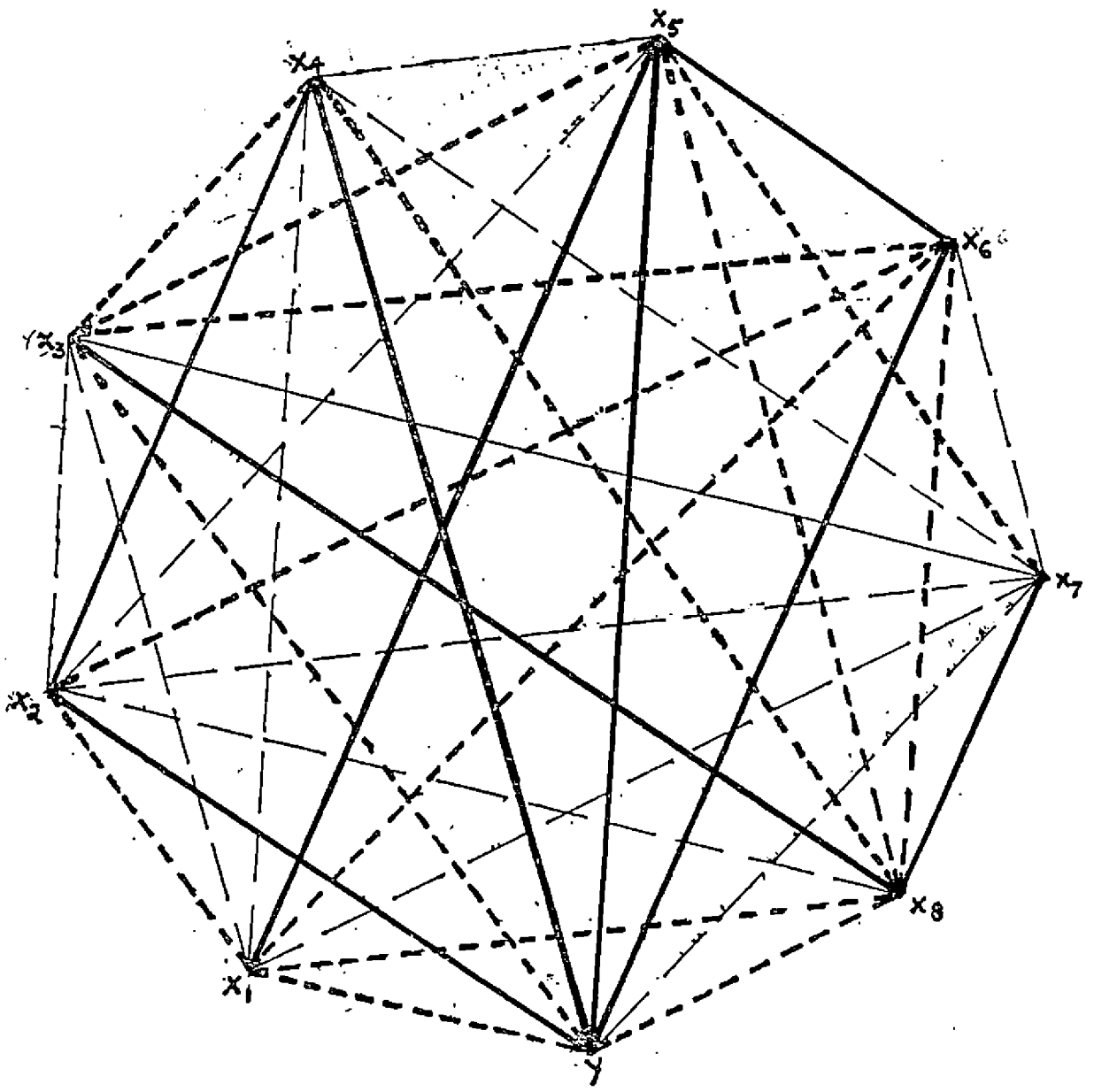
* Significant at 5% level
** Significant at 1% level

Table 10. Phenotypic correlation among yield and eight components in horsegram

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	y
x_1	..	0.1601	-0.0144	-0.0312	0.1180	0.1314	-0.1720	0.1501	0.0869
x_2	..	..	-0.1370	0.2860	-0.0471	-0.0516	-0.1076	-0.0116	0.4761**
x_3	..	..	..	0.0201	0.1442	0.0139	0.2661	0.8000**	0.1965
x_4	..	..	..	..	-0.1077	0.1414	-0.1056	0.1193	0.3870*
x_5	..	..	..	..	..	0.3803*	-0.0144	0.0855	0.4195**
x_6	..	..	..	..	..	..	-0.0787	0.0376	0.4996**
x_7	..	..	..	..	..	..	..	0.0423	-0.1933
x_8	..	..	..	..	..	..	..	..	-0.1345
Y	..	..	..	..	..	..	..	..	..

** Significant at 1% level

Fig. 2. CORRELATION DIAGRAM OF YIELD AND EIGHT YIELD COMPONENTS IN HORSE GRAM



to maturity showed positive non significant correlation with yield. 100-seed weight exhibited a non significant negative correlation with yield.

As far as the association among the various characters was concerned, a positive significant correlation was observed between plant height and length of pods; number of primary branches and number of pods per plant; days to 50 per cent flowering and days to maturity; length of pods and number of seeds per pod and 100-seed weight and days to maturity. The maximum value was for that between days to 50 per cent flowering and days to maturity (0.8160), followed by 100-seed weight and days to maturity (0.6030). A significant negative correlation was observed between days to 50% flowering and 100 seed weight (-0.5466).

All correlations between the rest of the characters were non significant.

4.3 Genetic divergence among the fifty genotypes

The fifty genotypes were subjected to divergence analysis using Mahalanobis D^2 technique. The entire plants could be grouped into eleven clusters. Non-hierarchial Euclidean cluster analysis was carried out using the Statistical Programme for Agricultural Research (SPAR) of IASRI, New Delhi.

Accordingly, the entire plants could be grouped into eleven clusters. The genotypes included in each cluster, the cluster mean value for each character and the range of characters in different clusters are given in Tables 11, 12 and 13 respectively.

4.3.1 Height of the plant

In cluster I, the maximum mean value of 46.88 was shown by V_{31} and the minimum of 37.13 by V_7. The mean value of this cluster was found to be 40.01 with a range of 9.75. In cluster II only a single member could be included, ie., V_{14} and its mean value was 52.64.

Cluster III showed a range of 19.30 with V_{40} and V_{36} showing the minimum and maximum values of 34.09 and 53.39 respectively. The mean value was 46.58, with a range of 19.30 which was relatively higher. In cluster IV, the range observed was 10.12, with minimum and maximum values of 45.16 (V_{18}) and 55.28 (V_{38}) respectively and a mean value of 50.58.

In cluster V, V_5 showed a minimum mean value of 36.48 and V_1, a maximum value of 41.39, with a range of 4.91. The mean value for the cluster was 39.05. Cluster VI had a single member, V_{23}, with a mean plant height of 49.51.

Table 11. Genotypes included in each different clusters

Cluster	Genotypes included
I	V_7, V_{22}, V_{25}, V_{31}, V_{47}
II	V_{14}
III	V_3, V_4, V_{36}, V_{39}, V_{40}
IV	V_{11}, V_{12}, V_{18}, V_{20}, V_{21}, V_{35}, V_{38}, V_{48}, V_{49}
V	V_1, V_2, V_5, V_9, V_{13}
VI	V_{23}
VII	V_{32}, V_{33}
VIII	V_{16}, V_{24}, V_{34}, V_{37}
IX	V_6, V_8, V_{30}, V_{45}, V_{46}
X	V_5, V_{17}, V_{26}, V_{27}, V_{28}, V_{29}, V_{50}
XI	V_{10}, V_{19}, V_{41}, V_{42}, V_{43}, V_{44}

Table 12. Cluster-mean value for each character in different clusters

Clusters	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	y
I	40.01	4.95	39.30	27.98	6.10	6.42	3.55	75.20	8.95
II	52.64	2.90	44.00	22.10	6.00	5.83	3.14	92.00	18.28
III	46.58	6.74	40.80	30.76	5.61	5.73	3.42	82.40	11.94
IV	50.58	5.12	40.83	29.31	6.25	6.36	3.81	85.50	10.49
V	39.05	3.82	44.70	23.14	6.64	6.05	3.63	91.60	9.00
VI	49.51	5.18	55.0	31.32	6.07	6.07	5.27	104.50	6.30
VII	30.49	4.09	65.25	26.05	6.39	6.39	3.55	109.38	10.02
VIII	52.96	6.67	56.88	38.42	6.11	6.34	3.18	110.50	10.54
IX	42.11	6.06	45.70	28.18	5.93	6.00	4.23	95.90	12.47
X	49.94	5.94	43.21	36.48	6.55	6.64	3.51	91.93	9.08
XI	40.87	5.76	39.25	40.38	5.80	6.00	3.84	86.75	9.41

Table 13. Range of character value in different clusters

Clusters	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	y
I	9.75	0.87	2.50	5.14	0.49	0.52	0.14	9.50	4.03
II	..	..	..	..	..	..	..	..	..
III	19.30	2.62	5.00	11.12	0.50	0.31	0.68	18.00	5.94
IV	10.12	2.23	5.50	14.22	0.50	0.48	0.48	22.50	8.13
V	4.91	1.57	8.00	13.26	0.72	0.50	0.79	18.00	3.43
VI	..	..	..	..	..	..	..	..	..
VII	0.50	0.38	2.50	2.83	0.41	0.03	0.20	11.00	7.06
VIII	1.95	4.35	12.00	27.62	0.66	0.54	0.30	20.50	5.21
IX	15.22	2.22	14.00	13.78	0.58	0.55	0.95	26.50	2.99
X	11.98	1.34	8.00	9.36	0.62	0.81	1.26	18.00	4.32
XI	11.47	1.78	7.00	13.86	0.33	0.38	0.51	15.50	5.68

The mean plant height in cluster VII was 30.49, with the minimum and maximum values shown by V_{32} and V_{33}, the only members. The range was the least in this case, ie. 0.50. In cluster VIII, V_{24} showed the minimum plant height (52.37 cm) and V_{37}, the maximum plant height (54.32 cm) with a range of 1.95 and mean value of 52.96. This cluster showed the highest mean value.

V_8 and V_{30} were the genotypes with the minimum (33.90 cm) and maximum (49.12 cm) mean height in cluster IX. The range was 15.22 with a mean value of 42.11 cm. In cluster X, the mean plant height exhibited by the members was 49.94. This cluster, with a minimum plant height of 45.22 (V_{28}) and maximum plant height of 57.20 (V_{27}) showed a range of 11.98. In cluster XI the plant height varied from a minimum of 35.31 (V_{43}) to a maximum of 46.78 (V_{19}), the range being 11.47. The mean value came to 40.87.

For the character plant height, cluster VII showed the lowest mean value of 30.49 and cluster VIII showed the highest mean value of 52.96. Regarding the range it was the widest in cluster III and the narrowest in cluster VII.

4.3.2 Number of primary branches

In cluster I the least number of primary branches was present in V_{31} (4.47) and the highest number in V_7 (5.34).

The mean value for the entire cluster was 4.95 with a range of 0.87. In cluster II, V_{14} was the sole member and hence the minimum value, maximum value and mean coincided at the 2.90. This was also the least mean value among all the clusters.

