VARIABILITY, CORRELATION, PATH COEFFICIENT AND GENETIC DIVERGENCE IN GREEN GRAM

(*Vigna radiata* (L.) Wilczek).

A

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ABSTRACT

VARIABILITY, CORRELATION, PATH COEFFICIENT AND GENETIC DIVERGENCE IN GREEN GRAM (*Vigna radiata* (L.) Wilczek)

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ABSTRACT

Variability, correlation, path coefficient and genetic divergence were studied in a set of 86 genotypes of green gram (*Vigna radiata* (L.) Wilczek) grown in a randomized block design with three replications at the Regional Pulse Research Station, Gujarat Agricultural University, Navsari during Summer 1996.

Analysis of variance revealed significant genotypic differences for all the eleven characters under study. A wide range of variation was apparent for all the characters. The genotypic coefficient of variation was highest for number of pods per plant followed by seed yield per plant, plant height, number of clusters per plant, number of pods per cluster and pod length. Heritability estimates were high for protein content, seed yield per plant, 100-seed weight, number of pods per plant, pod length, plant height, number of clusters per plant, number of pods per cluster, days to maturity and days to 50 per cent flowering. The expected genetic advance as a percentage of mean was high for number of pods per plant, seed yield per plant, plant height, number of clusters per plant and pod length. High hertitability coupled with high genetic advance was exhibited by number of

pods per plant, seed yield per plant, plant height and number of clusters per plant. Thus, phenotypic selection would be effective for the genetic improvement in these traits.

Correlation analysis revealed that seed yield per plant was found to be highly significant and positively correlated with plant height, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod at genotypic levels. These yield- contributing characters also possessed associations amongst themselves. The traits, 100-seed weight, days to 50 per cent flowering and days to maturity were negatively correlated with seed yield.

Path coefficient analysis indicated the highest positive direct effect for number of clusters per plant, followed by plant height, 100-seed weight, number of pods per plant, number of seeds per pod and days to 50 per cent flowering. The character, days to maturity exhibited high negative direct effect, while pod length showed negative low direct effect.

Based on these findings, it can be suggested that for improving seed yield in green gram, more emphasis should be given to plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100-seed weight.

The genetic diversity was assessed using Mahalanobis's D^2 statistic wherein eighty six genotypes were grouped in eight clusters. The clustering pattern of the genotypes was independent of their geographical distribution. Based on inter-cluster distance, cluster-III showed high genetic divergence with cluster-VIII, VI and V and cluster-IV with V. Therefore, it was concluded that the genotypes belonging to these groups can be utilized in developing diverse variability and improving seed yield in green gram. The

characters, number of pods per plant, seed yield per plant, number of clusters per plant, number of pods per cluster and plant height contributed maximum to the divergence.

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CERTIFICATE

This is to certify that the thesis entitled **"Variability, correlation, path coefficient and genetic divergence in green gram (*Vigna radiata* (L.) Wilczek."** submitted by **Shri C. R. Patel** in partial fulfillment of the requirements for the award of the degree of **Master of Science (Agriculture)** in the subject of **Plant Breeding and Genetics** of the Gujarat Agricultural University is a record of bonafide research work carried out by him under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma or other similar title.

Place : Navsari
Date : December २९, 1997

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DECLARATION

This is to declare that the whole of the research work reported in this thesis in partial fulfilment of the requirements for the degree of **Master of Science (Agriculture)** in **Plant Breeding and Genetics** by the undersigned is the result of investigation done by me under the direct guidance and supervision of **Dr. N. M. Desai**, Associate Professor, Department of Agricultural Botany, N. M. College of Agriculture, Gujarat Agricultural University, Navsari Campus, Navsari and that no part of the work has been submitted for any other degree so far.

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Place : Navsari

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INTRODUCTION

I INTRODUCTION

Green gram (*Vigna radiata* (L.) Wilczek) an important seed legume in the pulse family, including chickpea, pigeon pea, urdbean, cowpea etc., playsa vital role in meeting the quantitative and qualitative requirements of food and protein throughout the world. It is known as mungbean, moong and goulden gram. It is popularly known as Mug in Gujararti, Mung in Oriya, Sonamung in Bengali, Moong in Hindi and Punjabi and Pachaipayaru in Tamil. The important moong-growing states are Maharashtra, Gujarat, Tamil Nadu, Andhra Pradesh, Bihar and Uttar Pradesh.

The centre of origin for green gram is not exactly known. According to Vavilov (1926), it might be originated in Hindustan and Central Asiatic regions. Green gram belongs to the family leguminosae and sub family papilionoideae with chromosomes 2n = 22.

In India, green gram occupies an area of about 3.47 million hectares, with an average production of 1.35 metric tonnes and 389 kg/ ha, productivity (Anonymous, 1994-95). In Gujarat state, it occupies an area of about 181.5 thousand hectares, with an average production and productivity of 714 metric tonnes and 393 kg/ ha, respectively (Anonymous, 1994-95). Green gram seed contains about 20 - 26 per cent protein and 62 - 65 per cent carbohydrate (Thakur, 1979). Its bio-product is used as animal feeds and compost manure.

Green gram is cultivated throughout the tropics and subtropics as a minor pulse crop, although it has been grown since ancient times in many countries, viz., Africa, India, Australia, Burma, Bangladesh, Indonesia, Sri Lanka, Thailand and Philippines.

Man has started domesticating and cultivating crop plants from the time immemorial but only the staple food crops received attention as compared to other food crops, like pulses. This may be one of the reason that the productivity of pulse crops reviewed comparatively very low. Another probable reason for the low yield of pulses are that the fertile and good soils were reserved for growing staple food crops, while pulses are being grown under marginal lands of low fertility and moisture stress, lack of good management practices and lack of high yielding varieties.

The average yield of green gram is very low and the year-to-year variation in yield is also remarkably high. Hence, one of the major objectives of the present breeding programme is to try to enhance the productivity and stabilize the yield performance. This is possible only when there is high genetical potential for yield and greater degree of adaptability. It is believed that pulses may have lower genetic potential than cereals as they give lower yield than cereals. The available evidence, however, indicates that the pulse crops have as high or a higher genetic potential for yield than cereals (Jain, 1975).

Although some research work was carried out in India, it was not sufficient enough to produce stable high yielding green gram varieties. As this crop is under-exploited, there is an immense need to start a planned genetic research work with collection of germplasm, study of variability and genetic divergence, evaluation, testing, selection of best genotypes for hybridization, selection of suitable, stable, high-yielding segregants from advance generations and release of varieties for sole cropping, inter cropping, relay cropping systems adaptable to both high and low management.

A wealth of variability is the prime requirement for the improvement of any crop. Therefore, in order to assess the extent of genetic

variation present in breeding material, the knowledge of genetic parameters such as genotypic coefficient of variability, phenotypic coefficient of variability, heritability and expected genetic advance is a pre-requisite in the genetic crop improvement.

Yield, a dependent character, is the resultant effect of a number of quantitative characters. The study of association between pairs of these characters and yield provides a basis for further breeding programmes. In order to estimate the direct and indirect contribution of an individual character towards yield, path coefficient analysis is used.

The selection of parents for hybridization is one of the crucial decisions that a plant breeder has to take. However, there are various methods for identifying such material. Among all the methods, Mahalanaobis's D^2 technique is the most efficient tool for estimating genetic divergence and for identifying the desirable parents for any crossing programme. Therefore, there is a need to study the genetic divergence among various cultivars in order to evaluate their usefulness as progenitors in hybridization programme.

Therefore, the present investigation was carried out to study the genetic variability, heritability, expected genetic advance, correlation, path coefficient and genetic divergence in eighty six genotypes of green gram with the following objectives :

1. To ascertain the nature and magnitude of genetic variability for yield and its components, heritability estimates and expected genetic gain through phenotypic selection.

2. To estimate phenotypic and genotypic correlations between yield and other characters for suggesting suitable selection criterion on the basis of genotypic correlations.

3. To analyse path coefficients for assessing the direct and indirect effects of individual character on yield.

4. To know the extent of genetic distance among different genotypes within a group (cluster) and to provide a basis for selection of parents for hybridization.

REVIEW OF LITERATURE

II REVIEW OF LITERATURE

The crop improvement depends upon the extent, nature and magnitude of genetic variability in the material and the extent to which it is heritable. Yield is the complex and polygenic character and highly influenced by environment. Therefore, it is necessary for a plant breeder to know the role of environment for expression of trait. To ascertain the variability for improving seed yield, knowledge of inter-relationship between yield and its component characters and among the component characters is essential. Path coefficient analysis provides precise information about the cause and effect situation and helps in determining the selection criteria in crop improvement. Genetic divergence helps in the selection of genetically divergent parents for their exploitation in hybridization programme.

Literature relevant to the research work done on various aspects in Green gram (*Vigna radiata* (L.) Wilczek) has been reviewed in the following sub headings.

2.1 Variability, heritability and genetic advance

2.2 Correlation and path coefficient analysis

2.3 Genetic divergence (D^2 statistic)

2.1 Variability, heritability and genetic advance

Assessment of genetic variability in the population is the first step in crop improvement because the progress of any breeding programme depends largely on the extent of variability present in population.

Genetic variability is determined with the help of certain genetic parameters such as coefficient of variation, heritability and genetic advance.

Heritability is the heritable portion of phenotypic variance and it is a good index of transmission of a character from parents to their offspring (Falconer, 1981). The knowledge of heritability helps the plant breeder in selection for a particular character. Heritability is the ratio of genotypic variance to phenotypic variance. Its estimation is important, because it determines the additives effects of genes. If the heritability of a character is high, the phenotypic value provides a fairly close measure of the genotypic value and thus the breeder can base his selection on the phenotypic performance. For predicting the effect of selection, heritability estimates along with genetic advance are more useful than the heritability estimates alone (Johnson *et al.*, 1955).

Singh and Malhotra (1970 a) observed genetic variability in a collection of seventy five indigenous and exotic green gram strains. They found wide range of variation for pods per plant, 100-seed weight and seed yield per plant. High GCV coupled with high genetic advance was recorded for pods per plant, seed yield per plant and 100-seed weight. They found relatively low GCV for days to flowering, days to maturity, pod length and seeds per pod. Heritability values were high for 100-seed weight, days to flowering and days to maturity while low for seed yield.

Chowdhury *et al.* (1971) studied variability in 21 varieties of green gram and observed a wide range of variation for pods per plant, plant height, days to flowering and seed yield. Plant height, days to flowering, pod length and 100-seed weight showed high heritability estimates accompanied with high genetic advance.

Veeraswamy *et al.* (1973) observed variability in 25 varieties of green gram. They found high genotypic coefficient of variation for clusters

per plant, pods per plant and plant height. High heritability accompanied with high genetic advance was noticed for plant height, clusters per plant.

Malhotra *et al.* (1974) studied genetic variability in 75 varieties of green gram and reported that the characters such as clusters per plant, pods per plant, seeds per pod and 100-seed weight had high genetic advance and the efficiency of this set of discriminant function was the highest as compared to direct selection for seed yield.

Reddy (1977) reported high variability in green gram for plant height, clusters per plant, pods per plant, seeds per pod, seed weight and yield. High heritability as well as moderate expected genetic advance were noted in respect of plant height, clusters per plant, pods per plant, seeds per pod and 100-seed weight. Days to 50 per cent flowering, days to maturity and pod length exhibited high heritability but low expected genetic gain.

Chopra and Gupta (1978) observed a wide range of phenotypic variability in green gram for days to maturity, number of pods per plant, days to flowering, grain yield per plant, plant height and number of clusters per plant. A comparatively high genetic coefficient of variation (GCV) was observed in number of pods per plant, seed yield per plant and plant height. The estimate of heritability was maximum for days to flowering, days to maturity, plant height, while genetic advance was maximum for number of pods per plant.

Arunachalam (1979) studied 196 selections of Indian bean and reported that protein content was ranged from 10.79 to 28.78 per cent. Yield per plant, pod number and plant height had high genetic coefficient of variation. The heritability estimates revealed that the variability in all characters was highly heritable. Additive gene action was evident for pods per plant and pod number.

Krishnaiah *et al.* (1979) studied 20 cultivars of green gram. They reported high heritability for maturity, pod number and seed number. Genetic advance of good magnitude had been recorded for pod number, yield and seed number.

Paramasivan and Rajasekaran (1980) evaluated 90 varieties of green gram for yield and yield components. They found high genotypic coefficient of variation (GCV) for plant height and pods per plant. Heritability was high for plant height, clusters per plant, pod length, pods per plant, days to flowering, days to maturity, seeds per pod, 100-seed weight and seed yield per plant. In case of 100-seed weight, pod length, cluster number, pod number and seed yield had high heritability with high genetic advance.

Patel and Shah (1982) reported phenotypic and genotypic coefficients of variability, broad sense heritability and genetic advance in 20 strains of black gram. Pod length and plant height had high genotypic coefficients of variation, heritability and genetic advance. High heritability with low genetic advance was observed for seeds per pod, 100-seed weight and pods per plant.

Parida and Singh (1984) observed high heritability for 100-seed weight, seeds per pod and pods per plant but it was low for yield per plant. Seed yield per plant and clusters per plant had high genetic advance in the F_1 generation.

Misra (1985) studied five genetic parameters in 30 varieties of green gram. High heritability was observed for pods per plant, plant height, clusters per plant, yield per plant and days to maturity. High heritability, coupled with high genetic advance for clusters per plant, pods per plant, plant height and yield per plant, was observed.

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Javia (1986) evaluated 50 genotypes of green gram. He reported high GCV and PCV for number of pods per plant, plant height and seed yield. High heritability was seen with high genetic advance for 100-seed weight and seed yield.

Ali and Shaikh (1987) observed variability in 30 genotypes of green gram. Highest genotypic and phenotypic coefficient of variation was observed in all characters, except days to maturity and seed yield per plant. Pod length, plant height, number of clusters per plant and number of pods per plant were the most important contributors to seed yield.

Patil *et al.* (1987) studied 89 green gram varieties during kharif and revealed that variability for all the seven traits was significant. Heritability was the highest for days to flowering, followed by 100-seed weight, plant height and seeds per pod.

Ramana and Singh (1987) investigated 37 varieties of green gram in rabi and kharif seasons. High GCV was found for pods per plant and yield per plant. High heritability was observed with high genetic advance for yield per plant, pods per plant, clusters per plant and plant height. Seed weight and days to first flower had high heritability, but low values of genetic advance.

Pandey *et al.* (1988) observed pods per plant was the most variable character, followed by seed yield per plant. High heritability coupled with moderate to high genetic advance and genetic coefficient of variation was found for seed yield per plant, pods per plant and plant height.

Ilhamuddin *et al.* (1989) estimated variability, heritability and genetic advance in eight quantitative characters. Significant differences between cultivars were noted for all the characters. High genotypic and phenotypic variances were recorded for plant height and 1000-seed weight.

Genotypic and phenotypic coefficients of variation were highest for yield per plant.

Miah and Bhaora (1989) observed high value for expected genetic advance for number of days to flowering, plant height, number of pods and seeds per plant and suggested that selection would be effective using these traits.