V_{39} and V_{40} showed the minimum (5.18) and maximum (7.80) number of primary branches respectively among the members of cluster III. The mean value came to 6.74 which was the highest among all the clusters and the range was 2.62. The members of cluster IV had primary branch number ranging from 3.63 (V_{49}) to 5.86 (V_{21}) with 2.23 as the range and 5.12 as the cluster mean.

The mean number of primary branches in cluster V was 3.82 with V_1 showing the minimum value of 2.89 and V_9 the maximum value of 4.46. The range was 1.57. V_{23} was the only member of the cluster VI, with a mean of 5.18. Cluster VII showed the least range of 0.38 for primary branch number, with the two members V_{32} and V_{33} showing value of 4.28 and 3.90 respectively. The mean value for the cluster was 4.09.

In cluster VIII; V_{24} had the lowest number of primary branches (5.62) and V_{34} had the highest number (9.97) the range being 4.35. This cluster showed the widest range for

this particular character. The main value was 6.67. The genotypes in cluster IX showed a range of 2.22, with V_{46} having the least number of primary branches (5.09) and V_6, the highest number (7.31) at harvest. The cluster had a mean value of 6.06.

In cluster X, V_{15} with a mean of 5.24 primary branches and V_{50} with a mean value of 6.58 primary branches at harvest, showed the minimum and maximum values respectively, with a range of 1.34. The cluster mean was shown to be 5.94 branches per plant. Cluster XI had a mean value of 5.76 and a range of 1.78. The minimum value was exhibited by V_{41} (4.72) and the maximum value by V_{42} (6.50).

The lowest mean value for this character was recorded for cluster II (2.90) and the highest value was shown by cluster VIII (6.67). Range was also the widest in cluster VIII (4.35) and the narrowest in cluster VII (0.38).

4.3.3 Days to 50 per cent flowering

Cluster I was one of the two clusters which showed a least range of 2.5, for days to 50 per cent flowering. The genotype V_{47} took the minimum number of days (38.0) to attain 50 per cent flowering, while, it was maximum in V_{22} (40.50). The mean value was 39.30. In cluster II, the sole

member V_{14} took 44.00 days to attain 50 per cent flowering. In cluster III, the minimum value was 38.5 (V_{40}) and the maximum value was 43.5 (V_{43}), with a range of 5.0 and mean value of 40.80.

Cluster IV had a mean value of 40.83 and a range of 5.5. The maximum value was 44.5 (V_{12} and V_{49}) and the minimum value was 39.0 (V_{18} and V_{48}). In cluster V_{13} required the maximum number of days (49.0) to attain 50% flowering, while V_5 took only 41.0 days. The range was 8.0 with a mean value of 44.7.

Cluster VI, with V_{23} as its only member, showed a mean value of 55.0. Cluster VII had the highest mean value for number of days to 50% flowering among all the clusters, ie., 65.25 days. The extreme values exhibited were 64.0 days (V_{33}) and 66.5 days (V_{32}).

In cluster VIII, the minimum and maximum values were exhibited by V_{24} (51.5 days) and V_{37} (63.5 days) respectively. The range was 12.0 and mean value was 56.88. Cluster IX showed the widest range of 14.0 with a minimum value of 40.0 (V_8) and a maximum value of 54.0 (V_6). The mean value of the cluster was 45.70.

Cluster X had a mean value of 43.21 and a range of 8.0, with the minimum and maximum values of 39.5 (V_{28}) and 47.5

(V_{29}) respectively. In cluster XI, the maximum value was exhibited by V_{43} (41.5) and the minimum value by V_{42} (34.5) the range being 7.0. The mean value for the cluster was 39.25, this being the lowest among all the clusters.

On an average the members of cluster XI took the shortest period to reach 50% flowering (39.25 days) and those of cluster VII, the longest period (65.25 days). The range was widest for cluster IX (14.0) and narrowest for cluster I (2.5).

4.3.4 Number of pods per plant

Cluster I had a mean value of 27.98 pods per plant with V_{25} having the minimum pods per plant (25.72) and V_{22} the maximum number (30.86). The range was 5.14. In cluster II the single member V_{14} had a mean number of pods of 22.10. This was the lowest value among all the clusters.

Cluster III showed a mean value of 30.76 for pod number per plant. The minimum number was in V_{40} (23.88 pods per plant) and the maximum was in V_4 (35.00 pods per plant) with a range of 11.12. V_{35} and V_{38} showed the minimum (21.92) and maximum (36.14) values respectively for number of pods per plant, in cluster IV. The mean value for the cluster was 29.31 and it showed a range of 14.22.

Cluster V showed a range of 13.26 for number of pods per plant with a maximum value of 30.34 (V_9) and a minimum value of 17.08 (V_1). The mean value was 23.14. Cluster VI, with its single member V_{23}, had a mean of 31.32 pods per plant. The lowest value for range, was exhibited by cluster VII (2.83), with the two members V_{32} and V_{33} showing the mean values 27.46 and 24.63 respectively. The mean value for the cluster was 26.05.

In cluster VIII, the genotype V_{34} showed the lowest number of pods per plant (28.12) and V_{37} the highest (55.74). The range 27.62, was the maximum among all the clusters and the mean value of the cluster was 38.42. Cluster IX exhibited a mean pod number of 28.18 pods per plant. The range was 13.78 with V_6 showing the minimum value (20.84) and V_{30}, maximum value (34.62).

V_{17} and V_{50} of cluster X showed the lowest and highest number of pods per plant respectively, the values being 33.48 and 42.84 in that order. This gave a range of 9.36 and a cluster mean of 36.48. Cluster XI exhibited the highest mean value of 40.38 for number of pods per plant, with a range of 13.86. The lowest and highest values were 31.14, for V_{16} and 45.00 for V_{43} respectively.

The mean value was lowest for cluster II (22.10) and highest for cluster XI (40.38). Cluster VIII had maximum range (23.62) and cluster VII had the minimum range (2.83).

4.3.5 Length of pods

Length of pods showed a range of 0.49 in cluster I with a minimum of 5.84 for V_{31} and a maximum of 6.33 for V_{22}. The cluster had a mean value of 6.10. V_{14}, the sole member of cluster II showed a mean length of 6.00 cm for pods. In cluster III V_{30} had the shortest pods of 5.30 cm length and V_{36} the largest with 5.80 cm. The range was 0.50 and this cluster had the lowest mean value for this character.

Cluster IV showed a minimum pod length of 5.99 for V_{35} and a maximum length of 6.49 for V_{12}. The range was 0.5 and mean value was 6.25. Cluster V had a low range of 0.72, with V_5 showing the minimum pod length (5.90) and V_2 the maximum length (6.62). The mean value was 6.64.

Cluster VI had a mean pod length of 6.07 cm for the single member V_{23}. The two members of cluster VII, V_{32} and V_{33} had pod length means of 6.61 and 6.20 respectively with a mean of 6.39 and a range of 0.41.

In cluster VIII, the length of pods ranged from a minimum of 5.72 (V_{24}) to a maximum of 6.38 (V_{34}) with a range of 0.66. The mean value of cluster was 6.11. A mean

pod length of 5.93 was shown by the members of cluster IX, with the extreme values shown by V_{30} (5.69) and V_{45} (6.27). A range of 0.58 was exhibited.

The highest cluster mean for pod length was seen in cluster X (6.55 cm), the genotype V_{20} having the shortest pods (6.11 cm) and V_{29} having the longest pods (6.75 cm). The range was 0.62. The lowest range for pod length was exhibited by cluster XI with a value of 0.33 resulting from a minimum value of 5.80 and a maximum value of 6.13. The cluster mean was 5.80. Minimum mean length of pods was in cluster III (5.61) and maximum in cluster X (6.39). Range was highest for cluster V (0.70) and lowest for cluster XI (0.33).

4.3.6 Number of seeds per pod

The character, number of seeds per pod showed a range of 0.52 in cluster I, with the minimum number of seeds per pod in the genotype V_7 (6.15 seeds) and the maximum number in V_{22} (6.67). The cluster showed a mean value of 6.42 seeds per pod. V_{14} of cluster II had a mean of 5.83 seeds per pod. In cluster III, V_3 showed a minimum seeds per pod of 5.55 and V_{39}, the maximum number of 5.86, with a mean of 5.73. The cluster had a range of 0.31. The mean value was lowest for this cluster.

Cluster IV had a minimum value of 6.13 (V_{23}) and a maximum value of 6.61 (V_{21}). The range was 0.48 with a mean value of 6.36. The corresponding values in cluster V were 5.70 (V_{13}), 6.20 (V_2), 0.5 and 6.05.

Cluster VI with the single member V_{23} had a mean value of 6.07. In cluster VII the least value for range was seen which is 0.03. This results from a minimum of 6.37 for V_{33} and a maximum of 6.40 of V_{33}. Mean value was 6.39 for the cluster as a whole.

In cluster VIII, the lowest value for seed number per pod was exhibited by V_{37} (6.06) and the highest value by V_{16} (6.60), the range being 0.54. The cluster mean was 6.34. The cluster IX showed the corresponding values of 5.74 (V_{46}) 6.29 (V_{45}) 0.55 and 6.00.

Maximum cluster mean was shown by cluster X with 6.64 seeds per pod. The genotype values ranged from 6.20 (V_{20}) to 7.01 (V_{50}) with the range also being the maximum (0.81) among all clusters. For cluster XI, the minimum value, maximum value range and cluster mean were 5.84, 6.22, 0.38 and 6.00 respectively.

The minimum and maximum mean value for this character was exhibited by cluster II (5.83) and cluster X (6.64)

respectively. Maximum and minimum range was for cluster X (0.81) and cluster VII (0.03).

4.3.7 100 seed weight

In cluster I, the range of 100 seed weight was the least (0.14) with 3.45 being the minimum value (V_{31}) and 3.76, the maximum (V_{22}). The mean weight for the cluster was 3.55. V_{14} included in cluster II showed a cluster mean of 3.14.

In cluster III, V_{40} had the lowest seed weight of 3.03 and V_3 the highest 100 seed weight of 3.71. Thus the cluster exhibited a range of 0.68 and a mean value of 3.42. Cluster IV with a mean 100 seed weight of 3.81 had a range of 0.48 with the minimum value 3.70 for V_{18} and a maximum of 4.18 for V_{20}. The corresponding values in cluster V were 3.63, 0.79, 3.04 (V_5) and 3.85 (V_2). Cluster VI which included V_{23} alone had the maximum mean value among all the clusters ie., 5.27.

Cluster VII had a mean value of 3.55. The 100 seed weight of the two genotypes included were 3.45 for V_{32} and 3.65 for V_{33} the range being 0.20 The range shown was the least among the 11 clusters. A range of 0.30 was exhibited by the genotypes of cluster VIII, the minimum value being 2.97 (V_{37}) and maximum being 3.27 (V_{34}). The cluster had a

mean 100 seed weight of 3.18. The corresponding values for cluster IX were 0.95, 3.94 (V_{46}), 4.89 (V_8) and 4.23.

Cluster X had a mean value of 3.51 and a range of 1.26, range being the maximum among all the clusters. The genotype V_{27} shows minimum value (2.9) and V_{20} showed the maximum (4.18). In cluster XI, the mean value was 3.84 and range was 0.51. The minimum and maximum values were 3.61 (V_{42}) and 4.12 (V_{19}) respectively.

Cluster II showed the lowest mean number of seeds per pod (3.14) and cluster VI showed the highest number (5.27). For the range in this character the maximum and minimum values were exhibited by cluster IX (0.95) and cluster I (0.14).