Roquib and Patnaik (1990) observed variability in 25 fodder cowpea types and reported high estimates of heritability for plant height, number of seeds per plant, pod length, days to 50 per cent flowering, days to maturity and seed yield per plant.

Gayen *et al.* (1991) studied variability and reported that all the genotypes varied significantly with regard to the characters. Heritability for all the characters was more than 70 per cent except for the number of seeds per pod. The characters with low coefficient of variation were more responsive to selection.

Pundir *et al.* (1992) observed variability in green gram and stated that variability in terms of genotypic and phenotypic coefficients of variation indicated that the major yield components, like 100-seed weight, seeds per pod and pod length had low amount of variability. Low heritability was observed in clusters per plant, while 100-seed weight had high heritability. The characters like seeds per pod, seed yield, pods per plant and 100-seed weight had high genetic advance.

Borah and Hazarika (1995) studied genetic parameters, namely, genotypic and phenotypic variances, GCV and PCV for green gram. High genotypic variances were recorded only for plant height and number of pods per plant. High heritability along with high genetic advance and GCV values were observed for plant height, number of pods per plant, seed yield per

plant, number of clusters per plant. Days to flowering and days to maturity exhibited low estimates of genetic advance.

Veerabadhiran and Jehangir (1995) revealed that the seed yield, number of cluster and number of seeds per pod showed high genotypic coefficient of variation. High heritability was observed for plant height, days to 50 per cent flowering and number of clusters. Plant height showed highest genetic advance followed by days to flowering.

Veerabadhiran *et al.* (1996) studied genetic variation among 21 genotypes of green gram. They observed that the seed yield and plant height showed moderate genotypic coefficient of variation. High heritability coupled with high genetic advance as per cent of mean was noticed for plant height and seed yield per plant.

Byregowda *et al.* (1997) evaluated genetic variability among yield and yield components in green gram. They showed that sufficient variability was present in the seed yield and pods per plant. High heritability coupled with high genetic advance was observed for seed yield and pods per plant which was mainly attributed to additive gene action.

2.2 Correlation and path coefficient analysis

The concept of correlation was first put forward by Galton (1889) and later elaborated by Fisher (1918) and Wright (1921). In plant breeding, correlation measures the mutual relationship between yield and its component characters. Selection is done on phenotypic basis by a plant breeder. However, in quantitative characters the genotype is influenced by the environment and phenotypic expressions of traits. Hence, it is essential to measure the correlations at phenotypic and genotypic levels.

Path coefficient analysis is simply a standardized partial regression coefficient which splits the genotypic correlation coefficient into direct and indirect effects. Path analysis was initially suggested by Wright (1921) and it was applied for the first time in plant breeding by Dewey and Lu (1959). Path analysis helps in indirect selection through component characters for genetic improvement of yield. The indirect selection would be more efficient than direct selection for yield when the character has a high heritability and high correlation with yield (Searle, 1965).

Singh and Malhotra (1970 b) evaluated green gram for correlation and path coefficient analysis. They reported higher genotypic correlation coefficient than environmental correlation coefficient. Seed yield per plant had significant positive association with clusters per plant, pods per plant, seeds per pod and 100-seed weight.

Chandel *et al.* (1973) studied yield and yield components in 26 varieties of green gram. They reported that days to 50 per cent flowering, pods per plant and seed weight had direct positive effect on yield, while days to 50 per cent flowering, seeds per pod and number of pods per plant had high indirect positive effect.

Tomar *et al.* (1973) reported correlation and path coefficient among four yield components of green gram. They found that yield was genotypically positively correlated with pods per plant, pod length and seeds per pod. Path analysis indicated that pods per plant and pod length were important yield components as compared to seeds per pod.

Malhotra *et al.* (1974) observed traits association in green gram and found positive correlation of seed yield with pods per plant, seeds per pod and days to flowering. Path coefficient analysis showed that pods per

plant had the highest direct and indirect effect on seed yield per plant. The direct influence of seeds per pod towards seed yield per plant was small. However, seed yield was indirectly influenced through pods per plant.

Pokle and Patil (1975) studied path coefficient analysis in green gram. Seeds per pod had a greater direct effect on yield. It was indicated that number of seeds per pod and number of pods per plant were most important yield contributing characters than other characters.

Yohe and Poehlman (1975) reported in mung bean that there was positive and significant correlation of seed yield with number of pods per plant, 100-seed weight, plant height and number of seeds per pod.

Pokle and Nomulwar (1977) observed correlation for six characters for green gram. Fairly large number of genotypic correlations were of higher magnitude than the corresponding phenotypic correlations and lower than the environmental correlations. Plant yield was positively and significantly correlated with number of pods per plant and plant height.

Reddy (1977) evaluated correlation for yield and its components in green gram. Yield was significantly and positively correlated with clusters per plant, pods per plant and seeds per pod but negatively correlated with seed weight. Pods per plant were significantly correlated with yield, clusters per plant and seeds per pod but negatively correlated with seed weight.

Singh *et al.* (1977) reported correlation and path coefficient analysis in green gram. There was significant positive association of seed yield with clusters per plant, pods per cluster and pods per plant. Path coefficient analysis indicated that pods per plant, pods per clusters and seeds per pod had positive direct effect on seed yield per plant. Clusters per plant has negative indirect effects.

Singh *et al.* (1978) studied correlation and path analysis for seed yield and its components in green gram. High and significant phenotypic correlation of yield with days to 50 per cent flowering, days to maturity, plant height, pods per plant, pod length and seed weight was observed. Path coefficient analysis revealed that seed weight and days to 50 per cent flowering had high positive direct effect on seed yield.

Krishnaiah *et al.* (1979) reported correlation and path coefficients for yield and yield components in 20 cultivars of green gram. There were significant correlations between maturity and seed size, pod number and seed size and between seed number and seed size. Yield had no significant correlation with any yield component.

Sandhu *et al.* (1980) observed correlation coefficients between 11 characters of green gram in a collection of 435 strains. They observed positive association of seed yield with clusters per plant, pods per plant, pod length, seeds per pod and 100-seed weight.

Singh *et al.* (1980) studied correlation and path analysis in 82 varieties of green gram. They reported that pods per plant, clusters per plant and seeds per pod had positive phenotypic association with seed yield per plant. Path coefficient analysis showed that clusters per plant and pods per clusters had positive direct effect of higher magnitude on seed yield per plant.

Boomikumaren and Rathinan (1981) observed correlation coefficients in 49 diverse types of green gram. Plant height, clusters per plant, pods per cluster, pods per plant and seeds per pod were positively correlated with seed yield per plant, while pod length and 100-seed weight were negatively correlated with seed yield per plant. The seed weight showed negative correlations with all the characters except pod length.

Gupta *et al.* (1982) evaluated correlation and path coefficients between yield and eight yield contributing characters in green gram. They observed that seed yield was positively associated with days to maturity, clusters per plant, pods per plant and seeds per pod at genotypic level. The path analysis indicated that cluster per plant, pods per plant and seeds per pod were the main factors contributing for seed yield.

Liu *et al.* (1984) investigated genetic correlations and path analysis of quantitative characters in green gram. Seed weight per plant was positively correlated with plant height and cluster per plant. The 100-seed weight was negatively correlated with pod number per plant.

Parida and Singh (1984) investigated genetic correlation of quantitative characters in green gram. Pods per plant, clusters per plant and pods per cluster were correlated with each other and with yield per plant. Seeds per pod and plant height were positively and significantly correlated with yield per plant, pods per plant and clusters per plant.

Vidyadhar *et al.* (1984) evaluated 36 varieties of green gram for path analysis. Number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight and protein content showed significant positive association with seed yield. The number of cluster per plant had a significant direct effect followed by the number of seeds per pod and 100-seed weight. The protein content showed positive association with grain yield but it had a negative direct effect.

Khan (1985) studied green gram for correlation and path coefficient analysis. Number of pods were positively correlated with yield. Number of pods had a high positive direct effect on yield, while pod length and cluster number had a negative direct effect.

Choi *et al.* (1986) reported that in mung bean there was positive correlation of yield with number of pods, number of seeds per pod and negative correlation with days to flowering which was also negatively correlated with number of pods per plant.

Javia (1986) investigated correlation and path analysis in 50 genotypes of green gram. Seed yield was positively and significantly correlated with pods per plant. Path analysis revealed that pods per plant had the highest direct effect on seed yield followed by pod length and days to maturity.

Malik *et al.* (1987) studied correlation and path analysis on seed yield per plant with related characters of 40 genotypes of green gram. They showed seed yield was positively and significantly correlated with plant height, pods per plant and clusters per plant. Path analysis revealed that days to flowering and plant height had the highest direct positive effects on seed yield per plant. The direct effects of days to maturity, clusters per plant, pod length and seeds per pod on seed yield were high and negative.

Ramana and Singh (1987) reported character association in 37 varieties of green gram grown in rabi and kharif seasons. In general, phenotypic correlations were smaller than the genotypic correlations in both the seasons. Seed yield showed a significant positive correlation with plant height, pods per plant, clusters per plant and seeds per pod in both the seasons.

Patil and Deshmukh (1988) observed correlation and path coefficient analysis in mung bean. They observed that the seed yield was significantly and positively associated with 100-seed weight, seeds per pod and pods per plant. Path coefficient analysis indicated that number of days to

flowering and 100-seed weight had the greatest positive direct effect on seed yield, while, number of days to maturity and seeds per pod had negative direct effects on seed yield.

Raut *et al.* (1988) studied correlation and path analysis with 30 genotypes of green gram. The seed yield was positively correlated with number of seeds per pod and clusters per plant at the genotypic level. Path analysis indicated that 100-seed weight, number of seeds per pod, clusters per plant and pods per plant had high positive direct effect on seed yield.

Satyan *et al.* (1989) reported correlation in some quantitative characters of green gram. They showed that the seed yield was positively and significantly correlated with plant height, number of clusters per plant, number of pods per plant, number of pods per cluster and days to maturity.

Naidu and Satyanarayana (1991) studied correlation in 13-yield related characters of green gram. Significant positive correlations were found among plant height, pods per plant, seeds per pod and seed yield.

Naidu and Rosaiah (1993) reported that plant height, number of clusters, pods per plant and seeds per pod had positive correlation with seed yield.

Reddy *et al.* (1994) studied character association and path coefficient analysis in 36 varieties of green gram. They showed that the pods per plant, pods per clusters and seeds per pod had a strong positive association with seed yield. Path coefficient analysis revealed that the same yield components had a strong positive direct effect on seed yield.

Sharma and Gupta (1994) observed that seed yield was correlated with biological yield per plant, clusters per plant, pods per plant, plant height and 100-seed weight. Path analysis showed that biological yield

per plant had the greatest positive direct effect on seed yield, followed by pods per plant, days to maturity, days to flowering, 100-seed weight and pod length.

Naidu *et al.* (1994) evaluated path analysis in 20 genotypes of mung bean grown in different environments. They found that pods per plant had positive direct effects on seed yield, while clusters per plant had negative direct effects on yield.

Kumar *et al.* (1995) studied correlation and path coefficient analysis with 16 green gram genotypes. Pods per plant and 100-seed weight had significant and positive correlation with seed yield. Positive direct effects were observed for pods per plant, plant height and 100-seed weight. Hence selection based on their characters would bring improvement in seed yield in green gram.

Veerabadhiran and Jehangir (1995) studied correlation and path analysis in 24 genotypes of green gram. They observed high positive correlation values for number of pods, number of clusters and number of seeds per pod with yield and the significant inter correlations existing among themselves revealed that these characters may be considered for improvement of yield.

Golsangi *et al.* (1996) studied correlation and path analysis in cowpea. They suggested that seed yield showed significant positive association with number of pods per plant and pod length. Path coefficient analysis showed that number of pods per cluster, number of clusters per plant and pod length had positive direct effect on yield.

2.3 Genetic divergence (D^2 statistic)

Genetic diversity is a basic criterion to the crop plants, whether through natural selection or hybridization. Several methods have been developed for measuring divergence between populations using multivariate analysis such as, multiple regression (Hotelling, 1936), discriminant function (Fisher, 1936) and D^2 statistic (Mahalanobis, 1936). Out of these methods D^2 statistic is a powerful tool in specifying the degree of divergence among populations at genotypic level and to assess the relative contributions of different components to the total divergence.

Gupta and Singh (1970) observed genetic divergence in 36 strains of green gram for yield and its components, viz.., number of seeds per pod, pod length, days to 50 per cent flowering and seed weight. Seed weight and pod length contributed maximum towards the total divergence.

Narsinghani *et al.* (1978) studied genetic divergence in pea and revealed that seed size, height and days to maturity were the important characters contributing towards the divergence.

Shanmugam and Rangaswamy (1982) studied genetic divergence in 45 varieties of green gram. They found that the grouping of genotypes in cluster was not related to geographical origin and based on average inter-cluster distances. The clusters XV, XVI and XIII were found to be highly divergent from all the other clusters.

Das and Gupta (1984) evaluated multivariate analysis by applying Mahalanobis's D^2 statistic and Cannonical analysis in black gram and did not find any relationship between genetic divergence and geographical origin. Thousand-grain weight made the greatest contribution to local divergence.

Singh and Tripathi (1985) observed a genetic divergence in 100 pea germplasms. They found that grouping of varieties in different clusters was not related to their geographical origin. Among the 14 clusters, the maximum inter-cluster distance was observed between cluster I and XIV, followed by cluster VII and XIV. Cluster XI was more diverse than others.

Marangappanavar (1986) studied multivariate analysis in 46 genotypes of cowpea and reported that 32 Indian genotypes occurred in 36 to 16 clusters, while 14 foreign varieties occurred in 10 clusters and stated that inter cluster spatial patterns were not consistent with varietal geographical distributions.

Misra (1986) studied genetic divergence in 30 Indian varieties of green gram and found that cluster analysis assigned the varieties to 10 groups and revealed that genetic diversity was not related to geographical diversity.

Ramana and Singh (1987) observed genetic divergence in 39 genotypes of mung bean grown in rabi and kharif seasons and reported that a total of 21 genotypes occurred in cluster I in the rabi and 28 in cluster III in the kharif; a considerable number of genotypes was common to cluster I in both seasons. Days to flowering and 100-seed weight contributed most to genetic divergence in the kharif and rabi seasons, respectively.

Singh and Pathak (1987) studied genetic divergence in 20 genotypes of mung bean. Genotypes were grouped into six clusters and the members of each clusters were geographically unrelated. Cluster II with 8 genotypes, had the maximum values for pods per plant and seed yield per plant. They recommended the use of genotypes from two divergent clusters in hybridization to obtain useful segregates in subsequent generations.

Thiagarajan *et al.* (1988) studied genetic divergence in seven parents and their hybrids in cowpea. The genotypes were grouped into 7 clusters based on D^2 values. The characters which contributed to most genetic divergence were days to 50 per cent flowering, 100-seed weight and plant height.

Natarajan *et al.* (1988) observed genetic diversity in 45 genotypes of green gram. The genotypes were grouped into five clusters with seed weight and days to flowering making the greatest contribution to divergence.

Natharajan and Palaniswamy (1990) reported genetic divergence in eight genotypes and 15 hybrids of mung bean indicating that petiole weight, stem weight, root weight and harvest index as the main source of genetic divergence.

Sonawane and Patil (1991) evaluated 47 indigeneous and 17 exotic strains of cowpea and reported that there is a substantial genetic diversity between the strains with D^2 values and genotypes were grouped into 6 clusters. The clustering pattern revealed that genetic divergence was not necessarily associated with geographical diversity. They suggested hybridization programme on the basis of inter cluster divergence and cluster means.

Birari and Ghanekar (1992) studied genetic diversity in 36 genotypes of Indian bean. They suggested that CO.5 and NO. 692 were highly divergent from all others for their yields. Hebbal 3 for earliness, CO.1 for high seed number and CO.269, EC 1876 and Golangaon local for their seed quality. Cannonical analysis supported the divergence pattern obtained by D^2 analysis.

Genetic diversity in seven genotypes of mung bean and their 21 F_1's were studied by Chandra *et al.* (1993) and concluded that the plant height, number of clusters per plant and number of pods per plant had contributed most to genetic divergence.

Holkar and Yadava (1995) observed genetic divergence in 36 genotypes of mung bean and suggested that the biological yield, harvest index and number of pods per plant made the greatest contribution to genetic divergence and suggested for use as selection criterion for improvement of seed yield.

Veerabadhiran *et al.*(1996) studied genetic divergence in 21 genotypes of green gram. The genotypes were grouped into 3 clusters. Maximum inter cluster distance was observed between cluster I and II indicating their divergence in origin.

MATERIALS AND METHODS

III MATERIALS AND METHODS

3.1 Location and climatic condition

The present experiment was conducted at the Regional Pulse Research Station, Gujarat Agricultural University, Navsari Campus, Navsari during summer 1996. The soil of the experimental plot was heavy black with pH 7.3 to 7.6. Geographically, Navsari is situated at 20°-37′ N latitude and 72°-54′ E longitude and at an altitude of 11.98 meters above mean sea level. The meteorological data for the summer season are given in Appendix I.

3.2 Experimental material

The experimental material for the present investigation consisted of eighty six genotypes of green gram (*Vigna radiata* (L.) Wilczek) obtained from the germplasm maintained at the Gujarat Agricultural University, Sardar Krushinagar. The details of the materials used in the present investigation are given in Table 3.2.1.

3.3 Experimental details

The experiment consisting of eighty six genotypes was laid out in randomized block design (RBD) with three replications. Each plot consisted of 4 rows of 3 meters long spaced at 30 cm. All recommended agronomic practices and plant protection measures were followed for successful raising of the crop.

3.4 Characters studied

For recording the observations, five plants were randomly selected in each genotype. The details regarding observations are as under.

Table 3.2.1 : Details of the green gram genotypes

Sr. No.	Entry	Pedigree	Source
1.	GM-9018	GUJ-1 x TAP-7	G.A.U., Sardar Krushinagar
2.	GM-9110	GM-85-86 x Pusa 105	"
3.	GM-9321	Sel. from Bechraji local	"
4.	GM-9307	PDM-84-143 x MGD-418	"
5.	GM-9208	Local selection	"
6.	GM-9411	Sel. from GM-8562	"
7.	GM-84-13	GUJ-2 x TAP-7	"
8.	GM-9206	GM-85-68 x ML-337	"
9.	GM-9023	PDM-54 x TAP-7	"
10.	GM-9406	PDM-84-143 x MGD-418	"
11.	GM-9317	Sel. from MGD-164	"
12.	GM-88-44	IPS-44 Sel.	"
13.	HUM-2	-	Banaras Hindu University, BHU, Varanasi
14.	GM-9315	Sel. from MGD-855	G.A.U., Sardar Krushinagar
15.	GM-9402	RMG-275 x ML-131	"
16.	GM-8801	Sel. from GM-82-13	"
17.	GM-9403	GM-83-1 x MGD-534	"
18.	GM-8906	IPS-10 x K-851	"
19.	Guj-3	PIMS-4 x 9011	"
20.	GM-86-14	GUJ-1 x Pusa-8732	"
21.	GM-9410	Sel. from GM-8907	"
22.	GM-8213	K-851 x ML-69	"
23.	GM-9106	Sel. from GUJ-2	"
24.	GM-9316	Sel. from MGD-170	"
25.	HUM-7	-	Banaras Hindu University, BHU, Varanasi
26.	GM-87-16	(PIMS-4 x ML-5) x (T-44 x ML-5)	G.A.U., Sardar Krushinagar
27.	GM-84-4	TAP-7 x T-44	G.A.U., Sardar Krushinagar
28.	GM-9404	GM-82-13 x RMG-275	"

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Table 3.2.1 (Contd.....)

Sr. No.	Entry	Pedigree	Source
29.	GM-9302	PDM-84-143 x K-851	"
30.	GM-9006	Sel. from local	"
31.	GM-9304	PDM-54 x MGD-418	"
32.	PS-16	-	C.S.A.U., Kanpur
33.	GM-9202	GM-82-13 x Pusa 8731	G.A.U., Sardar Krushinagar
34.	GM-84-26	K-851 x PIMS-4	"
35.	GM-88-35	Sel. from IPS-6	"
36.	GM-9419	Local selection	"
37.	GM-9008	PIMS-4 x K-851	"
38.	GM-9310	PDM-54 x TAP-7	"
39.	GM-9320	Sel. from Bechraji local	"
40.	GM-9408	Sel. from GM-9011	"
41.	GM-9318	Sel. from MGD-10	"
42.	GM-9010	PIMS-4 x ML-5	"
43.	GM-9415	GUJ-1 x ML-537	"
44.	K-851	-	C.S.A.U., Kanpur
45.	GM-9303	PDM-54 x MGD-418	G.A.U., Sardar Krushinagar
46.	GM-9306	GM-85-60 x RMG-275	"
47.	GM-9104	GM-85-65 x ML-406	"
48.	GM-9307	PDM-84-143 x MGD-418	"
49.	GM-9207	GM-87-33 x MGD-340	"
50.	GM-9409	Sel. from GM-8560	"
51.	GM-9311	GUJ-1 x Vijapur local	"
52.	GM-9317	MGD-416 Sel.	"
53.	GM-8904	K-851 x ML-5	"
54.	GM-9103	GM-85-16 x Pusa-105	G.A.U., Sardar Krushinagar
55.	GM-9412	Sel. from GM-9108	"
56.	GM-84-6	K-851 x PIMS-4	"
57.	GM-86-19	Sel. from GUJ-1	"
58.	GM-9420	Local selection	"

Table 3.2.1 (Contd.....)

Sr. No.	Entry	Pedigree	Source
59.	GM-86-17	GUJ-1 x Pusa-105	"
60.	GM-9407	PDM-84-143 x MGD-418	"
61.	GM-9413	Sel. from GM-8904	"
62.	GM-9401	RMG-275 x ML-131	"
63.	Pusa-9072	-	IARI, New Delhi
64.	GM-9111	Sel. from GM-88-33	G.A.U., Sardar Krushinagar
65.	GUJ-2	Local selection	"
66.	GM-9002	GUJ-2 x MH-309	"
67.	GM-9305	GM-82-13 x RMG-275	"
68.	GM-88-10	Sel. from GM-82-13	"
69.	GM-9309	GM-82-7 x MUM-2	"
70.	GM-9314	Sel. from MGD-186	"
71.	GM-9001	PIMS-4 x K-851	"
72.	GM-9308	GM-85-60 x Pusa-131	"
73.	GM-9405	GM-82-13 x RMG-275	"
74.	GM-9301	PDM-84-143 x K-851	"
75.	GM-9021	PDM-54 x TAP-7	"
76.	GM-3	-	"
77.	LGG-472	-	P.A.U., Ludhiana
78.	RMG-337	-	Navgaon (Rajasthan)
79.	RUM-120	-	"
80.	RUM-112	-	Navgaon (Rajasthan)
81.	RUM-351	-	"
82.	Pusa-9531	-	IARI, New Delhi
83.	Pusa-9532	-	"
84.	Pusa-9571	-	"
85.	CO-4	-	TAU, Coimbatore
86.	TARM-1	-	BARC, Trombay

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3.4.1 Days to 50 % flowering

The number of days from date of sowing to date of appearance of flower in 50 per cent plants were recorded.

3.4.2 Days to maturity

The total number of days from date of sowing to date of maturity in plants was recorded.

3.4.3 Plant height (cm)

The height of plant was recorded in centimeters from the base of main shoot to the tip of main shoot at maturity.

3.4.4 Number of clusters per plant

The peduncles which possessed one or more pods were considered as clusters per plant.

3.4.5 Number of pods per cluster

Total pods per plant divided by the number of clusters per plant represented the number of pods per cluster.

3.4.6 Number of pods per plant

Total number of pods on individual plant was recorded.

3.4.7 Number of seeds per pod

Total number of seeds per pod was counted from randomly selected plant.

3.4.8 Pod length (cm)

It was measured in centimeters from the base to the tip of the pod.

3.4.9 100-seed weight (g)

Weight of randomly selected hundred seeds was recorded in grams on electronic balance.

3.4.10 Seed yield per plant (g)

The total seeds obtained from each selected plant was weighed in grams and the average was recorded.

3.4.11 Protein content (%)

Protein per cent was estimated by using semi micro Kjeldahl method (Jackson, 1967) at Department of Agriculture Chemistry, N.M.College of Agriculture, Navsari.

Abbreviations :

The following abbreviations are used for various terms in this dissertation :

1.	Genotypic variance	$\sigma^2 g$
2.	Phenotypic variance	$\sigma^2 p$
3.	Error variance	$\sigma^2 e$
4.	Standard error	S.E.
5.	Standard error of mean	S.Em.
6.	Critical difference	C.D.

7.	Coefficient of variation	C.V.
8.	Genotypic coefficient of variation	GCV
9.	Phenotypic coefficient of variation	PCV
10.	Heritability (broad-sense)	H(b)
11.	Genetic advance	GA
12.	Co-variance	$Co\sigma^2$
13.	Genotypic correlation coefficient	rg
14.	Phenotypic correlation coefficient	rp
15.	Environmental correlation coefficient	re
16.	Genetic divergence	D^2
17.	Number of replications	r
18.	Grams	g
19.	Centimeters	cm

3.5 Statistical procedure

Statistical analysis was carried out using mean values of five randomly selected plants. Various genetic parameters, viz., variability, correlation, path coefficient and D^2-value were estimated.

The data recorded for different characters were subjected to analysis of variance with the formula suggested by Panse and Sukhatme (1978).

Analysis of variance of the experimental design :

Analysis of variance

Source of variation	D.F.	Mean square	Expected mean square
Replications	(r-1)	M_1	$\sigma^2e + g\sigma^2r$
Genotypes	(g-1)	M_2	$\sigma^2e + r\sigma^2g$
Error	(r-1).(g-1)	M_3	σ^2e

Where,

g = Number of genotypes

r = Number of replications

M_1, M_2, M_3 = Mean square of replication, genotypes and error, respectively

3.5.1 Estimate of coefficient of variability

All the statistical analyses were carried out at the Computer Centre of N.M. College of Agriculture, Navsari.

3.5.1.1 Genotypic variance (σ^2g)

It is the variance contributed by genetic causes or the occurrence of differences among individuals due to differences in their genetic make up. It was calculated by the formula given by Miller *et al.* (1958) for randomized block design.

$$\sigma^2g = \frac{M_2 - M_3}{r}$$

Where,

σ^2g = Genotypic variance

M_2 = Mean square of treatments (genotypes)

M_3 = Environmental (error) mean square

r = Number of replications

3.5.1.2 Phenotypic variance (σ^2p)

It is the sum of variances contributed by genetic causes and environmental factors. It was calculated as under :

$$\sigma^2p = \sigma^2g + \sigma^2e$$

Where,

σ^2p = Phenotypic variance

σ^2g = Genotypic variance

σ^2e = Error variance

3.5.1.3 Environmental variance (σ^2e)

The mean square for error represented the variation attributed to environmental causes.

$$\sigma^2e = M_3$$

Where,

σ^2e = Error variance

M_3 = Error mean sum of square

3.5.2 Parameters of variability

(i) Mean

The mean value of each character was worked out by dividing total by corresponding number of observations.

$$\bar{X} = \frac{\sum Xij}{n}$$

Where,

$\bar{X}$ = Mean

$\sum Xij$ = Any observation in i^{th} treatment and j^{th} replication

n = Number of observations

(ii) Range

It is difference between the lowest and the highest value for each character.

(iii) Standard error (S.Em.)

Standard error of mean was calculated with the help of error mean square from analysis of variance table.

$$S.Em = \left[\frac{\sigma^2 e}{r} \right]^{0.5}$$

Where,

S.Em. = Standard error of mean

$\sigma^2 e$ = Error mean square

r = Number of replication

(iv) Critical difference (C.D.)

Critical difference for all the characters was calculated; to compare treatment means by following formula

C.D. = S.Em. x $(2)^{0.5}$ x 't' at 5 % error d.f.

Where,

S.Em. = Standard error of the difference of treatment means to be compared.

't' = Tabulated value of 't' at 1 per cent or 5 per cent degree of freedom of error mean square

(v) Coefficient of variation (C.V.)

The coefficient of phenotypic and genotypic variation was calculated by formula suggested by Burton (1952).

$$C.V.\% = \left[\frac{\sigma^2 e}{\bar{X}} \right]^{0.5} \times 100$$

(a) Phenotypic coefficient of variation (PCV)

$$PCV\ \% = \left[\frac{\sigma^2 p}{\bar{X}} \right]^{0.5} \times 100$$

(b) Genotypic coefficient of variation (GCV)

$$GCV\ \% = \left[\frac{\sigma^2 g}{\bar{X}} \right]^{0.5} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic standard deviation

$\sigma^2 g$ = Genotypic standard deviation

$\bar{X}$ = Grand mean of character

(vi) Heritability (broad-sense) H(b)

Heritability means the proportion of variability which is heritable in nature to total variability. It is due to genetic causes whereas non-heritable variability is contributed by error variance.

Broad sense heritability was calculated by the formula suggested by Burton and Devane (1953) as under.

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

Where,

H(b) = Heritability (broad-sense)

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

(vii) Genetic advance (GA)

It means improvement in performance of selected lines over the original population.

The formula given by Johnson *et al.* (1955) was used to calculate genetic advance.

$$GA = H(b) \times K \times \sigma p$$

Where,

GA = Genetic advance

H(b) = Heritability (broad-sense)

K = Selection differential (K = 2.06 at 5 % selection intensity Allard, 1960)

σp = Phenotypic standard deviation

(viii) Genetic advance expressed as percentage of mean

The expected genetic gain expressed in percentage of mean was calculated by the method suggested by Johnson *et al.* (1955).

$$\text{Genetic advance (in \% of mean)} = \frac{GA}{\bar{X}} \times 100$$

Where,

$\underline{G}A$ = Expected genetic advance

$\bar{X}$ = Mean of character under study

3.5.3 Correlation coefficient

For phenotypic, genotypic and environmental correlation coefficients for all the characters were worked out. The data were subjected to covariance analysis from which different component of mean sum of product were estimated.