4.3.8 Days to maturity

Cluster I showed a mean value of 75.20 which was the lowest among all clusters. The range was 9.50. V_{22} had the minimum duration of 71.0 days and V_{31}, the maximum duration of 80.50 days. Cluster II, with the only genotype V_{14}, had a mean duration of 92.00 days Cluster III showed a mean value of 82.40 with a range of 18.0 days. V_{40} had the minimum duration of 72.5 days within this cluster and V_{36} had the maximum value of 90.5 days.

In cluster IV, V_{48} took the minimum days for maturity (73.0 days) and V_{49} the maximum (95.5 days) with a range of 22.5. The mean of the cluster was 85.5. Cluster V had a mean value of 91.6 and a range of 18.0. The minimum and maximum values were 85.0 (V_2) and 103.0 (V_{13}). Cluster VI had a mean duration of 104.50 days.

In cluster VII, the range was 11.0 and the mean was 109.38, the mean being second highest among all the clusters. The minimum value was 104.0 (V_{32}) and the maximum was 115.0 (V_{33}). The corresponding values in cluster VIII were 20.5, 110.38, 98.0 (V_{34}) and 118.5 (V_{37}). This cluster had the highest mean duration.

Cluster IX had a mean duration of 95.90 and a range of 26.5, this being the widest range. V_{46} (88.5 days) and V_6 (115.0 days) showed the minimum and maximum duration within the cluster. Cluster X had corresponding values of 91.93, 18.0, 83.5 (V_{28}) and 101.5 (V_{29}) respectively.

Cluster XI had a range of 15.5 and a mean of 86.75 days. The maximum duration was exhibited by V_{19} (91.0 days) and minimum by V_{43} (75.5 days).

The extremities in mean duration were shown by members of cluster III (82.4) and cluster VIII (110.38). Range varied from 18.0 (cluster X) to 26.5 (cluster IX).

4.3.9 Yield per plant

Of all the genotypes in cluster I, V_3 had the minimum yield of 6.17 g per plant and V_{25} had the maximum, of 10.53 g per plant, the range being 4.03. The mean yield for the cluster was 8.95. Cluster II, with the genotype V_{14} alone had the highest mean yield of 18.28. In cluster III a mean yield of 11.94 was observed with a range of 5.94. The minimum value was for V_3 (9.92) and maximum was for V_{39} (15.86).

V_{35} and V_{38} had the minimum (8.10) and maximum (16.23) values for mean yield in cluster IV and the range was the highest (8.13). The cluster mean was 10.49. Cluster V had a mean value of 9.00 with a range of 3.43. The maximum and minimum values for yield were exhibited by V_2 (10.04) and V_{13} (6.61).

Cluster VI had a single member with the lowest cluster mean of 6.30. The two members of cluster VII had values of 13.55 for V_{32} and 6.49 for V_{33} with a mean yield of 10.02 and a range of 7.06.

Cluster VIII had a range of 5.21 and mean yield of 10.54. The minimum and maximum values are 7.48 (V_{24}) and 12.67 (V_{37}). Cluster IX showed corresponding values of 2.99, (which was the lowest among all clusters) 12.47, 11.32 (V_6) and 14.31 (V_{45}) respectively.

In cluster X, V_{27} showed the minimum mean yield of 6.55 and V_{17} showed a maximum yield of 10.87, the range being 4.32. Cluster mean was 9.08. The corresponding values exhibited by cluster XI were 6.38 (V_{10}) 12.06 (V_{19}) 5.68 and 9.41 respectively.

Mean yield was lowest for cluster VI (6.30) and highest for cluster II (18.27). Range was maximum in cluster IV (8.13) and minimum in cluster IX (2.99).

The average distance of the cluster members from clusters centroids are given in Table 14. The maximum distance was shown by cluster VIII (2.578) and minimum by cluster VII (1.578). Cluster II and VI had single members and hence the value is 0.000.

Table 14 gives the distance between cluster centroids. The least distance is between clusters III and XI (2.825) and the highest distance is between clusters II and VI (7.420).

The contribution of the various characters towards total divergence was also found out. 100 seed weight exhibited the maximum contribution towards the total divergence (16.35%) followed by yield (13.35%). The lowest contribution was by days to maturity (4.59%). The values are shown in Table 15.

Table 14. Average distance of cluster members from cluster centroids and distances between cluster centroids (Distance from centroids in parenthesis)

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	(1.830)	5.038	3.354	2.023	2.460	5.656	5.057	4.845	3.333	2.897	2.680
II	..	(0.000)	4.358	4.314	4.538	7.420	6.149	5.465	4.529	5.543	5.371
III	..	..	(2.001)	3.227	3.964	6.008	6.115	4.371	2.005	4.323	2.458
IV	..	..	..	(1.727)	2.470	4.700	5.001	3.874	2.603	2.015	2.739
V	..	..	..	..	(1.610)	4.591	3.715	4.820	2.787	3.534	3.316
VI	..	..	..	..	..	(0.000)	5.281	5.512	3.966	5.310	4.895
VII	..	..	..	..	..	..	(1.578)	4.501	4.431	4.948	5.432
VIII	..	..	..	..	..	..	..	(2.578)	4.072	3.199	4.275
IX	..	..	..	..	..	..	..	..	(2.009)	3.807	2.577
X	..	..	..	..	..	..	..	..	..	(1.608)	3.424
XI	..	..	..	..	..	..	..	..	..	..	(1.679)

Fig. 3. Cluster diagram of the genotypes studied

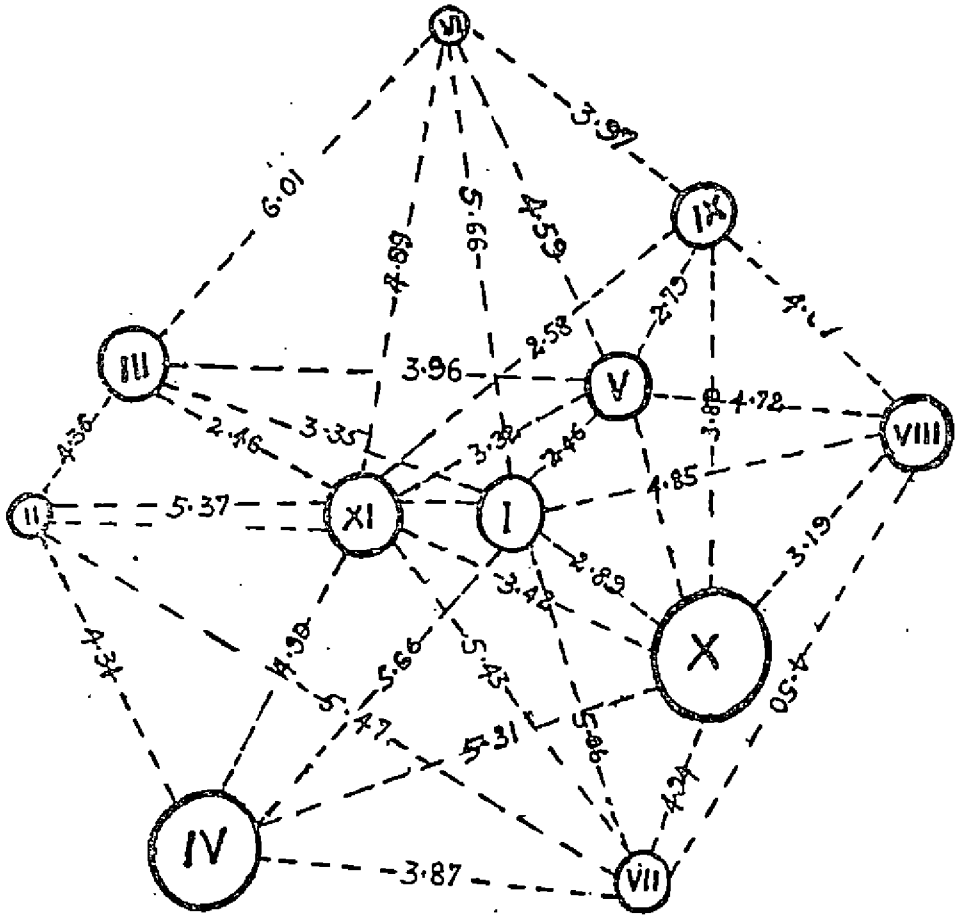


Table 15. Contribution of the characters towards total divergence in horse gram.

Characters	Percentage contribution towards total divergence
x_1	9.45
x_2	12.50
x_3	7.51
x_4	12.23
x_5	12.95
x_6	10.88
x_7	16.35
x_8	4.59
Y	13.35

4.4 Growth analysis

Growth analysis represents the estimates of photosynthesis in terms of dry matter accumulation and quantifies growth and yield components. The plants subjected to destructive sampling at ten days interval were dried and the dry matter accumulation was found out. From the data obtained, the various key growth indices were determined.

4.4.1 Total dry matter production (TDM)

The dry matter accumulation of the twelve representative genotypes of horse gram were studied and the results are indicated in Table 16. V_{34} showed the maximum TDM followed by V_{37} and V_{44}. The lowest value was shown by V_{22} (Fig. 4).

In all the genotypes TDM increased throughout the growth period till harvest. A slight decrease was noted at harvest. In almost all the genotypes, except V_{34} and V_{37}, the total dry matter production was only less than 10 per cent during pre-flowering period. In V_{34} it was 28.13 per cent and in V_{37} it was 22.66 per cent.

4.4.2 Crop growth rate (CGR)

It is the increase in unit area of the crop in unit time. The CGR at different intervals are given in Table 17.

Table 16. Total dry matter production per unit area at various growth slages (g)

Genotype	Days after sowing											
	10	20	30	40	50	60	70	80	90	100	110	120
V_6	0.48	3.06	11.80	27.55	74.25	123.55	227.80	356.25	351.03	379.75	375.75	370.10
V_{22}	0.62	3.72	13.25	32.65	127.80	188.70	245.75					
V_{31}	0.38	2.34	7.83	23.03	109.15	203.65	332.25	375.45				
V_{34}	0.47	2.75	10.83	23.75	135.90	236.38	355.00	445.75	479.5			
V_{35}	0.52	2.44	7.38	20.93	102.10	177.30	296.75	330.15				
V_{37}	0.56	3.66	8.25	22.65	100.98	156.65	345.75	417.20	419.85	454.25	445.50	442.10
V_{40}	0.60	1.85	9.55	25.70	135.68	177.85	255.70					
V_{42}	0.51	3.79	9.25	23.43	129.00	204.60	314.33	304.00				
V_{43}	0.59	3.79	12.28	26.75	188.50	283.13	319.35					
V_{44}	0.47	3.19	14.10	31.25	176.5	242.25	354.85	387.50	419.50			
V_{46}	0.57	2.90	9.00	27.35	108.65	155.48	229.05	292.00				
V_{49}	0.52	2.21	8.10	25.18	120.80	166.75	249.20	330.60	310.68			