Analysis of covariance

Source of variation	D.F.	Mean square	Expected mean square
Replications	(r-1)	-	-
Genotypes	(g-1)	MS_1	σ^2e 1.2 + $r\sigma^2g$ 1.2
Error	(r-1).(g-1)	MS_2	σ^2e 1.2

Where,

r = Number of replications

g = Number of genotypes

$Co\sigma^2$ = Covariance

(i) Genotypic covariance ($Co\sigma^2g$ 1.2)

$$Co\sigma^2g\ 1.2 = \frac{MS_1 - MS_2}{r}$$

(ii) Phenotypic covariance ($Co\sigma^2p$ 1.2)

$$Co\sigma^2p\ 1.2 = Co\sigma^2g\ 1.2 + MS_2$$

(iii) Environmental covariance ($Co\sigma^2e$ 1.2)

$$Co\sigma^2e\ 1.2 = MS_2$$

Where,

MS_1 = Mean sum of product due to genotypes between character first and second

MS_2 = Mean sum of product due to error between character first and second

r = Number of replications

The genotypic, phenotypic and error variance and covariances were used to calculate genotypic and phenotypic correlation coefficient. The general formula may be expressed as follows :

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$$r\ 1.2 = \frac{Co\sigma^2\ 1.2}{\sqrt{(\sigma^2_{\ 1})(\sigma^2_{\ 2})}}$$

Where,

r 1.2 = Correlation coefficient for a pair of trait 1 and 2

$Co\sigma^2$ 1.2 = Covariance for a pair of trait 1 and 2

$\sigma^2_{\ 1}, \sigma^2_{\ 2}$ = Variance for trait 1 and 2

(a) Genotypic correlation coefficient (rg 1.2)

$$rg\ 1.2 = \frac{Co\sigma^2\ g\ 1.2}{\sqrt{(\sigma^2_{\ g1})(\sigma^2_{\ g2})}}$$

(b) Phenotypic correlation coefficient (rp 1.2)

$$rp\ 1.2 = \frac{Co\sigma^2\ p\ 1.2}{\sqrt{(\sigma^2_{\ p1})(\sigma^2_{\ p2})}}$$

Where,

$Co\sigma^2$ g 1.2 and $Co\sigma^2$ p 1.2 are genotypic and phenotypic covariance for a pair of trait 1 and 2, respectively

$\sigma^2_{\ g1}$ and $\sigma^2_{\ g2}$ are genotypic variance for trait 1 and 2, respectively and $\sigma^2_{\ p1}$ and $\sigma^2_{\ p2}$ are phenotypic variance for trait 1 and 2, respectively

3.5.4 Path coefficient analysis

The genotypic correlation coefficient was used to calculate the path coefficients. The analysis was carried out by the method suggested by Dewey and Lu (1959).

The genotypic correlation among the eleven characters were partitioned into their direct and indirect effects on causal variable and their direct and indirect effects on yield were estimated as under.

The path coefficients were obtained by solving a set of simultaneous equations as below :

$$r_{ny} = P_{ny} + r_{n2} \cdot P_{2y} + r_{n3} \cdot P_{3y} + \ldots\ldots\ldots + r_{nx} \cdot P_{xy}$$

Where,

r_{ny} = represents correlation between one component character and yield

P_{ny} = represents path coefficient between one character and yield

$r_{n2}, r_{n3}, \ldots\ldots, r_{nx}$ = represents correlation coefficient between that character and other yield component in term.

The following genotypic correlation matrix was formed :

Matrix-A Matrix-B Matrix-C

$$\begin{bmatrix} r_1y \\ r_2y \\ r_3y \\ \vdots \\ \vdots \\ r_ny \end{bmatrix} = \begin{bmatrix} r_{11} & r_{12} & r_{13} \ldots\ldots & r_{1n} \\ r_{21} & r_{22} & r_{23} \ldots\ldots & r_{2n} \\ r_{31} & r_{32} & r_{33} \ldots\ldots & r_{3n} \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ r_{n1} & r_{n2} & r_{n3} \ldots\ldots & r_{nn} \end{bmatrix} \times \begin{bmatrix} p_1y \\ p_2y \\ p_3y \\ \vdots \\ \vdots \\ p_ny \end{bmatrix}$$

or A = B x C

Where,

$r_{12} = r_{21}$ and so on and

r_{1y} = correlation between first component character and yield

The technique given by Goulden (1962) was followed for inversion of 'B' matrix using partitioning method of matrix inversing the following correlation matrix as per Doolittle method given by Steel and Torrie (1960).

Path coefficient (P_{ij}) was obtained as follows :

$$P_{ij} = (B^{-1}) = A$$

Where, (B^{-1}) is the inverse of mutual correlation matrix of character

The indirect effect for a particular character through other character was obtained by multiplication of direct path and particular correlation coefficient between those two characters, respectively.

$$\text{Indirect effect} = r_{ij} \times P_{ij}$$

Where,

$i = 1, 2, 3, \ldots\ldots, n$

$j = 1, 2, 3, \ldots\ldots, n$

$P_{ij} = P_{1y} \times P_{2y} \times P_{3y} \times \ldots\ldots \times P_{ny}$

The residual effect i.e. variation in dependent character yield due to uncontrolled-causes was estimated by subtracting this value from unity.

$$R = \sqrt{1 - (P_n r_n)}$$

3.5.5.1 Wilk's criterion

After testing the difference in regard to individual character through 'Anova' a simultaneous test of significant difference in regard to the pooled effect of the eleven characters was carried out using Wilk's criterion (Wilk's, 1932 and Rao, 1952).

$$\text{Wilk's criterion} = \frac{|E|}{|E + V|}$$

$$= \frac{\text{Determinant of error sum of squares and sum of product matrix}}{\text{Determinant of (error + genotype) sum of squares and sum of product matrix}}$$

3.5.5.2 D^2 statistics

Rao (1952) described the Multivariate analysis of genetic divergence using Mahalanobis's D^2 statistic. Transformation of original means of various characters (X_i's) to uncorrelated variates (Y_i's) was carried out by pivotal condensation as the common dispersion matrix calculated on computer. This made D^2 value as a simple sum of squares of differences in transformed values for various characters. The generalised distance between any two population is defined as :

$$D^2_p = b_1d_1 + b_2d_2 + \ldots\ldots + b_pd_p$$

Where,

$X_1, X_2, X_3 \ldots\ldots, X_p$ as a multiple measurements available on each individual $d_1d_2 \ldots\ldots$, dp as $X_1^{-1} - X_1^{-2}$, $X_2^{-1} - X_2^{-2} \ldots\ldots$ $Xp^{-1} - Xp^{-2}$, respectively, being the difference in the mean of two populations.

In terms of variance and covariance, the D^2 value is obtained as follow :

$$D^2_{\ p} = Wij\ (Xi^{-1} - Xi^{-2})\ (Xj^{-1} - Xj^{-2})$$

Where,

Wij = is the inverse estimated variance covariance matrix.

3.5.5.3 Determination of clusters

No formal rules can be laid down for formation of clusters because a cluster is not a well defined term. The only criterion appears to be that any two groups belonging to the same cluster should atleast on an average show smaller D^2 than those belonging to two different clusters. There are several methods available for the formation of clusters viz., Tocher's method (Rao, 1952).

After the formation of clusters average intra cluster distance was calculated by using the formula,

$$\frac{\sum Di^2}{n}$$

Where,

$\sum Di^2$ = Sum of distance between all possible combinations of the population included in the cluster

n = Number of populations in a cluster

The inter-cluster distance was calculated by measuring the distance between cluster-I and II, between cluster-I and III, between cluster-II and III and so on. Likewise one by one clusters were taken and their distances from other were calculated. For graphical presentation average intra and inter-cluster D^2 values were used to obtain mutual relationship between clusters.

EXPERIMENTAL RESULTS

IV EXPERIMENTAL RESULTS

The results obtained in the present investigation on variability, correlation, path coefficient and genetic divergence in green gram (*Vigna radiata* (L.) Wilczek) are presented under the following headings :

4.1 Analysis of variance

4.2 Variability

4.3 Heritability and genetic advance

4.4 Correlation coefficient

4.5 Path coefficient analysis

4.6 Genetic divergence

4.1 Analysis of variance

The analyses of variance indicating the mean sum of squares for all the eleven characters studied, are summarized in Table 4.1. The genotypic differences were highly significant for all the eleven characters under study indicating considerable amount of genetic variability among the genotypes tested in the present study.

The mean values of different genotypes in respect of eleven characters studied are presented in Appendix - II.

4.2 Variability

The range, mean, phenotypic, genotypic and environmental variances, phenotypic and genotypic coefficients of variation, heritability and expected genetic advance as percentage of mean for eleven characters are presented in Table 4.2.

Table 4.1 : Analysis of variance for different characters in Greengram (*Vigna radiata* (L.) Wilczek)

Source of variance	D.F.	Seed yield per plant	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of cluster per plant	No. of pods per clusters	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100 seed weight (g)	Protein content (%)
Replication	2	0.470	0.703	6.375	34.500	0.351	0.042	0.133	0.209	3.159	0.004	-0.008
Treatment	85	13.366**	45.033**	61.397**	338.865**	8.448**	4.325**	491.125**	5.482**	8.475**	0.702**	5.275**
Error	170	0.019	5.597	5.713	5.004	0.325	0.341	3.021	0.038	1.087	0.004	0.005
S.Em. ±		0.113	1.932	1.951	1.826	0.465	0.477	1.419	0.160	0.861	0.054	0.050
C.D. at 5%		0.314	5.381	5.430	5.082	1.294	1.336	3.954	0.445	2.375	0.150	0.167
C.V. %		2.313	6.119	3.326	5.980	9.48	10.859	5.569	3.034	10.039	1.391	0.308

** - Significant at p = 0.01

Table 4.2 : Range, mean, genotypic, phenotypic and environmental variances, GCV, PCV, $H^2(b)$ and G.A. as % of $\bar{X}$ for different characters in greengram

Characters	Range	Mean	Genotypic variance	Phenotypic variance	Environmental variance	GCV (%)	PCV (%)	$H^2(b)$ (%)	G.A. as % of $\bar{X}$
Seed yield/ plant (g)	2.62 - 12.62	6.003	4.449	4.468	0.019	35.137	35.212	99.57	72.22
Days to 50 % flowering	31.33 - 54.89	38.660	13.145	18.742	5.597	9.378	11.198	70.14	16.18
Days to maturity	55.99 - 86.43	71.860	18.561	24.274	5.713	5.995	6.856	76.46	10.79
Plant height (cm)	13.90 - 59.80	37.406	111.287	116.291	5.004	28.202	28.829	95.70	56.83
No. of clusters per plant	3.00 - 10.33	6.011	2.708	3.033	0.325	27.376	28.973	89.28	53.28
No. of pods per cluster	3.27 - 8.73	5.381	1.328	1.669	0.341	21.416	24.009	79.57	39.35
No. of pods per plant	12.00 - 79.97	31.211	162.701	165.722	3.021	40.868	41.246	98.177	83.42
Pod length (cm)	4.17 - 10.37	6.464	1.815	1.853	0.038	20.842	21.059	97.95	42.49
No. of seeds per pod	7.23 - 14.57	10.387	2.463	3.550	1.087	15.109	18.139	69.38	25.93
100-seed weight (g)	3.72 - 6.01	4.721	0.233	0.237	0.004	10.225	10.312	98.31	20.88
Protein content (%)	21.30 - 25.91	23.854	1.757	1.762	0.005	5.557	5.565	99.72	11.43

4.2.1 Seed yield per plant (g)

The genotypic variation for seed yield per plant were found to be highly significant. The maximum seed yield per plant was recorded for GM-9304 (12.62 g), followed by GM-9303 (10.77 g) and GM-9320 (10.88 g). On the other hand, minimum seed yield per plant was recorded for GM-84-6 (2.62 g), followed by GM-9405 (2.63 g) and TARM-1 (2.77 g). The overall mean seed yield per plant was 6.003 g. The genotypic, phenotypic and environmental variances were 4.449, 4.468 and 0.019, respectively. The estimates of genotypic and phenotypic coefficients of variation were high (GCV = 35.137 % and PCV = 35.212 %).

4.2.2 Days to 50 % flowering

The minimum days to 50 per cent flowering was recorded for genotype GM-8906 (31.33 days), followed by GM-9420 (32.67 days) and GM-9303 (32.68 days), whereas maximum days to 50 per cent flowering was recorded for Rum-120 (54.89 days) , followed by RMG-337 (54.22 days) and CO-4 (50.67 days) with an overall average flowering days of 38.66. The genotypic, phenotypic and environmental variances were 13.145, 18.742 and 5.597, respectively. The genotypic and phenotypic coefficients of variation were small (GCV = 9.378 % and PCV = 11.198 %).

4.2.3 Days to maturity

The early maturing genotype was GM-8906 (55.99 days), followed by K-851 (57.44 days) and GM-9413 (62.00 days) and the late maturing genotype was RMG-337 (86.43 days), followed by Co-4 (85.33 days) and RUM-120 (84.77 days) with an average of 71.860 days. The genotypic, phenotypic and environmental variances were 18.561, 24.274 and

5.713, respectively. The genotypic and phenotypic coefficients of variation were small (GCV = 5.995 % and PCV = 6.856 %).

4.2.4 Plant height (cm)

The variation observed among the genotypes for this character was moderate. The dwarfest genotype was GM-9405 (13.90 cm), followed by GM-9410 (18.00 cm) and GM-9002 (19.73 cm). On the other hand, the tallest genotype was GM-9103 (59.80 cm), followed by CO-4 (58.43 cm) and GM-9419 (57.90 cm) with mean plant height 37.406 cm. The genotypic, phenotypic and environmental variances were 111.287, 116.291 and 5.004, respectively. The genotypic and phenotypic coefficients of variation were high (GCV = 28.202 % and PCV = 28.829 %).

4.2.5 Number of clusters per plant

This trait had a large range of variation from 3.00 to 10.33 with an average of 6.011. The maximum number of clusters was recorded in genotype GM-9409 (10.33), followed by GM-9304 (9.87) and RUM-120 (9.40). The minimum number of clusters was recorded in genotype GM-9314 (3.00), followed by GM-9002 (3.36) and GM-9311 (3.30). The genotypic, phenotypic and environmental variances were 2.708, 3.033 and 0.325, respectively. The genotypic and phenotypic coefficients of variation were high (GCV = 27.376 % and PCV = 28.973 %).

4.2.6 Number of pods per cluster

The magnitude of variability for this trait was small. The average number of pods per cluster was 5.381. The highest number of pods per cluster was observed in genotype GM-9208 (8.73), followed by GM-9412 (7.87) and CO-4 (7.50), while the lowest was observed in genotype GM-

9103 (3.27) followed by GM-88-10 (3.46) and GM-9314 (3.33). The genotypic, phenotypic and environmental variances were 1.328, 1.669 and 0.341, respectively. The genotypic and phenotypic coefficients of variation were high (GCV = 21.416 % and PCV = 24.009 %).