Fig.4. Total dry matter production in different genotypes

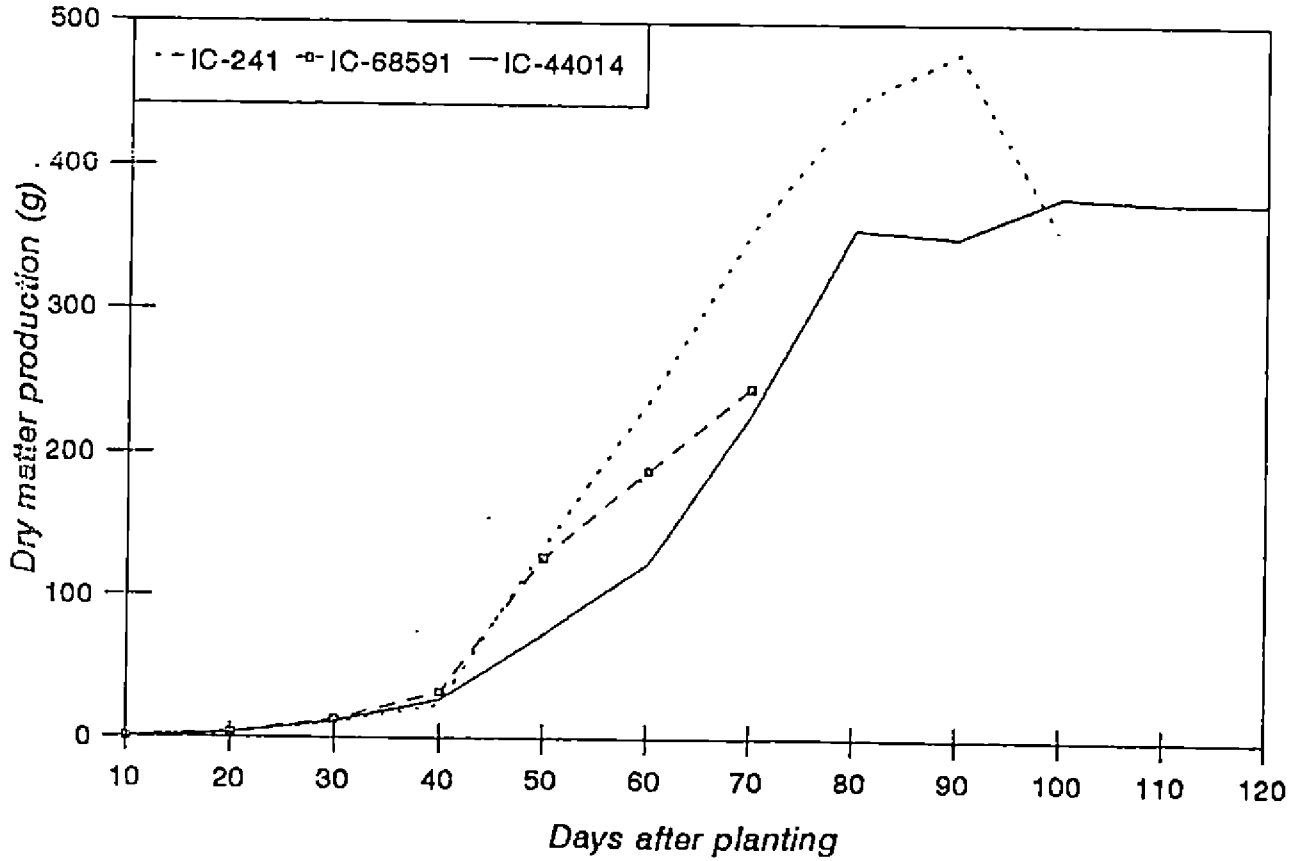
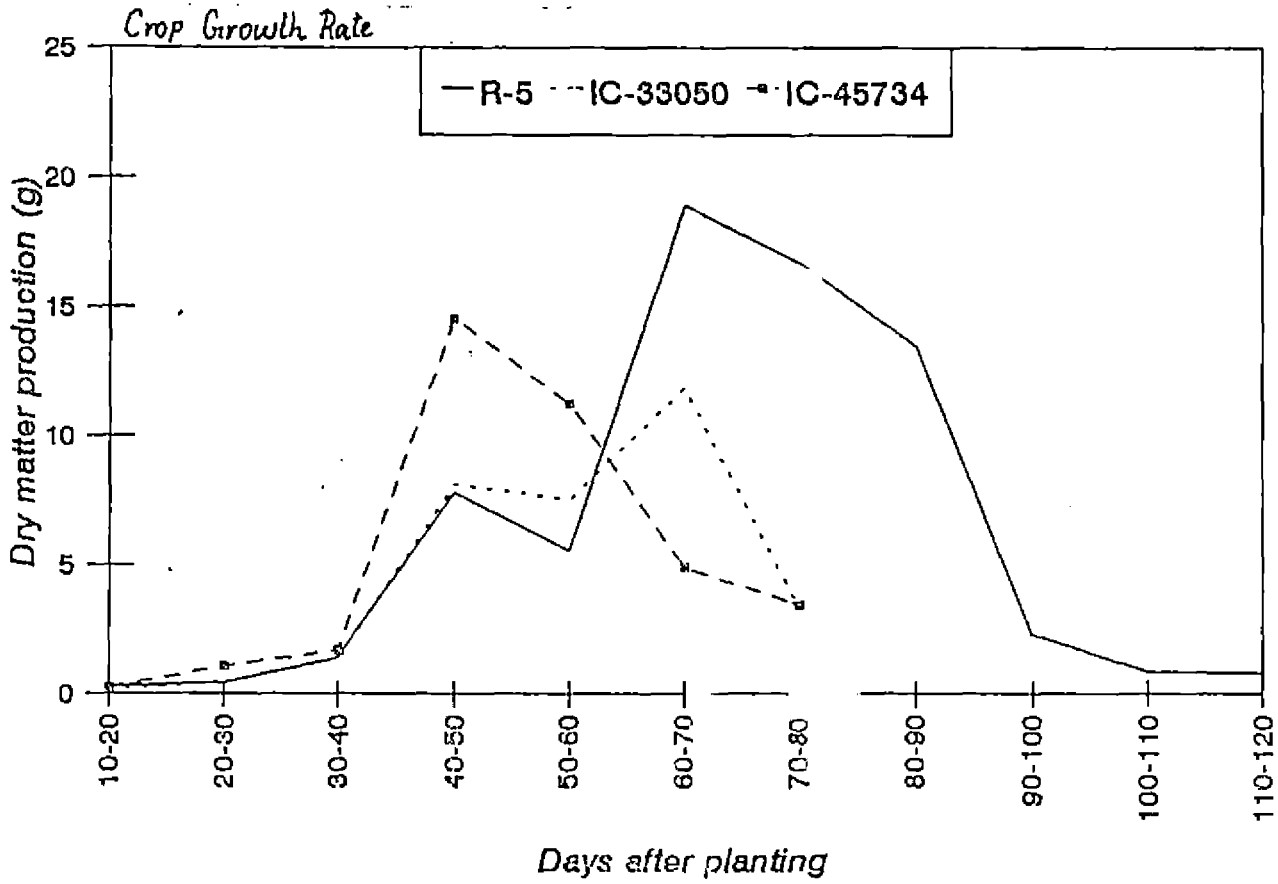


Table 17. Crop growth rate at various growth stages (g $day^{-1}m^{-2}$)

Genotype	Interval of sampling										
	10-20	20-30	30-40	40-50	50-60	60-70	70-80	80-90	90-100	100-110	110-120
V_6	0.26	0.87	1.58	4.67	6.93	10.43	12.84	12.52	2.87	0.41	0.41
V_{22}	0.31	0.95	1.94	9.52	6.09	5.71					
V_{31}	0.20	0.55	1.52	8.61	9.45	12.86	4.32				
V_{34}	0.23	0.81	1.24	11.25	10.09	11.82	9.75	3.18			
V_{35}	0.19	0.49	1.36	8.12	7.53	11.87	3.34				
V_{37}	0.31	0.46	1.44	7.83	5.57	18 91	16.75	13.44	12.35	7.875	2.812
V_{40}	0.13	0.77	4.62	11.00	77.90	4.25					
V_{42}	0.32	0.55	5.42	10.56	7.56	7.46	4.96				
V_{43}	0.32	2.85	7.45	16.18	9.43	7.62					
V_{44}	0.27	1.09	7.72	14.52	11.26	4.19	3.47				
V_{46}	0.23	0.61	1.84	8.13	4.68	7.36	6.39				
V_{49}	0.17	0.59	4.71	9.56	4.62	8.23	8.14	3.97			

Fig.5. Crop growth rate in different genotypes



The values increased steadily from sowing to 40-50 days after sowing (DAS) in short duration varieties and to 60-70 DAS in long duration varieties and then decreased gradually. A higher CGR was shown by V_{37} at 60-70 DAS (18.91) and lowest by V_{35} (8.12[illegible]) at 40-50 DAS (Fig. 5).

4.4.3 Net assimilation rate (NAR)

Net assimilation rate is the increase in plant weight per unit area of assimilatory surface, per unit time. The NAR values at 10 days interval are shown in the table 18.

Net assimilation rate values did not exhibit drastic difference in the early stages but beyond 50-60 DAS the varieties showed significant difference. The peak value at 40-50 DAS was highest for V_{40} (1.48) and lowest for V_{49} (0.12) (Fig. 6).

4.4.4 Relative growth rate (RGR)

It is an index of rate of increase in biomass per unit area over the existing biomass. During the initial stages there was not much difference in RGR among the varieties. RGR slightly decreased during the initial stages, then reached a peak at 40-50 DAS and again decreased (Table 19). The value was highest for V_{22} (0.13) and the lowest for V_{43} (0.06) at the peak period (Fig. 7).

Table 18. Net assimilatin rate at various growth stages (g $m^{-2}day^{-1}$)

Genotype	Interval of sampling										
	10-20	20-30	30-40	40-50	50-60	60-70	70-80	80-90	90-100	100-110	110-120
V_6	0.18	0.14	0.16	0.20	0.11	0.20	0.19	0.02	0.01	0.01	0.01
V_{22}	0.21	0.16	0.14	0.31	0.25	0.13					
V_{31}	0.18	0.18	0.18	0.29	0.22	0.18	0.08				
V_{34}	0.16	0.10	0.07	0.33	0.17	0.14	0.01				
V_{35}	0.14	0.08	0.08	0.23	0.18	0.25	0.08				
V_{37}	0.20	0.06	0.10	0.12	0.23	0.33	0.09	0.12	0.01	0.01	0.01
V_{40}	0.18	0.12	0.84	1.48	0.72	0.09					
V_{42}	0.10	0.09	0.07	0.23	0.21	0.15	0.09	0.01			
V_{44}	0.01	0.18	0.09	0.31	0.11	0.02	0.07	0.07			
V_{46}	0.14	0.09	0.09	0.22	0.14	0.11	0.11				
V_{49}	0.12	0.16	0.14	0.18	0.12	0.16	0.15	0.77			

Fig.6. Net assimilation rate in different genotypes

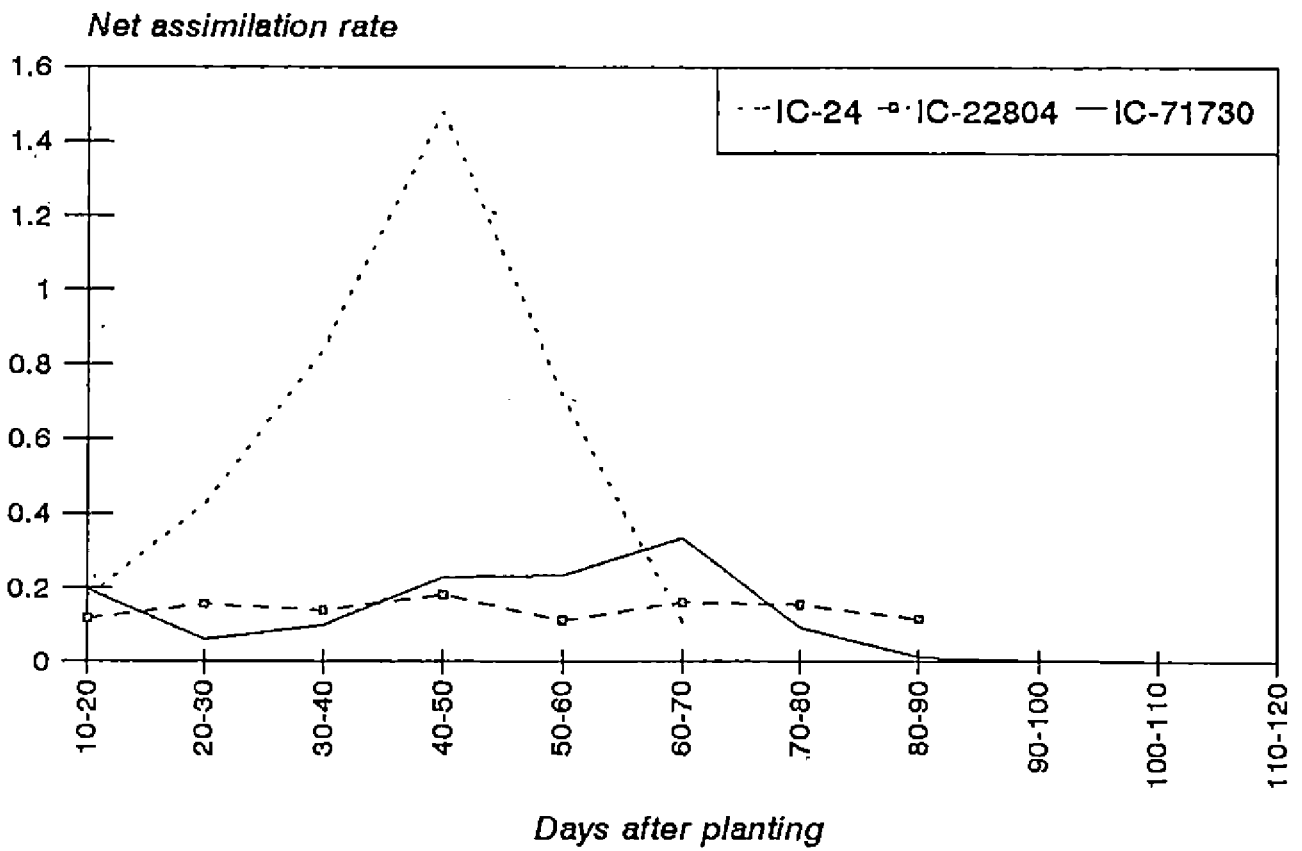
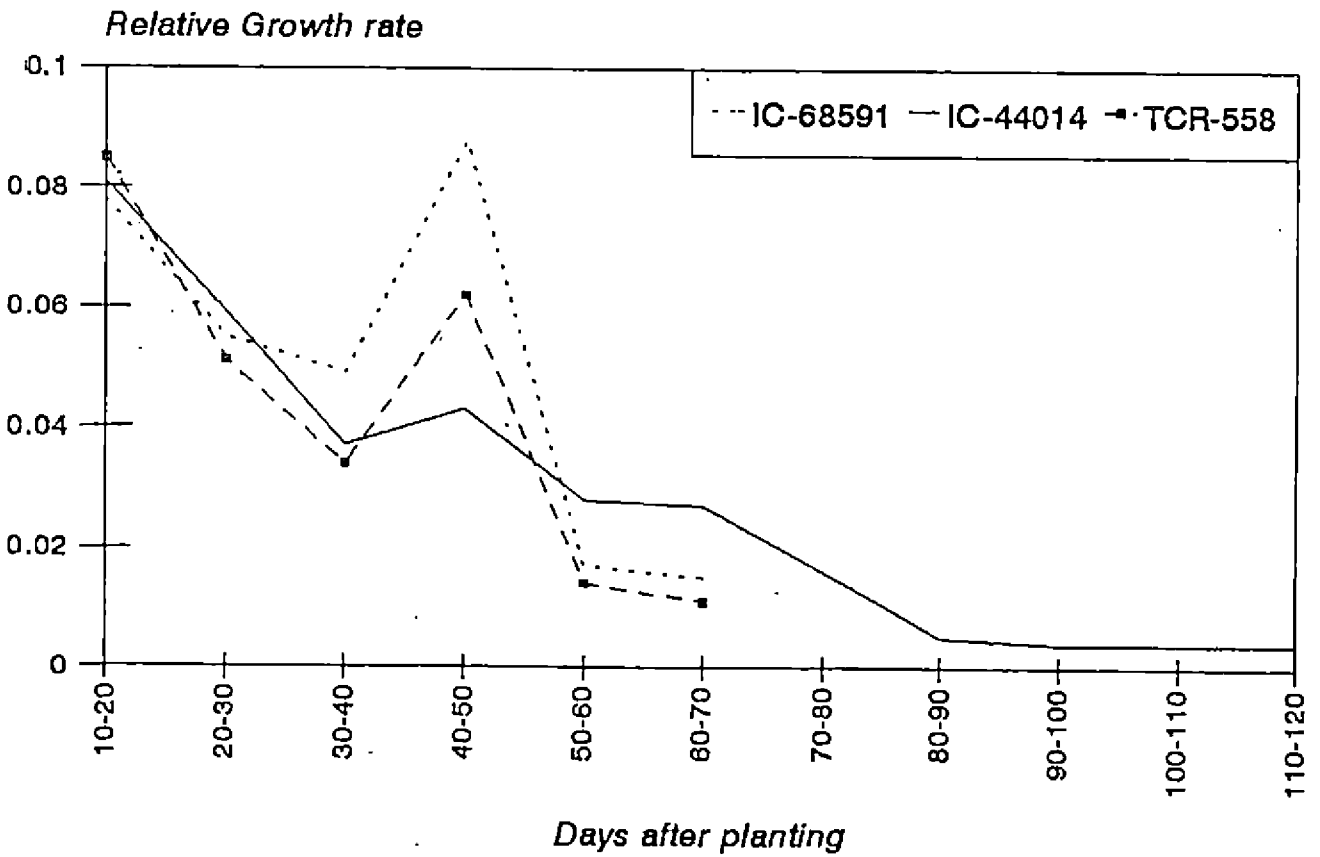


Table 19. Relative growth rate at various growth stages (g $m^{-1}g^{-1}day^{-1}$)

Genotype	Interval of sampling										
	10-20	20-30	30-40	40-50	50-60	60-70	70-80	80-90	90-100	100-110	110-120
V_6	0.08	0.06	0.37	0.04	0.03	0.03	0.02	0.02	0.01	0.01	0.01
V_{22}	0.08	0.06	0.07	0.13	0.02	0.02					
V_{31}	0.08	0.05	0.05	0.11	0.03	0.21	0.02				
V_{34}	0.08	0.06	0.03	0.08	0.02	0.02	0.99	0.05			
V_{35}	0.07	0.05	0.05	0.07	0.02	0.14	0.01				
V_{37}	0.08	0.04	0.04	0.07	0.02	0.02	0.01	0.01	0.01	0.01	0.01
V_{40}	0.05	0.07	0.04	0.08	0.01	0.01					
V_{42}	0.09	0.04	0.04	0.08	0.02	0.02	0.02				
V_{43}	0.09	0.05	0.03	0.08	0.01	0.01					
V_{44}	0.08	0.07	0.04	0.08	0.01	0.01					
V_{46}	0.07	0.05	0.05	0.06	0.02	0.01	0.01	0.01			
V_{49}	0.06	0.06	0.05	0.07	0.01	0.13	0.17				

Fig.7. Relative growth rate in different genotypes



4.4.5 Leaf area index (LAI)

Leaf area index showed a similar trend as NAR. It first increased, reached a peak at 40-50 DAS stage for short and medium duration types and at 60-70 DAS for long duration types. Then there was a slight decrease (Table 20). The highest value was recorded by V_{40} (2.98) at 40-50 DAS (Fig.8).

During the final harvest the following observations were also made (Table 21).

1. Number of branches per m^2: V_{49} showed the lowest value (71.84 branches m^{-2}) and V_{34} the highest value (450.18 branches m^{-2}).

2. Number of pods per m^2: V_{37} had the highest number of pods per square meter of land (666.72) and V_6 and the lowest number (250.80).

3. Weight of pods per m^2: This was highest for V_{44} (400.2 g m^{-2}) and lowest for V_{22} (115.14 g).

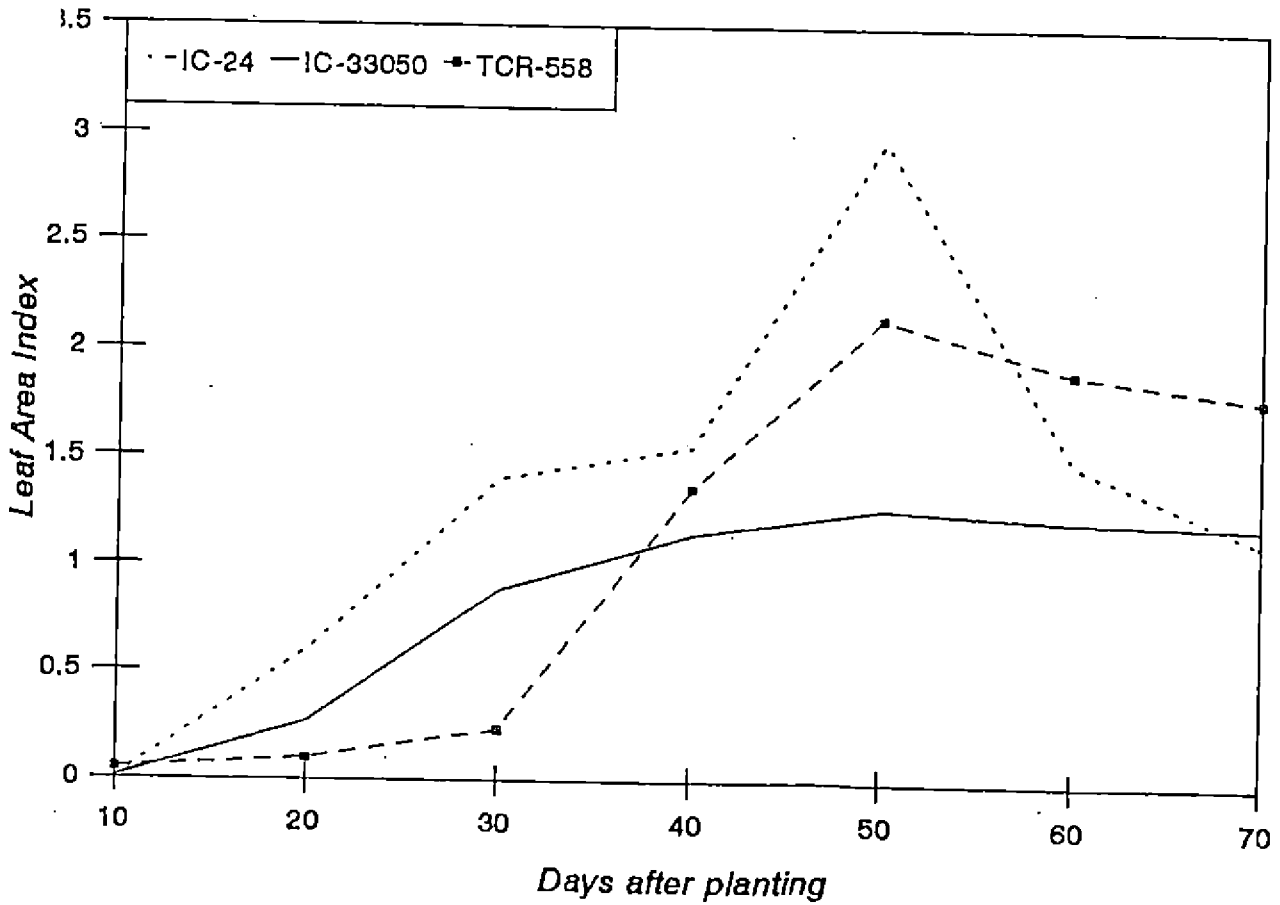
4. Weight of seed per m^2: V_{37} showed the maximum weight of seeds m^{-2} (152.4 g) and V_{31}, the minimum (74.04 gm^{-2})