4.2.7 Number of pods per plant

This trait showed wide range of variation from 12.00 to 79.97 pods per plant with mean number of pods 31.211. The maximum number of pods per plant was recorded for genotype GM-9208 (79.97), followed by GM-8213 (76.40) and GM-9303 (60.13). On the other hand, minimum number of pods per plant was recorded for genotype GM-9018 (12.00), followed by GM-9002 (13.90) and RMG-337 (15.00). This character had the maximum genotypic and phenotypic variances out of all the characters (Vg = 162.701, Vp = 165.722 and Ve = 3.021). The values of genotypic and phenotypic coefficients of variation were also high (GCV = 40.868 % and PCV = 41.246 %).

4.2.8 Pod length (cm)

The pod length ranged from 4.17 to 10.37 cm with mean pod length 6.464cm. The maximum pod length was exhibited by the genotype GUJ-2 (10.37 cm) followed by GM-9308 (9.40 cm) and RMG-337 (9.23 cm). The minimum pod length was exhibited by the genotype GM-9408 (4.17 cm) followed by GM-9303 (4.20 cm) and GM-9410 (4.26 cm). The genotypic, phenotypic and environmental variances were 1.815. 1.853 and 0.038, respectively. The estimates of genotypic and phenotypic coefficient of variation were high (GCV = 20.842 % and PCV = 21.059 %).

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4.2.9 Number of seeds per pod

The number of seeds per pod ranged from 7.73 to 14.57 with an average of 10.387. The highest number of seeds per pod was observed in genotype GM-9420 (14.27) followed by GUJ-2 (13.67) and Pusa-9532 (13.60). The lowest number of seeds per pod was observed in genotype GM-9311 (7.83) followed by GM-9106 (8.00) and GM-9305 (8.03). The genotypic, phenotypic and environmental variances were 2.463, 3.550 and 1.087 respectively. The genotypic and phenotypic coefficients of variation were medium (GCV = 15.109 % and PCV = 18.139 %).

4.2.10 100-seed weight (g)

The range exhibited for 100-seed weight is from 3.72 to 6.01 g with mean test weight 4.721 g. The maximum seed weight was recorded for genotype GM-9402 (6.01 g) followed by RUM-120 (5.73 g) and GM-9111 (5.96 g). The minimum seed weight was recorded for genotype TARM-1 (3.72 g) followed by GM-9208 (3.89 g) and GM-9412 (3.96 g). The genotypic, phenotypic and environmental variances were small (0.233, 0.237 and 0.004, respectively). The genotypic and phenotypic coefficients of variation were medium (GCV = 10.225 % and PCV = 10.312 %).

4.2.11 Protein content (%)

Protein content ranged from 21.30 (GM-88-44) to 25.91 (GM-9002) per cent with mean value of 23.854 per cent. The genotypic, phenotypic and environmental variances were 1.757, 1.762 and 0.005, respectively. The estimates of genotypic and phenotypic coefficients of variation were small (GCV = 5.557 % and PCV = 5.565 %).

4.3 Heritability and expected genetic advance in per cent of mean

The estimates of heritability in broad sense [$H^2(b)$] for all the characters under study are presented in Table 4.2. High estimates of heritability were recorded by protein content (99.72 %) followed by seed yield per plant (99.57 %), 100-seed weight (98.31 %), number of pods per plant (98.17 %), pod length (97.95 %), plant height (95.70 %), number of clusters per plant (89.28 %), number of pods per cluster (79.57 %), days to maturity (76.46 %) and days to 50 per cent flowering (70.14 %). Moderate heritability was observed for the number of seeds per pod (69.38 %).

The estimates of expected genetic advance in respect of different characters at selection intensity of 5 per cent were calculated. Since these values are not comparable, they were expressed as expected genetic advance in percentage of mean and are presented in Table 4.2. It ranged from 83.42 (number of pods per plant) to 10.79 (days to maturity) per cent. The very high genetic advance expressed as percentage of mean was obtained for seed yield per plant (72.22 %), plant height (56.83 %), number of clusters per plant (53.28 %), while the remaining characters had shown moderate to low genetic advance expressed as percentage of mean.

4.4 Correlation coefficient

The correlation coefficients between seed yield and its components and among the component characters were estimated at phenotypic and genotypic levels. The phenotypic (r_p) and genotypic (r_g) correlation coefficients of eleven different characters are presented in Table 4.3.

Table 4.3 : Phenotypic and genotypic correlation coefficients among eleven characters in greengram

Characters	(r)	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100-seed weight (g)	Protein content (%)
Seed yild/ plant (g)	P	-0.021	-0.152	0.405**	0.414**	0.263*	0.317**	0.011	0.228*	-0.008	0.102
	G	-0.016	-0.168	0.415**	0.441**	0.296**	0.320**	0.011	0.274**	-0.008	0.103
Days to 50 % flowering	P		0.452**	-0.101	0.170	0.096	-0.153	0.164	-0.175	0.127	-0.061
	G		0.642**	-0.101	0.216*	0.135	-0.183	0.198	-0.230*	0.156	-0.073
Days to maturity	P			-0.134	0.148	0.061	-0.090	0.056	-0.100	0.024	0.021
	G			-0.150	0.186	0.084	-0.103	0.069	-0.166	0.029	0.024
Plant height (cm)	P				0.324**	0.159	0.365**	-0.086	0.186	-0.380**	-0.006
	G				0.342**	0.184	0.373**	-0.089	0.233*	-0.392**	-0.005
No. of clusters per plant	P					0.416**	0.166	0.134	0.162	-0.153	0.083
	G					0.522**	0.176	0.143	0.178	-0.167	0.088
No. of pods per cluster	P						0.198	-0.015	0.045	-0.110	0.013
	G						0.223*	-0.017	0.088	-0.127	0.017
No. of pods per plant	P							-0.312**	0.041	-0.239*	0.008
	G							-0.316**	0.049	-0.241*	0.008
Pod length (cm)	P							0.150	0.185	0.185	-0.029
	G							0.189	0.189	-0.029	
No. of seeds per pod	P								-0.088	0.120	
	G								-0.117	0.142	
100-seed weight (g)	P									-0.115	
	G									-0.116	

* - Significant at p = 0.05

** - Significant at p = 0.01

The results of correlation between different pairs of eleven characters are described as below.

4.4.1 Seed yield per plant

Seed yield per plant showed positive and highly significant correlation with plant height (r_p = 0.405 and r_g = 0.415), number of clusters per plant (r_p = 0.414 and r_g = 0.441), number of pods per plant (r_p = 0.317 and r_g = 0.320), number of pods per cluster (r_p = 0.263 and r_g = 0.296), number of seeds per pod (r_p = 0.228 and r_g = 0.274) at both phenotypic and genotypic levels, while number of pods per cluster and number of seeds per pod was only significant at phenotypic level. Seed yield per plant was positively correlated with pod length, protein content and negatively correlated with days to 50 per cent flowering, days to maturity, 100-seed weight but did not reach the level of significance.

4.4.2 Days to 50 % flowering

Days to 50 per cent flowering showed positive and highly significant correlation with days to maturity (r_p = 0.452 and r_g = 0.642) at both the levels. The number of clusters per plant was positively correlated with days to 50 per cent flowering but significant only at the genotypic level. The correlations of this character with number of pods per cluster, pod length and 100-seed weight were positive and non-significant. Number of seeds per pod (r_p = - 0.175 and r_g = - 0.230) possessed negative and significant correlation with days to 50 per cent flowering and reached the level of significance at genotypic level only. Plant height, number of pods per plant and protein content had non-significant negative correlations with days to 50 per cent flowering at both the levels.

4.4.3 Days to maturity

Days to maturity showed no significant association with other traits. The correlations of this character with number of clusters per plant, number of pods per cluster, pod length, 100-seed weight and protein content were positive and non-significant at both levels. The character plant height, number of pods per plant and number of seeds per pod showed low and negative correlations with days to maturity at both the levels.

4.4.4 Plant height

This character exhibited positive and highly significant correlations with number of clusters per plant ($r_p = 0.324$ and $r_g = 0.342$) and number of pods per plant ($r_p = 0.365$ and $r_g = 0.373$) at phenotypic and genotypic levels. Number of seeds per pod ($r_p = 0.186$ and $r_g = 0.233$) showed positive and significant correlation with plant height at genotypic level. However, the number of pods per cluster had non-significant positive correlation with plant height. 100-seed weight ($r_p = 0.380$ and $r_g = 0.392$) showed negative and highly significant correlation with plant height at both the levels. Plant height was negatively correlated with pod length and protein content but did not reach the level of significance.

4.4.5 Number of clusters per plant

Number of clusters per plant showed positive and highly significant correlation with number of pods per cluster ($r_p = 0.416$ and $r_g = 0.522$) at phenotypic and genotypic levels. This character showed positive correlation with number of pods per plant, pod length, number of seeds per pod and protein content but did not reach the level of significance. 100-seed

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weight showed negative and non-significant correlation with number of clusters per plant.

4.4.6 Number of pods per cluster

Number of pods per cluster had positive and significant correlations with number of pods per plant (r_p = 0.198 and r_g = 0.223) at genotypic level only. The character number of seeds per pod and protein content showed positive and non-significant correlation with number of pods per cluster. Pod length and 100-seed weight showed low and negative correlations with this trait at both the levels.

4.4.7 Number of pods per plant

Correlation of this character with number of seeds per pod and protein content was low and positive at both the levels. Pod length (r_p = - 0.312 and r_g = - 0.316), 100-seed weight (r_p = - 0.239 and r_g = - 0.241) showed negative and highly significant correlation with number of pods per plant at both the levels.

4.4.8 Pod length

Correlation of pod length with number of seeds per pod and 100-seed weight was positive and non-significant. However, protein content showed negative correlation with pod length at both the levels.

4.4.9 Number of seeds per pod

Number of seeds per pod exhibited positive correlation with protein content and negative correlation with 100-seed weight but did not reach the level of significance at phenotypic and genotypic sites.

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weight showed negative and non-significant correlation with number of clusters per plant.

4.4.6 Number of pods per cluster

Number of pods per cluster had positive and significant correlations with number of pods per plant (r_p = 0.198 and r_g = 0.223) at genotypic level only. The character number of seeds per pod and protein content showed positive and non-significant correlation with number of pods per cluster. Pod length and 100-seed weight showed low and negative correlations with this trait at both the levels.

4.4.7 Number of pods per plant

Correlation of this character with number of seeds per pod and protein content was low and positive at both the levels. Pod length (r_p = - 0.312 and r_g = - 0.316), 100-seed weight (r_p = - 0.239 and r_g = - 0.241) showed negative and highly significant correlation with number of pods per plant at both the levels.

4.4.8 Pod length

Correlation of pod length with number of seeds per pod and 100-seed weight was positive and non-significant. However, protein content showed negative correlation with pod length at both the levels.

4.4.9 Number of seeds per pod

Number of seeds per pod exhibited positive correlation with protein content and negative correlation with 100-seed weight but did not reach the level of significance at phenotypic and genotypic sites.

4.4.10 100-seed weight

100-seed weight exhibited low and negative correlation with protein content at both phenotypic and genotypic levels.

4.5 Path coefficient analysis

Seed yield per plant was considered as the resultant variable, while, the remaining ten yield contributing characters as the causal variables. The genotypic correlation coefficients were worked out between seed yield per plant and each of the ten causal variables and among themselves to study the direct and indirect effects on seed yield per plant. The data on the direct and indirect effects of these variables on seed yield per plant are presented in Table 4.4.

4.5.1 Days to 50 % flowering

The genetic correlation between days to 50 per cent flowering and seed yield per plant was negative and non-significant (- 0.016). Its direct effect on seed yield was positive (0.149). The indirect effects of this trait via number of clusters per plant (0.067) and 100-seed weight (0.033) were positive and moderate and through the number of pods per plant (0.008) was positive and low. The negative indirect effect via days to maturity (- 0.160) was high, while this effects through the number of seeds per pod (- 0.040) and number of pods per plant (- 0.035) were moderate and through plant height (- 0.025), pod length (- 0.006) and protein content (- 0.007) were low.

4.5.2 Days to maturity

The genotypic correlation of days to maturity with seed yield per plant was negative and non-significant (- 0.168). The direct effects of this trait on seed yield was negative and highest (- 0.249). The indirect effect via

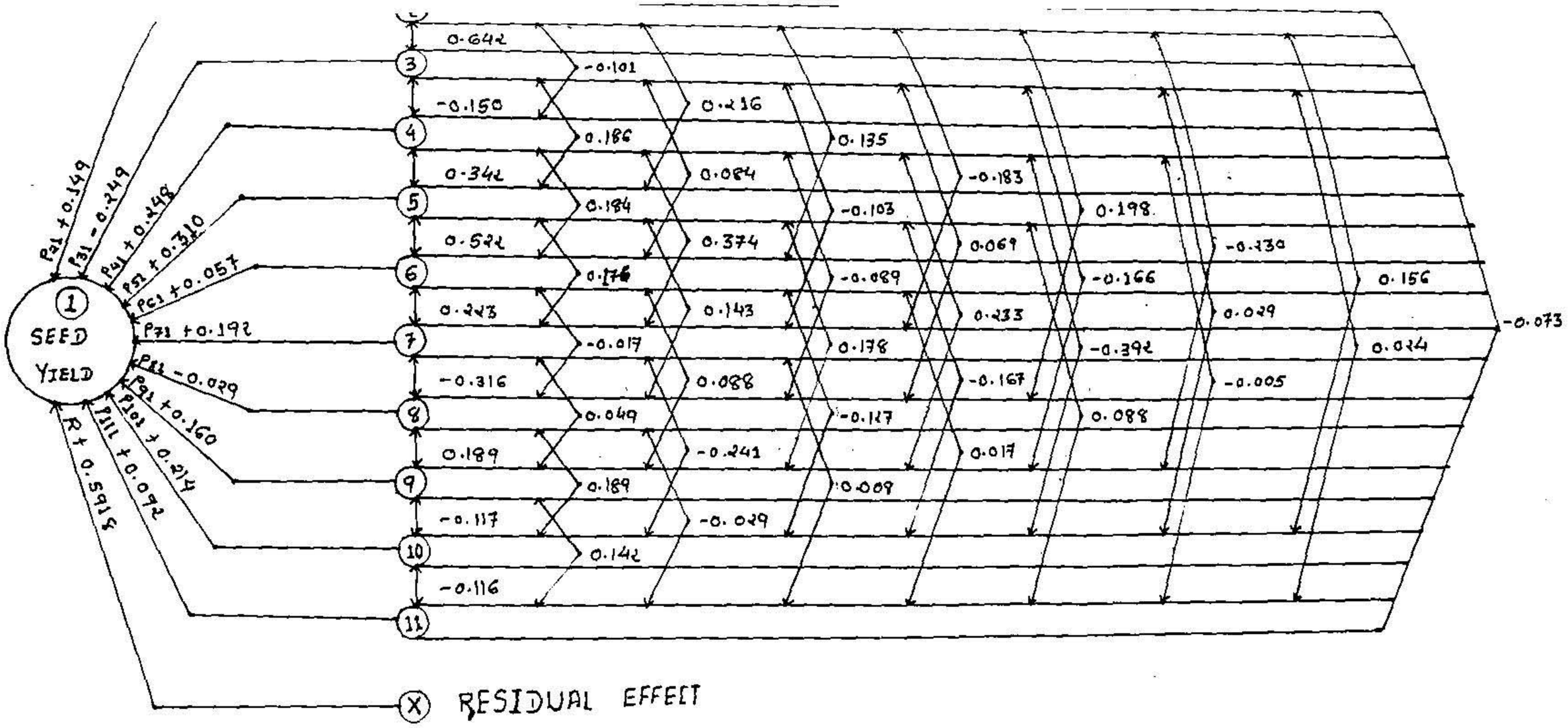
Table 4.4 : Direct and indirect effects of different characters on (seed) yield in greengram