5. Number of seeds per pod: V_{22} had the highest number of seeds per pod (6.67) and V_{46}, the lowest number (5.75).

Table 20. Leaf area index at various growth stages (m^2m^{-2})

Genotype	Days after sowing											
	10	20	30	40	50	60	70	80	90	100	110	120
V_6	0.08	0.12	0.26	0.31	1.28	1.42	1.99	1.96	1.95	1.94	1.95	1.90
V_{22}	0.01	0.12	0.57	1.29	1.31	1.29	1.27					
V_{31}	0.01	0.08	0.25	1.53	1.57	1.56	1.41					
V_{34}	0.01	0.48	1.43	2.03	2.94	2.94	2.53	1.56	1.40			
V_{35}	0.01	0.47	0.88	1.15	1.22	1.27	1.20					
V_{37}	0.01	0.12	0.35	0.87	1.47	1.73	2.10	2.07	2.01	1.96	1.95	
V_{40}	0.01	0.60	1.41	1.85	2.98	1.49	1.13					
V_{42}	0.01	0.10	1.23	1.50	1.51	1.44	1.39					
V_{43}	0.05	0.10	0.24	1.36	2.15	1.90	1.79					
V_{44}	0.01	0.27	0.09	1.43	1.48	1.46	1.42	1.21	1.20			
V_{46}	0.01	0.29	1.00	1.26	1.29	1.27	1.26	1.17				
V_{49}	0.09	0.23	1.00	1.36	1.56	1.51	1.48	1.39	1.01			

Fig.8. Leaf area index in different genotypes



6. 1000 seed weight: Weight of 100 seeds were calculated and from that, 1000 seed seed was found out. It was maximum for V_6 (41.0) and minimum for V_{30} (29.8).

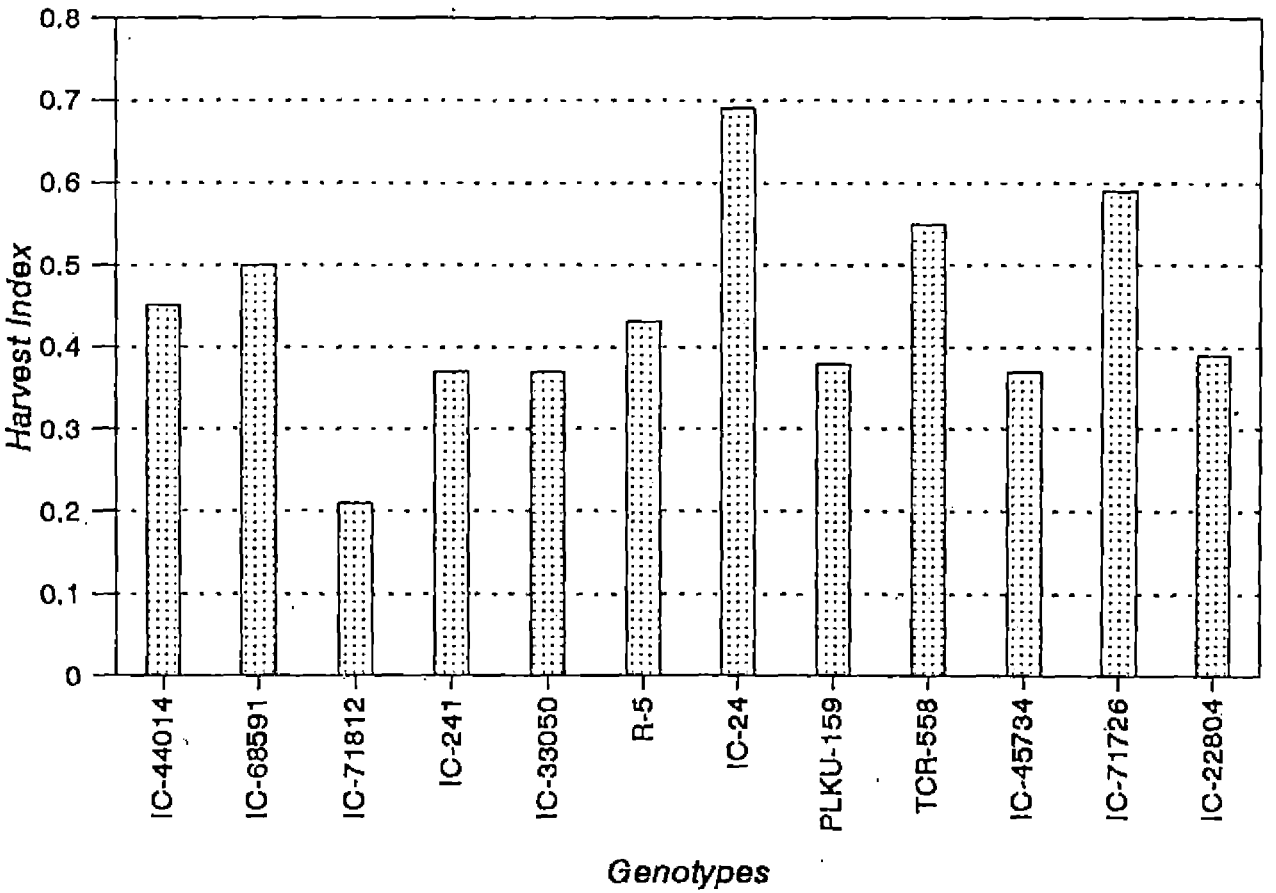
7. Biological yield: It represents the total biomass yield in terms of total dry matter production. The maximum biological yield was given by V_{34} (383.6 g) and the minimum by V_{22} (196.6 g).

8. Harvest index: It is the rate of economic yield to biological yield. V_{40} showed the maximum HI (0.69) and V_{31} the minimum (0.2) (Fig. 9).

Table 21. Yield and yield compenents at final harvest

	V_6	V_{22}	V_{31}	V_{34}	V_{35}	V_{37}	V_{40}	V_{42}	V_{43}	V_{44}	V_{46}	V_{49}
Branches per m^2	258.64	131.14	388.40	450.18	207.78	213.25	307.80	258.00	282.00	175.32	128.82	71.84
Pods per m^2	250.80	370.32	341.52	337.40	263.04	666.72	286.56	499.12	540.12	522.72	325.20	355.92
Weight of pods per m^2(g)	214.20	115.14	240.12	319.50	180.54	391.20	134.70	315.00	258.48	400.20	340.20	367.80
Weight of seeds per m^2(g)	135.84	97.62	74.04	143.04	97.32	152.40	142.56	93.96	140.64	124.92	137.88	97.88
Number of seeds per m^2	6.15	6.67	6.43	6.44	6.13	6.06	5.79	5.84	5.91	6.22	5.75	6.50
1000-seed weight (g)	41.00	37.60	34.50	32.40	38.00	29.80	30.30	36.10	37.10	37.30	39.40	39.20
Biological yield (g)	300.60	196.60	300.36	383.60	264.12	356.40	204.58	243.20	255.60	335.60	233.60	248.50
Harvest index	0.45	0.50	0.21	0.37	0.37	0.42	0.69	0.39	0.54	0.37	0.59	0.39

Fig.9. Harvest index of different genotypes



Discussion

DISCUSSION

Eventhough horse gram enjoys substantial variability in the genetic stock available in our country, attempts to study the extent of diversity and to utilise it effectively for crop improvement had been very meagre. Information regarding the genetic divergence present, heritability, genetic advance and correlation of characters is very important for the successful breeding programme. The present study has been undertaken with the above-said objectives.

5.1 Variability studies

Looking into the analysis of variance of the fifty genotypes of horse gram under study, for all the nine characters, it was seen that the varieties differed significantly from each other, with respect to all the characters. All characters showed significant difference at one per cent level.

The overall variation in a population can be generally split into variation due to genetic causes (Vg) and environmental effect (Ve) and the gene-environment interaction. It is tacitly assumed that, environmental contribution is independent of genotype. Thus the basic genetic model can be expressed as

$V_P = V_G + V_E$ where V_P = phenotypic variance

V_G = genotypic variance V_E = environmental variance

The various components of variance were studied in the fifty genotypes of horse gram. The estimates of gcv and pcv followed an almost similar trend of variability. This agrees with the findings of Apte, et al. 1991; Singh, 1990; Amaranatha et al., 1990; Shukla et al. 1988 and several other workers. The genotypic co-efficient of variation was highest for number of primary branches (22.2428). This was followed by number of pods per plant (21.8594), and yield (21.0345). It was lowest for number of seeds per pod (3.2871). A high co-efficient of variation for number of pods per plant had earlier been reported by Patil and Deshmuk (1982) in horse gram itself. The other characters showed a small gcv (< 20%).

Phenotypic co-efficient of variation was highest for yield (29.5641) followed by number of primary branches (26.3312) and number of pods per plant (24.7183). The environmental component was the highest for yield (20.7746).. Days to maturity had the lowest environmental co-efficient of variation (1.3376).

The high gcv obtained for the characters, primary branch number, number of pods per plant and yield suggested that, these traits were highly affected by the action of genes. The environmental influence was comparatively low. Selection, if practised in these traits, may provide some improvement in the above said characters. The existence of a high heritability component was also indicated for these characters. The higher value for environmental variance in yield, could be considered as a proof, for the complexity of the character, yield and the difficulty in its improvement by selection for yield as such.

According to Burton (1952), gcv, along with heritability estimates would give a better idea about the efficiency of selection, as the latter measures the proportion of the variability of a character that is transmitted to the progeny. A high heritability coupled with high gcv would indicate a less environmental influence on the character and high transmission index, while, a low heritability, even with a high gcv is not of much use for the improvement of the character by selection. This confirms that selection based on the characters, primary branch numbers and number of pods per plant can provide some improvement in horse gram.

Heritability studies indicated the highest value for 100 seed weight. Similar result had been reported by Singh (1990) in horse gram and Parameswarappa (1992) in blackgram. This was closely followed by days to maturity and length of pods. Plant height and days to 50% flowering also recorded high heritability. For number of seeds per pod, the heritability was moderate. The least heritable character was identified as yield (50.6218). A low heritability for grain yield per plant was reported by Singh (1990) also in horse gram. This was in accordance with the comparatively higher environmental influence, seen from the co-efficient of variation estimates. This low heritability also confirmed the complex nature of the character. Improvement through selection for this trait is doubtful, due to low transmissi-bility of the character to its progeny.