Characters	Direct effect on seed yield	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100-seed weight (g)	Protein content (%)	Genotypic correlation with seed yield
Days to 50 % flowering	0.149	-	-0.160	-0.025	0.067	0.008	-0.035	-0.006	-0.040	0.033	-0.007	-0.016
Days to maturity	-0.249	0.096	-	-0.037	0.058	0.005	-0.020	-0.002	-0.026	0.006	0.002	-0.168
Plant height (cm)	0.248	0.037	-0.015	-	0.106	0.011	0.072	0.003	0.037	-0.084	0.001	0.415**
No. of clusters per plant	0.310	-0.046	0.085	0.032	-	0.030	0.034	-0.004	0.029	-0.036	0.008	0.441**
No. of pods per cluster	0.057	-0.021	0.046	0.162	0.020	-	0.043	0.001	0.014	-0.027	0.002	0.296**
No. of pods per plant	0.192	0.026	0.093	0.054	0.013	-0.027	-	0.009	0.008	-0.051	0.001	0.317**
Pod length (cm)	-0.029	-0.017	-0.022	0.044	-0.001	-0.061	0.030	-	0.030	0.040	-0.003	0.011
No. of seeds per pod	0.160	0.041	0.058	0.055	0.005	0.009	-0.006	-0.037	-	-0.025	0.013	0.274**
100-seed weight (g)	0.214	-0.007	-0.097	-0.052	-0.007	-0.046	-0.006	-0.019	0.023	-	-0.011	-0.008
Protein content (%)	0.092	-0.006	-0.001	0.027	0.001	0.002	0.001	0.023	-0.025	-0.011	-	0.103

Residual effect = 0.5918

*** - Significant at p = 0.05**

**** - Significant at p = 0.01**



Diagramatic representation of factors influencing seed yield in green gram. Double arrowed lines indicate correlation coefficients and single arrowed lines indicate direct effects.

Where,

1. Seed yield per plant
2. Days to 50 % flowering
3. Days to maturity
4. Plant height
5. No. of clusters per plant
6. No. of pods per cluster
7. No. of pods per plant
8. Pod length
9. No. of seeds per pod
10. 100-seed weight
11. Protein content (%)

Fig. 1 : Genotypic path in green gram

days to 50 per cent flowering was positive and high (0.096), while the indirect effect via number of clusters per plant (0.058) was moderate and positive and via 100-seed weight (0.006), number of pods per cluster (0.005) and protein content (0.002) were low and positive. The negative indirect effects via plant height (- 0.037), number of seeds per pod (- 0.026), number of pods per plant (- 0.020) were moderate and via pod length (- 0.002) was low.

4.5.3 Plant height

Plant height had positive and strong association with seed yield per plant (0.415). So its direct effect on seed yield was also positive and high (0.248). This trait had high correlation with seed yield due to its high indirect effect through number of clusters per plant (0.106) and number of pods per plant (0.072), moderate indirect effect through days to 50 per cent flowering (0.037) and number of seeds per pod (0.037) and low indirect effect via number of pods per plant (0.011), pod length (0.003) and protein content (0.001). The negative indirect effect of plant height via 100-seed weight (- 0.084) was moderately high and through days to maturity (- 0.015) was low.

4.5.4 Number of clusters per plant

The genotypic correlation between number of clusters per plant and seed yield was positive and highly significant (0.441) due to its high direct effect on seed yield (0.310). The indirect effects of number of cluster per plant on seed yield via days to maturity was positive and high (0.085), while there were moderate indirect effects via plant height (0.032), number of pods per cluster (0.030), number of pods per plant (0.034) and number of seeds per pod (0.029). The indirect effect through protein content (0.008)

days to 50 per cent flowering was positive and high (0.096), while the indirect effect via number of clusters per plant (0.058) was moderate and positive and via 100-seed weight (0.006), number of pods per cluster (0.005) and protein content (0.002) were low and positive. The negative indirect effects via plant height (- 0.037), number of seeds per pod (- 0.026), number of pods per plant (- 0.020) were moderate and via pod length (- 0.002) was low.

4.5.3 Plant height

Plant height had positive and strong association with seed yield per plant (0.415). So its direct effect on seed yield was also positive and high (0.248). This trait had high correlation with seed yield due to its high indirect effect through number of clusters per plant (0.106) and number of pods per plant (0.072), moderate indirect effect through days to 50 per cent flowering (0.037) and number of seeds per pod (0.037) and low indirect effect via number of pods per plant (0.011), pod length (0.003) and protein content (0.001). The negative indirect effect of plant height via 100-seed weight (- 0.084) was moderately high and through days to maturity (- 0.015) was low.

4.5.4 Number of clusters per plant

The genotypic correlation between number of clusters per plant and seed yield was positive and highly significant (0.441) due to its high direct effect on seed yield (0.310). The indirect effects of number of cluster per plant on seed yield via days to maturity was positive and high (0.085), while there were moderate indirect effects via plant height (0.032), number of pods per cluster (0.030), number of pods per plant (0.034) and number of seeds per pod (0.029). The indirect effect through protein content (0.008)

was low. The negative indirect effect via days to 50 per cent flowering (- 0.046) and 100-seed weight (- 0.036) was moderate. The negative indirect effect of number of clusters per plant via pod length (- 0.004) was low.

4.5.5 Number of pods per cluster

The genotypic correlation between number of pods per cluster and seed yield was positive and significant (0.296). The direct effect of number of pods per cluster was positive and low (0.057). Among the indirect effects, this trait had high positive effect via plant height (0.162), moderate positive effect via days to maturity (0.046), number of pods per plant (0.043), while through number of clusters per plant (0.020), number of seeds per pod (0.014), pod length (0.001) and protein content (0.002) were positive and low. The negative indirect effect via days to 50 per cent flowering (- 0.021) and 100-seed weight (- 0.027) was low.

4.5.6 Number of pods per plant

The genotypic correlation between number of pods per plant and seed yield was positive and significant (0.317), due to its moderate direct effect on seed yield per plant (0.192). The indirect effect of days to maturity was positive and high (0.093) as also with plant height (0.054), while days to 50 per cent flowering (0.026) had moderate indirect effect of number of clusters per plant (0.013), while it was low with pod length (0.009), number of seeds per pod (0.008) and protein content (0.001). The negative indirect effect via 100-seed weight (- 0.051) and number of pods per cluster (- 0.027) was moderate and low.

4.5.7 Pod length

The genotypic correlation between pod length and seed yield per plant was low and positive (0.011). The direct effect of pod length was negative and low (- 0.029). The indirect effect of pod length via plant height (0.044), 100-seed weight (0.040), number of pods per plant (0.030) and number of seeds per pod (0.030) was positive and moderate. The negative indirect effect of pod length via number of pods per cluster (- 0.061) was moderate. The negative effects via days to 50 per cent flowering (- 0.017), days to maturity (- 0.022), number of clusters per plant (- 0.001) and protein content (- 0.003) were low.

4.5.8 Number of seeds per pod

The genotypic correlation between number of seeds per pod and seed yield was positive and significant (0.274) due to its moderate direct effect (0.160) on seed yield per plant. The indirect effect of number of seeds per pod via days to 50 per cent flowering (0.041), days to maturity (0.058) and plant height (0.055) were positive and moderate, while number of clusters per plant (0.005), number of pods per cluster (0.009) and protein content (0.013) were positive and low. The negative indirect effect via 100-seed weight (- 0.025) and number of pods per plant (- 0.006) were moderate to low.

4.5.9 100-seed weight

The genotypic correlation of 100-seed weight with seed yield per plant was negative and low (- 0.008) but its direct effect on seed yield was positive and high (0.214). Its indirect effects via number of seeds per pod (0.023) was positive and moderate. The negative indirect effect of 100-

seed weight via days to maturity (- 0.097) was high. The moderate indirect effect of 100-seed weight via plant height (- 0.052) and number of pods per cluster (- 0.046) were negative. It was low through pod length (- 0.019), protein content (- 0.011), days to 50 per cent flowering (- 0.007), number of clusters per plant (- 0.007) and number of pods per plant (-0.006).

4.5.10 Protein content

The genotypic correlation of protein content with seed yield was positive and high (0.103). Its direct effect on seed yield per plant was positive and low (0.092). Protein content had moderate and positive indirect effect on seed yield via. plant height (0.027), pod length (0.023) and low indirect effect via number of pods per cluster (0.002), number of clusters per plant (0.001) and number of pods per plant (0.001). The negative indirect effect of protein content via number of seeds per pod (- 0.025) was moderate while days to 50 per cent flowering (- 0.006), 100-seed weight (- 0.011) and days to maturity (- 0.001) were low.

4.6 Genetic divergence

Multivariate test, using Wilk's criterion, was carried out to test the differences among the 86 genotypes of green gram.

Based upon the observations of eleven characters, the Malhalanobis's D^2 statistic was computed for all possible 3655 pairs of 86 genotypes in order to assess the genetic diversity present among the genotypes under study.

4.6.1 Composition of clusters

Clustering of the 86 genotypes was carried out following Tocher method (Rao, 1952). In all, eight clusters were formed and their composition

Table 4.5 : The distribution of eighty-six greengram genotypes to different clusters on the basis of D^2 statistic

Clusters	Number of genotypes	Genotypes
I	15	GM-9307, GM-9411, GM9206, HUM-2, GUJ-3, GM-9410, GM-9316, PS-16, GM-9008, GM-9310, GM-9010, GM-9306, GM-9307, GM-9311, GM-8904
II	17	GM-9110, GM-9321, GM-84-13, GM-9023, GM-9403, GM-87-16, GM-9302, GM-84-26, GM-9408, GM-9318, GM-9415, GM-9207, GM-9409, GM-9317, GM-9103, GM-84-6, TARM-1
III	3	RMG-337, RUM-120, CO-4
IV	4	GM-8801, GM-8213, GM-9412, RUM-112
V	16	GM-9018, GM-88-35, Pusa-9072, GM-9305, GM-88-10, GM-9314, GM-9001, GM-9308, GM-9405, GM-9021, LGG-472, RUM-351, Pusa-9531, Pusa-9532, Pusa-9571
VI	9	GM-88-44, GM-9315, GM-84-4, GM-9404, GM-9006, K-851, GM-9104, GM-86-19, GM-9420
VII	14	GM-9406, GM-9402, GM-86-14, GM-9106, HUM-7, GM-86-17, GM-9407, GM-9413, GM-9401, GM-9111, GUJ-2, GM-9002, GM-9301, GM-3
VIII	8	GM-9028, GM-9317, GM-8906, GM-9304, GM9202, GM-9419, GM-9320, GM-9303

Table 4.6 : Average intra and inter-cluster (D) values for 86 genotypes of greengram

Clusters	I	II	III	IV	V	VI	VII	VIII
I	2.255	2.603	6.300	2.951	2.689	2.482	2.857	3.672
II	-	2.229	6.280	3.483	3.311	2.275	2.863	2.511
III		-	2.823	4.866	6.438	6.455	5.797	6.733
IV		-	2.239	4.305	3.122	3.671	3.744	
V			-	2.226	3.313	2.242	4.966	
VI				-	2.271	2.865	2.715	
VII					-	2.454	3.904	
VIII						-	2.736	

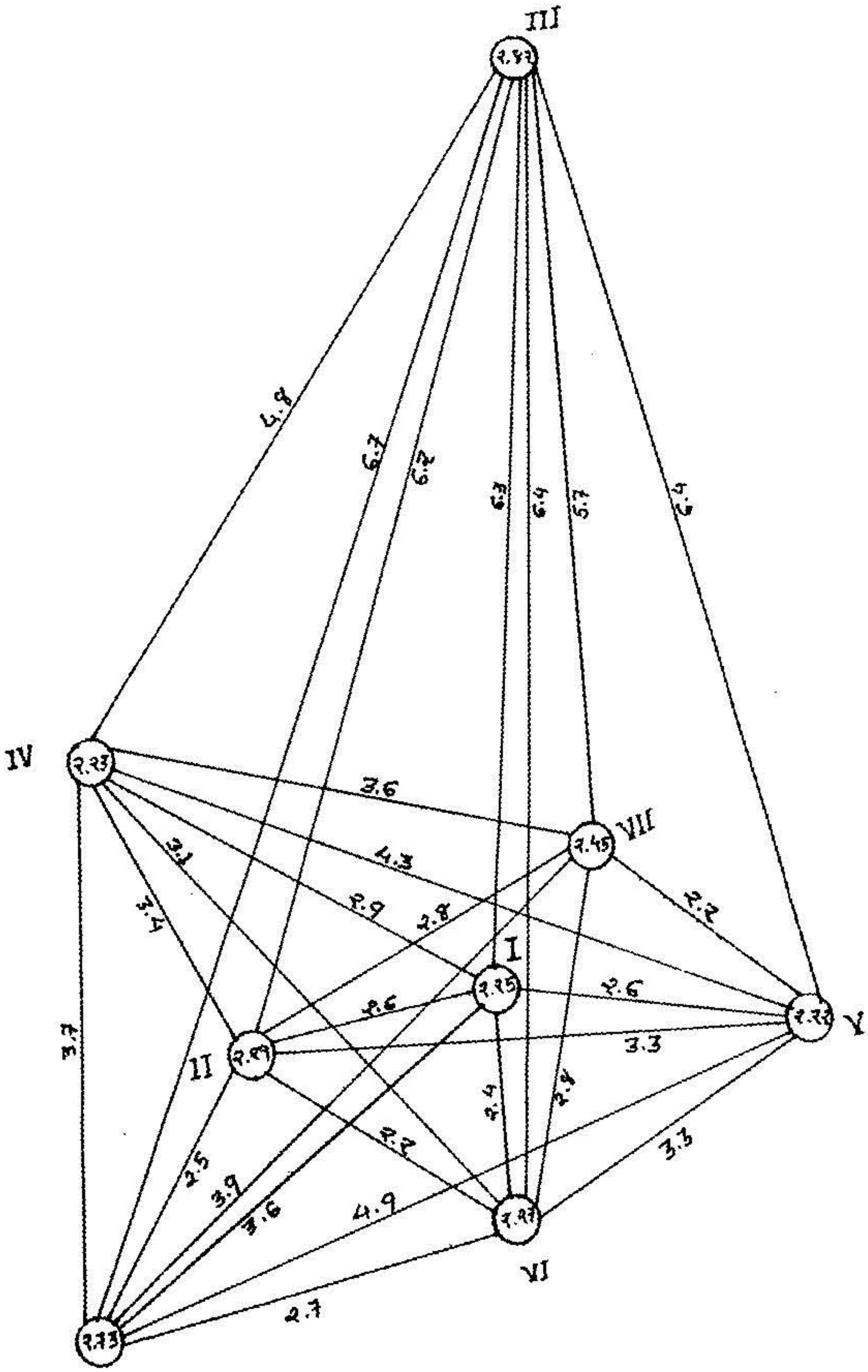


Fig. 2 : Mutual relationship among the D^2 clusters

is given in Table 4.5. Cluster-II was the largest cluster containing seventeen genotypes from G.A.U., Sardar Krushinagar (16) and B.A.R.C., Trombay (1). Out of sixteen genotypes included in the cluster-V, nine were from G.A.U., Sardar Krushinagar, four from I.A.R.I., New Delhi, one from P.A.U., Ludhiana and one from Navga on (Rajasthan). Cluster-I comprised fifteen genotypes which were from G.A.U., Sardar Krushinagar (13), B.H.U., Varanasi (1) and C.S.A.U., Kanpur (1). Fourteen genotypes were grouped in the cluster-VII from G.A.U., Sardar Krushinagar (13) and B.H.U., Varanasi (1). Cluster-VI contained nine genotypes out of which eight were from G.A.U., Sardar Krushinagar and one from C.S.A.U., Kanpur. Cluster-VIII comprised eight genotypes which were from G.A.U., Sardar Krushinagar. Cluster-IV contained four genotype from G.A.U., Sardar Krushinagar (3) and from Navgaeon (Rajasthan) (1). Cluster-III was smallest cluster comprising only three genotypes from T.A.U., Coimbatore (1) and (2) from Navgaeon (Rajasthan).

4.5.2 Intra and inter-cluster distance

Intra and inter-cluster distance (D) between all possible pairs of eight clusters were computed and presented in Table 4.6.

A study of the data revealed that the inter-cluster distance (D) ranged from 2.242 to 6.733. The maximum inter-cluster distance (D = 6.733) was observed between cluster-III and VIII followed by those between cluster-III and VI (D = 6.455). The minimum inter-cluster distance (D = 2.242) was observed between cluster-V and VII followed by the cluster-Ii and VI (D = 2.275).

Intra-cluster distance (D) ranged from 2.226 to 2.823. At intra-cluster level cluster-III had the highest value (D = 2.823) which was followed

Table 4.7 : Cluster means for eleven characters in 86 genotypes of greengram

Clusters	Seed yield per plant	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of cluster per plant	No. of pods per clusters	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100 seed weight (g)	Protein content (%)
I	5.61	39.17	71.04	41.30	5.45	5.07	48.37	5.85	8.78	4.65	22.62
II	6.04	37.94	71.59	46.35	6.61	5.23	43.24	5.98	11.31	4.35	24.97
III	6.63	53.26	85.51	34.09	9.07	7.08	22.30	8.34	10.06	5.03	23.66
IV	5.49	41.17	74.30	32.96	8.02	7.63	47.22	6.42	8.99	4.45	22.83
V	4.32	38.02	72.42	27.17	4.39	3.94	26.84	6.91	10.04	4.79	23.49
VI	6.30	36.54	70.78	36.75	6.34	6.01	49.00	5.79	12.29	4.79	22.92
VII	5.84	38.71	71.02	30.74	5.31	5.53	32.05	7.05	10.03	5.28	24.86
VIII	10.02	36.09	69.20	47.43	7.73	6.43	54.35	6.81	11.44	4.47	24.39
Mean	6.281	40.113	73.233	37.099	6.615	5.865	40.420	6.644	10.368	4.726	23.718
S.Em. ±	0.549	1.831	1.709	2.420	0.520	0.390	3.897	0.279	0.404	0.104	0.306
C.V. %	24.711	12.921	6.600	18.460	22.251	18.850	27.21	11.880	11.031	6.240	3.650

by the cluster-VIII (D = 2.736). The minimum intra-cluster distance (D = 2.226) was observed in cluster-V followed by cluster-II.

4.5.3 Cluster means of various characters

Cluster means of all the eleven characters are presented in Table 4.7. A marked inter-cluster variation was observed in the cluster means for some characters viz., days to 50 per cent flowering (C.V. % = 12.92), plant height (C.V. % = 18.46), number of clusters per plant (C.V. % = 22.25), number of pods per plant (C.V. % = 27.21), number of seeds per pod (C.V. % = 11.03), pod length (C.V. % = 11.88), number of pods per cluster (C.V. % = 18.85) and seed yield per plant (C.V. % = 24.71). Among the coefficient of variation the character number of pods per plant, seed yield per plant and number of clusters per plant were the main contributors to the total divergence.

Cluster means revealed that cluster-III required maximum days to 50 per cent flowering (53.26 days) and maturity (85.51 days). This cluster also showed highest mean values for number of clusters per plant (9.07) and pod length (8.34 cm) and lowest mean values for number of pods per plant (22.30). Cluster-II had highest protein content (24.97 %) and lowest mean value for 100-seed weight (4.35 g). Seed yield per plant (10.02 g), plant height (47.43 cm) and number of pods per plant (54.35) were highest in cluster-VIII and days to 50 per cent flowering (36.09 days) and days to maturity (69.20 days) were minimum in this cluster. Cluster-V had lowest mean values for seed yield per plant (4.32 g), number of clusters per plant (4.39), plant height (27.17 cm) and number of pods per cluster (3.94). The lowest mean values for protein content (22.62 %) and number of seeds per pod (8.78) were observed in the cluster-I. The maximum mean value for

number of pods per cluster (7.63) was observed in cluster-IV. The highest mean values for number of seeds per pod (12.29) and lowest mean value for pod length (5.79 cm) were observed in cluster-VI. While the cluster-VII had the higher mean value for 100-seed weight (5.28 g).

DISCUSSION

VI DISCUSSION

Evaluation of the germplasm is the pre-requisite to collect the basic information before initiating any breeding programme for the improvement of the crop. Success of the crop improvement programme is largely dependent on the extent of genetic variability present in the population. Environment has a great influence on many quantitative characters, in which the variability partitioned into heritable and non-heritable components like genetic coefficient of variation, heritability, genetic advance etc. are most important to the plant breeder for selection of the breeding method in crop improvement programme.

A knowledge of the inter-relationship of quantitative traits of economic importance with seed yield and among themselves is important for the improvement in a complex character like yield through selection. The correlation studies are helpful to some extent to the breeder, but they do not take into consideration the cause and effect relationship which restrict the practical utility of correlations in selection programme.

The technique of path coefficient analysis devised by Wright (1921) and utilized for the first time in plants by Dewey and Lu (1959) in crested wheat grass is efficient in disintegrating the total correlation between two variables into direct and indirect effects. This technique could be used to understand the cause of association between two variables and provides basis for selection of superior genotypes from the diverse breeding populations.

Mahalanobis's D^2 statistic is being used as an efficient tool in quantitative estimation of genetic diversity and selection of parents for hybridization programme.

5.1 Variability

The present study showed a wide range of phenotypic variability and highly significant varietal differences for all the characters indicating considerable amount of variability. This suggests that there is ample scope to identify high yielding, early and dwarf genotypes to improve different characters simultaneously, provided the material is subjected to judicious selection pressure.

All the eleven characters had a wide range of variability (Table 4.1). Similar results were reported for number of pods per plant, seed yield per plant, plant height and number of clusters per plant (Singh and Malhotra, 1970 a; Chowdhury *et al.*, 1971; Reddy, 1977; Chopra and Gupta, 1978; Javia, 1986), days to flowering and days to maturity (Chopra and Gupta, 1978), 100-seed weight and seeds per pod (Singh and Malhotra, 1970 a; Reddy, 1977).

It will be of great interest to consider the *per se* performance of different genotypes in respect of different quantitative characters of economic importance particularly earliness, seed size and seed yield. The varieties GM-8906, GM-9420 and GM-9303 were early in flowering. The boldest seed size was recorded by GM-9402 followed by GM-9111 and RUM-120. The highest yielding variety was GM-9304 which was at par with GM-9320.

The phenotypic range of variation is not the precise criterion of judging the amount of genetic variation present in population. The genetic parameters like variance components, genotypic coefficient of variation, heritability and genetic advance are important to study the extent of genetic variability more precisely. Since breeding potential of an experimental material depends on the amount of genetic variability which is a pre-requisite

for response to selection, the phenotypic variance was partitioned into its genotype and environment components to know the genetic variability present in each character.

The genotypic variance followed the trend of phenotypic variance and was greater than environmental variance for all the characters. This implied that phenotypic variability may be considered as a reliable measure of genotypic variability. In the present study, the phenotypic and genotypic variances were greater than the environmental variances for all the characters under study (Table 4.2). This indicated that selections for these characters would be effective.

With a view to compare different quantitative characters in respect of phenotypic and genotypic variability, phenotypic coefficient of variation and genotypic coefficient of variation were calculated. The genotypic coefficient of variation measures the range of variability present in a character and helps to compare the variability present in different characters. The highest amount of genotypic coefficient of variation was exhibited by number of pods per plant followed by seed yield per plant, plant height and number of clusters per plant. Moderate extent of genotypic coefficient of variation was exhibited by number of pods per cluster, pod length, number of seeds per pod and 100-seed weight, while characters such as days to 50 per cent flowering and protein content possessed lowest magnitude of genotypic coefficient of variation. High genotypic coefficient of variation for number of clusters per plant, plant height and number of pods per plant has also been reported by Veeraswamy *et al.* (1973), Ali and Shaikh (1987) and Borah and Hazarika (1995), for pod number, plant height and seed yield by Singh and Malhotra (1970 a), Chopra and Gupta (1978) and

Javia (1986), for plant height and pod length by Patel and Shah (1982), for number of pods per plant by Paramasivan and Rajasekaran (1980) and Ramana and Singh (1987), for seed yield, clusters per plant and seeds per pod by Veerabadhiran and Jehangir (1995).

Genetic coefficient of variation measures the amount of variation in character, but it is not possible to assess the amount of heritable variation based on this estimates. Burton (1952) suggested that genotypic coefficient of variation along with heritability estimates would provide better estimates of the amount of genetic gain expected through phenotypic selection.

5.2 Heritability and genetic advance

The heritability estimates were quite high for the characters, seed yield per plant, days to 50 per cent flowering, days to maturity, plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, 100-seed weight and protein content. It indicated that these characters were least influenced by environmental factors, with the character number of seeds per pod, having moderate heritability. The higher estimates of heritability obtained in the study may be due to the fact that the experiment was conducted only at a single location and for one year. Thus, the genotypic variance estimated from a single test contained interaction variance in addition to genetic variance resulting in the upward bias in the estimates of broad sense heritability.

High estimates of heritability in green gram were also reported for days to 50 per cent flowering (Chowdhury *et al.*, 1971; Reddy *et al.*, 1977; Ramana and Singh, 1987; Veerabadhiran and Jehangir, 1995), days to maturity (Singh and Malhotra, 1970 a; Chopra and Gupta, 1978; Misra,

1985), plant height (Veeraswamy *et al.*, 1973; Patel and Shah, 1982; Pandey *et al.*, 1988; Veerabadhiran *et al.*, 1996), number of clusters per plant (Reddy *et al.*, 1977; Paramasivan and Rajasekaran, 1980; Veerabadhiran and Jehangir, 1995), number of pods per plant (Krishnaih *et al* .,1979; Parida and Singh, 1984), pod length (Chowdhury *et al.*, 1971; Paramasiyan and Rajasekaran, 1980; Roquib and Patnaik, 1990), 100-seed weight (Reddy *et al.*, 1977; Parida and Singh, 1984; Patil *et al.*, 1987; Pundir *et al.*, 1992), protein content (Arunachala, 1979) and seed yield per plant (Paramasivan and Rajasekaran, 1980; Misra, 1985; Ramana and Singh, 1987; Borah and Hazarika, 1995; Veerabadhiran *et al.*, 1996; Byregowda *et al.*, 1997). However, Singh and Malhotra (1970 a) and Parida and Singh (1984) reported low estimates of heritability for seed yield in green gram.

The high heritability estimates have been helpful to the plant breeder as these enable the plant breeders to base the selection programme on phenotypic performance. Johnson *et al.* (1955) in their studies with F_4 and F_5 generations of a cross in soyabean suggested that heritability estimates in conjunctions with genetic advance were more reliable in predicting the resultant effect from selecting the best individuals. Ramanujum and Tirumalachar (1967) also discussed the limitations of estimating heritability in broad sense as it included both additive as well as epistatic gene effects and suggested that it would be reliable only if accompanied by high genetic advance.

The expected genetic advance expressed in percentage of mean was high for characters viz., number of pods per plant, seed yield per plant, plant height and number of clusters per plant. It was moderate for pod length, number of pods per cluster, number of seeds per pod and 100-seed weight.

while, it was of lower magnitude for days to 50 per cent flowering, protein content and days to maturity. The same results were also obtained on high genetic advance for seed yield per plant (Singh and Malhotra, 1970 a; Krishnaiah *et al.*, 1979; Parida and Singh, 1984, Ramana and Singh, 1987; Pundir *et al.*, 1992; Borah and Hazarika, 1995; Veerabadhiran *et al.*, 1996; Byregowda *et al.*, 1997), number of pods per plant (Chopra and Gupta, 1978; Mishra, 1985; Pandey *et al.*, 1988; Borah and Hazarika, 1995; Byregowda *et al.*, 1997), plant height (Chowdhury *et al.*, 1971; Pandey *et al.*, 1988; Miah and Bhaora, 1989; Borah and Hazarika, 1995; Veerabadhiran and Jehangir, 1995; Veerabadhiran *et al.*, 1996), and number of clusters per plant (Veeraswamy *et al.*, 1973; Malhotra *et al.*, 1974; Parida and Singh, 1984; Ramana and Singh, 1987; Borah and Hazarika, 1995).

Number of pods per plant, seed yield per plant, plant height and number of clusters per plant showed high heritability along with higher to moderate genotypic coefficient of variation and genetic advance indicating that most likely the heritability was due to additive gene effects and the genotypes under study were highly diverse and of great genetic potential with regard to these characters. Further improvement in these characters would be achieved by phenotypic selection. An advantage of this nature also deserved careful and sustained exploitation of genetic improvement in green gram.

High heritability was coupled with low genetic advance for days to 50 per cent flowering, days to maturity and protein content. This is due to non-additive effect.

5.3 Correlation coefficient

Prior to any breeding programme for the improvement in crops, it is imperative to obtain information regarding the inter-relationship of

different plant characters with yield and among themselves since it facilitates a quick assessment of high yielding genotypes in selection programmes. The real or true association could be known only through genotypic correlation which eliminates the environmental influence.

The correlations of seed yield with other ten characters and among the characters themselves were estimated at genotypic and phenotypic levels. In general, the value of genotypic correlations were higher than their phenotypic correlation which is in agreement with the findings of Singh and Malhotra (1970 b), Pokle and Nomulwar (1977) and Ramana and Singh (1977). This indicated that there was a high degree of inter-relationship between two variables at genotypic level. In few cases, however, the phenotypic correlations were slightly higher than their genotypic counterparts which implied that the non-genetic causes inflated the values of genotypic correlation because of the influence of environmental factors.