Heritability indicates only the effectiveness with which, selection of a genotype can be based on phenotypic performance, but it fails to indicate genetic progress (Johnson et al., 1955). Heritability and genetic advance, when calculated together would be more useful in predicting the resultant effects of selection. In the present study, high genetic advance was obtained for length of pods (50.0236) followed by number of pods per plant (39.4803), number of primary branches (38.6860), 100 seed weight (32.5937),

and days to 50 per cent flowering (32.27124). Genetic advance was moderate for yield (30.8296), plant height (29.6174) and days to maturity(26.2047) indicating that, selection based on these characters may not be very effective. Number of seeds per pod showed a very low genetic advance of 6.0913.

A relative comparison of heritability estimates and genetic advance expressed as per cent mean, gives an idea about the nature of gene action governing a character (Mishra et al., 1988). High heritability with high genetic advance for a character indicates the presence of additive gene effects, whereas a high heritability with low genetic advance indicates non-additive gene effects. Improvement by selection will be effective, only if high heritability is associated with high genetic advance. If the genetic advance is low, even if high heritability is present for the character, it cannot be considered beneficial (Panse, 1957).

The character, length of pods, showed high heritability coupled with high genetic advance expressed as percentage of mean, indicating substantial contribution of additive genetic variance in the expression of this character, as suggested by Panse (1957). This could be considered as a promising character for effective selection. Number of pods per plant, number of primary branches and 100-seed weight

had high heritability with medium-to-low genetic advance, revealing the possibility of non-additive gene effects, governing this character. Similar interpretations were given by Gadekar and Dhumale (1990) in rice bean. Yield again, had a lower gentic advance and heritability, confirming the ineffectiveness of selecting for yield as such. This observation on yield is contrary to the findings of Mishra and Dash (1991) in french bean and Dumbre et al. (1983) in cowpea, which showed a high heritability and genetic advance for yield.

It was also observed that a comparatively higher gcv, need not always be associated with higher heritability values, as in the case of yield and number of pods per plant. Also, characters like 100 seed weight, days to maturity and plant height, which had comparatively lower genetic advance showed high heritability values. This finding is in accordance with that by Singh (1990) in horse gram. This behaviour may be attributed to the variations in the extent of involvement of environmental components of variation, in the above-said traits.

Thus, considering the gcv, heritability and genetic advance together, the length of pods is a promising character for selection for yield.

5.2. Correlation studies

If selection is done on a character, it changes many other unselected characters. Hence it is necessary to study the correlated response to selection, of one character, so as to get information regarding the influence on other characters.

The correlation studies carried out, exhibited more or less, similar trend for phenotypic and genotypic correlations, but, in general, the genotypic correlation coefficients were higher than the phenotypic correlation coefficients. This itself is a clear indication of substantial interference of environment on the expression of the character (Singh, 1990)

Grain yield per plant showed the strongest positive correlation of 0.5327, with number of seeds per pod, followed by the with number of pod per plant length of pods and number of primary branches. Singh (1990) also obtained similar results in horse gram. These could be considered as major components of yield. The positive correlation of pods per plants with yield was observed to be a general rule, in almost all legume crops by several workers (Mahajan, 1993; Singh, 1990; Apte et al., 1991; Mishra et al., 1988 and Frey, 1975)

The positive correlation of seed yield with increase in length of pods, may be through an increase in the number of seeds contained in the pods. If the length is more, it subsequently leads to increased seed yield. An increase in rimary branch number, also increases the yield. This may e through an increase in number of pods per plant due to an ncrease in the primary branches, on which, they are borne, hich in turn leads to a higher yield (Singh, 1985). In contrast to some previous reports (Singh, 1990, in horse gram; Mishra et al., 1988 in chickpea, Apte et al., 1991 in cowpea) of a significant negative correlation of 100-seed weight with yield, non significant negative association was observed between 100-seed weight and yield in this crop, as was reported in soyabean by Mahajan (1993); Amaranatha (1990), Dixit and Patil (1984) in soyabean.

Among the yield components, number of primary branches showed a positive and significant relationship with number of pods per plant. It might be this effect, which leads to the significant positive association between number of primary branches and yield (Singh, 1985). A positive significant correlation was shown by plant height and length of pods.

Days to 50 per cent flowering exhibited significant negative correlation with 100 seed weight. The negative

correlations arise due to sequentially developing components which share a common pool of assimilates. As the first component utilises greater or lesser amount of assimilates, the next component compensates accordingly, by utilising more or less, as the case may be. The incorporation of such negatively associated characters necessitates the use of special breeding techniques like disruption selection or mutation breeding, to break the undesirable linkage, as reported by (Shukla, 1988).

Days to 50 per cent flowering had a very strong positive correlation with days to maturity. This is explainable, as delay in 50 per cent of the plant to flower, will subsequently delay the maturity period.

Length of pods and number of seeds per pod showed a significant positive correlation. As the pod length increased, the number of seeds per pod increased, thereby causing an increase in seed yield.

Hundred seed weight and days to maturity showed a significant positive association. As the duration of the crop increases, the transport of assimilates towards the seed and its subsequent storage in the seeds will be more. This could be a possible explanation for the association noticed.

Contrary to other reports, no relationship of 100-seed weight, with the rest of the characters was observed, may be, due to a low genetic variation for this character.

The positive association for the number of primary branches with number of pods per plant and of number of pods per plant, in turn, with seed yield suggested that, selection for plants with large number of primary branches would favour increased seed yield.

The phenotypic correlations also showed an almost similar trend, but, among the yield components, significant correlations were exhibited only between length of pods and number of seeds per pod and also between days to 50 per cent flowering and days to maturity. The characters, number of primary branches, number of pods per plant, length of pods and number of seeds per pod showed positive and significant association with yield. Other correlations were not significant.

Significant positive environmental correlation was observed between days to 50 per cent flowering and 100 seed weight, as against the genotypic and phenotypic correlations which were significant and negative for this pair of characters. Also, days to 50 per cent flowering and number

of seeds per pod showed significant positive relationship. This positive association points to the fact that, these characters are influenced to a large extent, by the environmental factors in respect of their genetic control.

In certain correlations, where phenotypic correlations are smaller than genotypic values the environmental correlations were small and positive (plant height and yield; days to 50 per cent flowering and length of pods, length of pods and yield, number of seeds per pod and days to maturity; 100 seed weight and days to maturity). This may be because, the genes governing the two traits are similar but the environments for the expression of these two traits may have small and dissimilar effects (Shukla, 1988).

In some cases, genotypic and phenotypic correlations had opposite signs (number of primary branches and number of seeds per pod, days to maturity and yield). Here the traits might have been effected by genetic and environmental sources of variation through different physiological mechanisms (Shukla, 1988). A high environmental correlation, as seen in the two cases, suggested a common influence of the environment involved in the development of the traits according to the same author.

5.3 Genetic divergence studies

The practical significance of genetic diversity had been well recognised by plant breeders. Multivariate analysis provides a powerful tool for assessing the diversity. The present attempt in horse gram was undertaken to unutilise the Mahalanobs D^2 statistic, to get an idea about the genetic diversity exhibited by the genotypes under study. This enable the selection of diverse parental lines for effective hybridisation.

The fifty genotypes from diverse origin (from Idukki and Ernakulam districts of Kerala, from Tirunelveli, Madurai, Dindigal and Tiruchendur districts of Tamil Nadu, from Delhi and also some of unknown origin) were analysed. Wilk's criterion test revealed highly significant difference among the 9 characters for 441 degrees of freedom.

The entire population could be grouped into 11 clusters according to the procedure given by Spark (1973). Non-hierarchial Euclidean cluster analysis in the Statistical Programme for Agricultural Research (SPAR-1) package of IASRI was used for this purpose. The optimum cluster number was found to be eleven, by graphical method.

Cluster I had 5 members, 2 of which were from Tamil Nadu, one from Kerala and two, of unknown origin. They were mostly early maturing and short types. Cluster II had a

single genotype from Delhi, with the largest number of pods per plant and 100-seed weight. Cluster III had five members - two from Dindigal, one from Madurai, one from Delhi and one of unknown origin. Cluster IV had genotypes from Delhi, Tamil Nadu and Kerala. The variation in yield was maximum in this cluster. In Cluster V, there were members from Kerala, Karnataka, Tamil Nadu and Delhi. Cluster VI had a sole member from Tamil Nadu. Cluster VII had two members one from Delhi and one from Tamil Nadu. One genotype from Delhi and three from Tamil Nadu were included in cluster VIII. Clusters IX and X included genotypes from all the three states. Cluster XI was composed entirely of the genotypes from Tamil Nadu.

The clustering pattern did not show any relationship with geographic origin. Geographically isolated genotypes could be identified to be in the same cluster. The five genotypes from Kerala were widely distributed in four clusters. Those from same area (V_9 and V_{17} from Idukki) were included in different clusters. Also two genotypes (V_2 and V_9) in cluster V were from different districts of Kerala - Idukki and Ernakulam. Genotypes from Delhi were distributed within eight out of the eleven clusters. Those from Tamil Nadu were included in all the eleven clusters. Similar results were reported by Ramakrishnan et al. (1979) in horse gram.

The diversity among the lines of the same geographical origin could be attributed to several reasons. It may be due to ecogeographical distribution (Sood et al., 1989). Populations from areas with complex environments may have, in the long run adjusted to several ecological riches and have accumulated enormous genetic variability (Chandel and Joshi, 1981). Some diversity could also be ascribed to the genetic drift and selection under diverse environment, which would cause greater diversity than geographic isolation alone (Murthy and Arunachalam, 1966). Also, the free exchange of seed material among different regions, and other human interference might have contributed to some diversity (Katiyar and Singh, 1979). Besides, in situations were geographically distant locations do not differ substantially in climate, biotype, soil and management, the geographical barrier may not be potent enough to accumulate variability as observed by Gupta and Singh, 1970 in greengram; Mahendiratta and Singh, 1971; Angadi, 1976 and Radhamanoharan, 1978 in cowpea and Chaudhary et al. 1975 in cluster bean. However, in some cases, effect of geographic origin influenced clustering, as seen in cluster XI, which was occupied entirely by genotypes from Tamil Nadu. This indicated that, though geographic distribution was not the sole criterion for clustering, its importance could still be traced as state by Katiyar and Singh, 1979 in chickpea.

As a general rule, genotypes with similar characteristics, though separated geographically, had come together. These genotypes might have been subjected to similar selection pressures, for particular utility product, for which, similar preference might have existed in different regions. This observation agreed with the findings of Chandel and Joshi (1981) in yellow-seeded pea

The average distance of cluster members from cluster centroids are given in Table 14. The clusters II and VI have the average distance given as 0.00 as these two have only a single member. Of the rest, cluster VII showed the least value and cluster VIII had the highest value. The distance between cluster centroids was maximum between II and VI followed by II and VII. So the members of these clusters could serve as best source of variability while making selection of parents to be used in hybridisation programmes.

The contribution of various characters towards total divergence revealed 100 seed weight to be the maximum contribution (16.35%). This result is in accordance with the findings of Ramakrishnan et al. (1979) in horse gram and also that of Dasgupta et al. (1987) in chickpea. The seed yield and length of pods were the next highest contributors (13.35 per cent and 12.95 per cent respectively).

Thus all the characters studied exhibited significant variability with the traits primary branch number, number of pods per plant and length of pods exhibiting good scope for improvement through selection. Hundred seed weight also showed good heritability and it contributed the maximum towards genetic divergence.

5.4 Growth analysis

The lack of a proper assessment of growth pattern in horse gram is a major constraint in the evolution of a good plant type. The various physiological parameters like growth rate, branching pattern, assimilation rate, partitioning of assimilates etc. will be important for the selection of an ideal plant type, which will be useful for further crop improvement. So the selection on the basis of physiological attributes is of prime importance and this will be facilitated by growth analysis technique. The present study was conducted with this idea in mind.

Total dry matter accumulation is the result of a balance between photosynthetic activity and respiratory losses (Sinha et al., 1990). The pre-requisites for any high yielding crop is its ability to produce higher amount of total dry matter (TDM) and its appropriate distribution to the different plant parts.

Total dry matter production showed an increase, almost upto maturity . This agrees with the findings of Kumari and Singh (1990) in ground nut. Only at the harvest stage, there was a slight reduction in TDM and that too, mostly, in the long duration varieties. Maximum TDM was for V_{34}, followed by V_{37}. The seed yield was also high for these two varieties (143.04 and 152.40 $g.m^{-2}$ respectively). Total dry matter at final harvest was closely correlated with seed yield in all varieties. Improvement in seed yield should therefore primarily aim at an increase in TDM. Since TDM productionis an indication of the increase of growth during various stages, the growth pattern at various developmental stages also is important.

In all the varieties, studied the increase in dry matter production was greatest during the middle phase of growth (40-50 DAS for short and medium duration types and at 60-70 DAS for long duration types). In all varieties except V_{34} and V_{37}, the TDM production during pre-anthesis was less than 10 per cent of the total, whereas it was high in V_{34} (28.34%) and V_{37} (22.60%). It is seen that in these varieties with more dry matter production, during pre anthesis the seed yield was high but the efficiency of partitioning of dry matter was poor thereby leading to lower harvest index. Such a low dry matter production during pre-

anthesis had been observed in some chick pea varieties by Pandey et al. (1976).

Net assimilation rate (NAR) among varieties did not differ significantly during the period upto 50-60 DAS. The NAR was maximum during the period 40-50 DAS. But there were occasional peaks and this could be attributed to the dropping of lower leaves, which did not contribute much towards photosynthesis but retained respiratory activity. The same trend was noticed by Prasad et al. (1978) in gram and Kalubarme and Pandey (1979) in green gram. The initial decline in NAR might be due to (i) excessive mutual shading as leaf area index (LAI) was high during this period and (ii) an increase in old leaves with low photosynthetic efficiency. Kalubarme and Pandey (1979) and Saini and Das (1979) have recorded a similar trend in green gram. The increase in NAR during 40-50 day after sowing (DAS) may be the result of greater demand for assimilates by the rapidly growing seeds. An increase in the production of photosynthates by green pods could be another reason as observed by Koller et al. (1970).

It is seen here that NAR is related to yield per day. V_{40} has the highest NAR at its peak period and correspondingly it showed the highest yield per day per unit

area (2.46) (Table 18). Those with lower NAR values at the peak period had comparatively lower yield per unit area. Thus it can be considered as a measure of photosynthetic efficiency.

Crop growth rate (CGR) also showed a similar trend, increasing upto the middle growth period of 40-50 DAS in short and medium duration varieties and 60-70 DAS in long duration varieties. Thereafter, the CGR declined till maturity. The initial rate of increase in CGR was poor and this might be associated with poor growth of stem and leaves. Rapid increase in CGR after flower formation resulted in increased accumulation of dry matter in reproductive organs. A higher NAR in turn leads to increase in CGR. Koller et al. (1970) also reported similar observations in soyabean.

Relative growth rate (RGR) increased during the initial stages, reached a peak during 40-50 DAS for short and medium duration types and 60-70 DAS for long duration types and then declined. The initial peak in RGR might be due to a similar increase in leaf area at this stage. A decrease after 40-60 days might be due to an increase in NAR. This agrees with the findings of Kalumbarme and Pandey (1979) in green gram.

Leaf area index (LAI) increased for all varieties upto maturity and a very slight decrease was noticed at final stages. This parameter represents the number of leaves per unit area. LAI was highest in the case of V_{40}. This also had shown the highest NAR, thus indicating a positive association between the two parameters. An increase in LAI causes an increase in photosynthetic area and thus the net assimilation increases. During the final stages the decline shown might be due to the fall of older leaves, which do not retain photosynthetic efficiency but have respiration activity. Similar findings were reported by Prasad et al. (1989) in garden pea, Kalubarme and Pandey (1979) in green gram and Mehra (1987) in pigeonpea.

Harvest index is the ratio of economic yield to biological yield. This was highest for V_{40}. In this case the TDM was not very high but the high HI was due to a better partitioning of TDM to the seed (178.19 g seed yield out of 255.7 g TDM). In V_{34} and V_{37} which had higher TDM values, the partioning to the reproductive dry matter was inefficient thereby, leading to a lower HI. In these genotypes, a higher percentage of TDM had been produced during pre-anthesis stage (28.34% and 22.60% respectively) than those in others. Similar findings were reported by Prasad et al. (1989) in Kalubarme and Pandey (1979) in green gram and Mehra et al. (1987) in pigeon pea. In V_{40} it was

10.05 per cent. Thus there was a higher partitioning to the vegetative dry matter in these varieties. LAI and NAR were also low in these cases. In the genotype V_{46} also, a better partitioning of dry matter to reproductive pods had led to a higher HI. The importance of efficient partioning of dry matter for higher harvest index had earlier been reported by Prasad and Karmakar (1989) in garden pea, Kalumbarme and Pandey (1979) in greem gram, Uprety et al. (1981) in soyabean, Mehra (1987) in pigeonpea and Singh (1990) in horse gram. The present findings agree with these reports.

From the morphological attributes, on a per unit area basis at final harvest, the highest harvest index was found for V_{40}. It also had the highest NAR and LAI. The partitioning of assimilates towards reproductive parts was most efficient in this genotype giving a HI of 0.69

It can thus be concluded that a plant type with highest NAR and LAI and TDM values at the middle of its growth phase and with very efficient dry matter partioning to reproductive parts is to be evolved while aiming at ideotype breeding.

Summary

SUMMARY

Studies on genetic divergence and variability, in fifty genotypes of horse gram were undertaken in the Department of Agricultural Botany, College of Horticulture, Vellanikkara during the year 1992-93. The experiment was aimed at evaluating the population in two perspectives - genetic studies and growth analysis.

Twenty five plants were randomly selected for taking observations on nine economic cnaracters. The data obtained were subjected to suitable statistical analysis, so as to estimate the variability and correlations and also to group the genotypes into homogenous clusters.

The salient findings could be summaried as follows:

1. The fifty genotypes of horse gram showed considerable variation with reference to the nine characters studied.

2. Estimates of phenotypic, genotypic and environmental variance showed that, a large proportion of variability was due to genetic factors, in all characters except number of seeds per pod and yield. The coefficients of variation were also in confirmation with this result.

12. The relative contribution of the different characters towards total divergence was studied and it was found to be the highest for 100 seed weight. This contributed 16 per cent towards the total genetic divergence.

13. The total dry matter production, in the twelve representative genotypes subjected to growth analysis was found to increase till the harvest period. It was the highest for the genotype V_{34} and the lowest for V_{22}.

14. Crop growth rate at different growth stages showed that, as a general rule, the value was at its peak during the middle growth stage.

15. Net assimilation rate was also highest at the middle stage of growth, ie. 40-50 days after planting in short duration types and at 60-70 days after planting in long duration types.

16. Relative growth rate also exhibited a peak value at the middle growth phase.

17. The genotypes showed the maximum leaf area index at 40-50 days after planting in short duration genotypes and at 60-70 days after planting in long duration types.

3. Heritability in the broad-sense was high (over 70 per cent) for all characters except number of seeds per pod and yield. These two traits showed moderate heritability. Heritability was highest for 100 seed weight and days to maturity.

4. Genetic advance estimated over the mean was highest for length of pods and it was lowest (less than 10) for number of seeds per pod.

5. Correlation studies revealed a significant positive genotypic correlation between yield and the characters, number of primary branches, number of pods per plant, length of pods and number of seeds per pod, as they might be governmed by additive genes. Hence these characters can be improved through straight selection. The character number of seeds per pod had shown a high heritability, but very low genetic advance, thereby questioning the scope for improvement through straight selection, for this trait.

6. Results of correlation studies revealed a higher genotypic correlation than genotypic correlation in most cases. Both the values were comparable in magnitude for any pair of characters.

7. Strong, significant and positive correlations were noticed between the characters plant height and length of pods; number of primary branches and number of pods per plant; days to 50 per cent flowing and days to maturity; length pods and number seed per pods and 100 seed weight and days to maturity.

8. Characters exhibiting significant associations with seed yield per plant were also inter correlated, thereby showing the possibility of simultaneous improvement.

9. Results of divergence studies revealed eleven clusters of which, the clusters II and VI had only a single member each.

10. The clustering pattern confirmed that there was no relationship between genetic distance and geographical distribution.

11. The average distance between cluster centroids was found to be the maximum for clusters II and VI and the maximum distance of the cluster members from cluster centroids was observed in cluster VIII. The members from the clusters II and VI can be expected to give the maximum hetrosis, if included in hybridization programmes, since the distance between cluster centroids is a measure of intercluster distance.

18. The harvest index was maximum for V_{40} and the minimum for V_{31}.

19. A better partitioning of the dry matter towards the reproductive portion was found to be an important criterian for a better harvest index.

20. From the growth analysis performed it can be concluded that a plant with the maximum leaf area and net assimilation rate at the middle growth stage with an efficient partitioning of dry matter towards the reproductive partition could be selected as an ideal plant type.

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GERMPLASM EVALUATION IN HORSE GRAM (*Dolichos biflorus*. L.)

BY

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ABSTRACT OF A THESIS

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ABSTRACT

The present study was undertaken in the Department of Agricultural Botany, College of Horticulture, Vellanikkara during October 1992 to February, 1993 to study assess the variability existing in a population of 50 genotypes of horse gram. Evaluations based on the physiological parameters were also carried out.

The results revealed the presence of sufficient genetic variability in the different genotypes studied, which were of different geographical origin. High heritability and genetic advance exhibited by the characters, length of pods and number of pods per plant point towards the possibility of these traits to be improved by direct selection. Environmental effect was found to be comparatively higher for yield and number of seeds per pod.

Correlation studies indicated maximum correlation of yield with number of seeds per pod and number of pods per plant. Association studies among the different traits showed positive significant correlations between the character pairs, plant height and length of pods, number of primary branches and number of pods per plant, days to 50 per cent flowering and days to maturity; length of pods and

number of seeds per pod and 100 seed weight and days to maturity.

Divergence analysis gave eleven clusters of which, cluster II and VI showed maximum distance of the cluster members from cluster centroids. The members of these two clusters could be considered superior as parents, for hybridization programmes. The maximum mean value for yield was exhibited by members of cluster II. The maximum contribution towards genetic divergence was made by the character 100 seed weight.

Growth analysis based as physiological parameters like dry matter production, NAR, CGR, LAI and HI suggested th an ideal plant type will be one in which maximum dry matter production, net assimilation rate and leaf area index was observed during the middle growth stage. An efficient partitioning of dry matter towards the reproductive parts was also an essential criterian.