In the present investigation, seed yield per plant was found to be highly significant and positively correlated with plant height, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod indicating that these attributes were mainly influencing the seed yield in green gram. Thus, selection practices for the improvement in one character will automatically result in the improvement in the other, even though direct selection for improvement has not been made for the yield character. Similar results exhibiting highly significant and positive correlation between seed yield and other traits as obtained in the present investigations were also reported for plant height (Yohi and Poehlman, 1975; Pokle and Nomulwar, 1977; Singh *et al.*, 1978; Ramana and Singh, 1987), number of clusters per plant (Reddy, 1977; Singh *et al.*,

1977; Sandhu *et al.*, 1980; Satyan *et al.*, 1989), number of pods per cluster (Singh *et al.*, 1977; Boomikumaren and Rathinan, 1981; Satyan *et al.*, 1989; Reddy *et al.*, 1994), number of pods per plant (Singh and Malhotra, 1970 b; Yohi and Poehlman, 1975; Pokle and Nomulwar, 1977; Javia, 1986; Mallik *et al.*, 1987; Golsangi *et al.*, 1996) and number of seeds per pod (Tomar *et al.*, 1973; Reddy, 1977; Sandhu *et al.*, 1980; Singh *et al.*, 1980; Boomikumaren and Rathinan, 1981; Reddy *et al.*, 1994; Veerabadhiran and Jehangir, 1995). Seed yield per plant also exhibited positive correlation with pod length (Sandhu *et al.*, 1980; Vidyadhar *et al.*, 1984). While, its association with days to 50 per cent flowering, days to maturity and 100-seed weight were negative and non-significant. Similar results were obtained by (Choi *et al.*, 1986) for days to flowering, for 100-seed weight (Reddy, 1977; Boomikumaren and Rathinan, 1981). This indicated that selections for improvement of one character, if successful, will result in the decline in other character. Protein content had very low and positive correlation with seed yield per plant which was negligible.

In the present investigation, days to 50 per cent flowering had highly significant and positive correlation with days to maturity suggesting that days taken to maturity can be predicted by days taken to flower. Similar finding was observed by Singh and Malhotra (1970 b), Yohe and Poehlman (1975), Patil and Deshmukh (1988). The positive and significant correlation of days to 50 per cent flowering with number of clusters per plant and significant and negative association with number of seeds per pod are also reported by Ramana and Singh (1987).

Days to maturity was found to have positive correlation with number of clusters per plant, number of pods per cluster, pod length, 100-seed weight and protein content. While, negative association with plant height and number of pods per plant.

Plant height showed highly significant and positive association with number of clusters per plant, number of pods per plant and number of seeds per pod. Highly significant and negative association with 100-seed weight. Similar findings were obtained by Boomikumaran and Rathinan (1981); Parida and Singh (1984); Natarajan *et al.* (1988) and Borah and Hazarika (1995), for 100-seed weight by Veerabadhiran and Jehangir (1995).

Number of clusters per plant had strong positive association with number of pods per cluster, while it had positive association with number of pods per plant, pod length, number of seeds per pod and protein content and negative association with 100-seed weight. Similar findings were reported by Parida and Singh (1984) and Veerabadhiran and Jehangir (1995).

Number of pods per cluster was found to have significant and positive correlation with number of pods per plant which was also reported by Reddy *et al.* (1994) and positive association with number of seeds per pod and protein content. Negative association was found between pod length and 100-seed weight (Boomikumaran and Rathinan, 1981).

Number of pods per plant had highly significant and negative correlation with pod length and 100-seed weight with positive and non-significant correlation with number of seeds per pod and protein content.

Similar results were obtained by Singh and Malhotra (1970 b) and Natarajan *et al.* (1988) for pod length and 100-seed weight except protein content.

Pod length showed positive and non-significant correlation with number of seeds per pod and 100-seed weight and negative correlation with protein content which was also reported by Reddy *et al.* (1994).

In general, correlation involving number of seeds per pod and 100-seed weight was low. Singh and Malhotra (1970 b) and Singh *et al.* (19780 also observed negative correlation of these characters. Correlation involving protein content with all characters was non-significant and low.

If the genetic correlation is high the two characters can be regarded as the same, and if there are no special circumstances affecting the heritability or the intensity of selection, it will make little difference in environment, if the selection is carried (Falconer, 1960).

On the basis of the present investigation on inter-relationship, it can be presumed that for improving seed yield in green gram, an ideal plant would be tall with late flowering and maturity time and having more number of clusters per plant, pods per cluster and pods per plant. Hence, these characters could be utilized as selection criteria for improving seed yield.

5.4 Path coefficient analysis

In the selection programme, when less number of variables are considered, correlation study alone can serve the purpose. However, when variables increase the situation becomes complex. For overcoming this

complexity path analysis (Wright, 1921 and Dewey and Lu, 1959) method is adopted to partition the correlation into direct and indirect effects, so that relative merits of each trait is established and their number is reduced in selection programmes.

In order to obtain a clear idea of the inter-relationship of various component characters with yield, direct and indirect effects were calculated using path coefficient analysis at genotypic level.

From the present studies, it was revealed that the highest positive direct effect on seed yield was recorded by number of clusters per plant followed by plant height, 100-seed weight, number of pods per plant, number of seeds per pod, days to 50 per cent flowering, protein content and number of pods per cluster. Similar results were reported by Singh *et al.* (1980); Gupta *et al.* (1982); Vidyadhar *et al.* (1984); Raut *et al.* (1988) and Golsangi *et al.* (1996) for number of clusters per plant. For number of pods per plant and 100-seed weight by Chandel *et al.* (1973); Raut *et al.* (1988) and Sharma and Gupta (1994), for days to 50 per cent flowering by Chandel *et al.* (1973); Singh *et al.* (1978); Mallik *et al.* (1987) and Patil and Desmukh (1988), for plant height by Mallik *et al.* (1987), for number of pods per cluster by Singh *et al.* (1977); Singh *et al.* (1980); Reddy *et al.* (1994) and Golsangi *et al.* (1996), for number of seeds per pod by Pokle and Patil (1975); Gupta *et al.* (1982); Vidyadhar *et al.* (1984) and Reddy *et al.* (1994). Negative direct effect on seed yield was found with days to maturity and pod length. Similar results were reported by Mallik *et al.* (1987) and Patil and Desmukh (1988) for days to maturity and for pod length by Khan (1985) and Mallik *et al.* (1987).

Number of clusters per plant showed high correlation with seed yield which was mainly due to its high positive direct and indirect effects via days to maturity, moderate indirect effect via plant height, number of pods per plant and number of pods per cluster and low indirect effect via number of seeds per pod. The impact of other indirect effect was negligible except days to 50 per cent flowering and 100-seed weight. Plant height also exhibited very high correlation with seed yield per plant due to its moderate direct effect, high indirect effects via number of clusters per plant and low indirect effects via number of pods per plant, days to 50 per cent flowering and number of seeds per pod. Indirect effects via 100-seed weight was high and negative and via days to maturity was low and negative. Similar results were reported by (Vidyadhar *et al.*, 1984) for number of clusters per plant and for plant height by (Patil and Deshmukh, 1988).

Number of pods per plant possessed high correlation with seed yield per plant due to its moderate effect, high indirect effect via days to maturity, moderate indirect effect via plant height and days to 50 per cent flowering while low indirect effect via number of clusters per plant. The negative indirect effect via 100-seed weight and number of pods per cluster. Indirect effect via rest of the characters were negligible. High indirect effect of number of pods per plant via days to maturity was also reported by Singh and Malhotra (1970 b).

The number of seeds per pod showed moderate correlation with seed yield per plant due to its moderate direct effect, while there was high indirect effect via plant height, days to 50 per cent flowering and days to maturity and low indirect effect via number of clusters per plant. Negative

indirect effect was observed via number of pods per plant and pod length. However, indirect effect via other characters were negligible. High indirect effect via plant height, days to 50 per cent flowering and days to maturity were also reported by Singh and Malhotra (1970 b); Natarajan *et al.* (1988) and Veerabadhiran and Jehangir (1995), negative indirect effect via number of pods per plant and pod length was reported by Vidyadhar *et al.* (1994) and Veerabadhiran and Jehangir (1995).

Number of pods per cluster was found to have significant correlation with seed yield per plant, while it had high indirect effect via plant height with moderate indirect effect via days to maturity and number of pods per plant. There was negative indirect effect via 100-seed weight and days to 50 per cent flowering. Similar results were reported by Patel (1989).

Days to 50 per cent flowering showed negative correlation with seed yield but its direct effect was positive. The positive indirect effect of days to 50 per cent flowering via days to maturity indicated that even in late flowering types the seed yield was enhanced with the advancement of the days to maturity. Similar results were reported by Sandhu *et al.* (1980).

Days to maturity was found to have negative correlation with seed yield due to its high negative direct effect. The negative indirect effect of days to maturity via days to 50 per cent flowering showed that with a fixed maturity period the seed yield was adversely affected with delayed onset of flowering. It shows that seed yield was mostly a function of flowering duration. Kumar *et al.* (1995) and Sandhu *et al.* (1980) reported similar results.

The character 100-seed weight exhibited negative correlation with seed yield, but, on partitioning, the direct effect of this character was positive and moderate. Indirect effects of all the characters were negative particularly via number of pods per plant and pod length. Similar results were reported by Singh and Malhotra (1970 b) and Chandel *et al.* (1973).

Pod length showed positive correlation with seed yield per plant but its direct effect was negative. A negative direct effect of pod length on seed yield was also reported by Chandel *et al.* (1973); Sandhu *et al.* (1981) and Kumar *et al.* (1995). Apparently an increase in pod length makes less amount of photosynthates available for storage in the seed.

The protein content showed positive correlation with seed yield per plant due to its positive direct effect.

In general, indirect effects of the characters, viz; plant height, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod were high, while moderate to low indirect effects were observed via plant height, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod. Therefore, indirect selection practiced on these characters will result in the improvement of respective characters and ultimately seed yield.

An important consideration for formulating the path diagram is that all the important causal factors affecting the seed yield are included. Since, yield is very complex character affected by so many factors, it might not be feasible to include all the characters. Under these circumstances, provision is made for residual path which would take care of all such factors

which were excluded from such studies. In the present study the residual effect at genotypic level was 0.5918 which suggested that there might be a few more component traits responsible to influence the seed yield per plant than those studied.

For the improvement of seed yield, emphasis should be made on all yield contributing characters which are influencing it directly or indirectly. In the present study, overall picture of path analysis reveal that for improving yield in green gram, weightage in selection should be given more to the number of clusters and pods per plant, more number of seeds per pod, tall plant, late flowering time and increased 100-seed weight.

5.5 Genetic divergence

Plant breeders are always interested to assess the genetic diversity among the germplasm, varieties or advance breeding material available with them so as to utilize them in direct breeding programme because **(i)** genetically diverse parents are likely to produce high heterotic effects (Griffing and Lindston, 1954) and **(ii)** the distantly related parents within the same species when utilized in cross breeding programme are likely to produce wider spectrum of variability.

To a plant breeder, single character is not of so much importance as the combined merit of a number of desirable traits become more important when he is concerned with a complex trait like yield. So, for improving yield, selection of parents based on a number of characters having quantitative divergence is required which can be fulfilled by D^2 statistic developed by Mahalanobis (1936).

In the present study, D^2 statistic estimated on eighty six green gram genotypes for eleven characters showed that generalized distance (D) between two populations varied from 2.226 to 6.733 which was an indicator of the diversity present in the material evaluated.

5.5.1 Clustering pattern

On the basis of D^2 statistic, eight clusters were formed from eighty six genotypes. The clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of the same geographical area were grouped in different clusters indicating that there is no formal relationship between geographical diversity and genetic diversity. Many workers have arrived at similar conclusion in different pulse crops. Some of the examples are the studies of Gupta and Singh (1970), Sanmugam and Rangaswamy (1982), Natarajan *et al.* (1988), Veerabadhiran *et al.* (1996), for green gram and, for cowpea, Narsinghani *et al.* (1978), Singh and Tripathi (1985), Sonawane and Patil (1991) for black gram,Das and Gupta (1984) and Indian bean Birari and Ghanekar (1992).

Considerable higher intra and inter-cluster D values revealed very interesting trend of genetic diversity. Intra-cluster D values of various clusters were found to be comparatively small indicating thereby the presence of substantial genetic diversity even within the cluster. The maximum inter-cluster distance was found between cluster-III and VIII followed by cluster-III and VI and cluster-III and V.

In heterosis breeding genotypes of diverse clusters are known to play an important role of potential parents and when each genotype of

different cluster are inter crossed they are likely to produce heterotic combinations.

5.5.2 Cluster means

In the present study cluster-VIII had the highest mean values for seed yield per plant, plant height and number of pods per plant, cluster-VII for 100-seed weight, cluster-VI for number of seeds per pod, cluster-IV for number of pods per cluster, cluster-II for protein content, whereas cluster-III was superior for number of cluster per plant, pod length and prolong duration of days to flowering and days to maturity. Therefore, inter crossing of such genotypes involved in these clusters will be useful for inducing variability in the respective traits.

The clustering pattern could be utilized in crossing the parents and deciding the cross combinations which may generate highest variability for various traits. The superior genotypes for breeding programme can also be selected on the basis of cluster means and inter-cluster distance. Therefore, for creating wide spectrum of variability and increasing yield inter crossing of genotypes of cluster-VIII for seed yield per plant, plant height and number of pods per plant. Cluster-VII, VI, IV and II for 100-seed weight, number of seeds per pod, number of pods per cluster and protein content while cluster-III for number of clusters per plant, pod length and prolonged duration of days to flowering and days to maturity. Whereas for inducing earliness genotypes of cluster-VIII will be desirable.

SUMMARY AND CONCLUSION

VI SUMMARY AND CONCLUSIONS

The investigation reported here on green gram (*Vigna radiata* (L.) Wilczek) was carried out in a randomized block design with three replications at Regional Pulse Research Station, Gujarat Agricultural University, Navsari during Summer-1996. A set of eighty six genotypes was utilized to study the variability parameters, correlation, path coefficient analysis and genetic divergence taking one qualitative and ten quantitative characters including seed yield.

- The analysis of variance for all the characters with all the eighty six genotypes showed differences among the genotypes studied, indicating sufficient amount of variability present in the material.

- The genotypic and phenotypic variances were higher for plant height and number of pods per plant.

- The highest genetic coefficient of variation was observed for number of pods per plant followed by seed yield per plant, plant height, number of pods per cluster and pod length thereby indicating considerable amount of variability in the material for these characters.

- High heritability were found for all the characters except number of seeds per pod, indicating that these characters were less influenced by environment and direct selection for these components would be effective for further improvement in yield level.

- High genetic advance as per cent of mean recorded for number of pods per plant, seed yield per plant, plant height, number of clusters per plant and pod length indicated operation of additive gene action for these traits. Moderate to high heritability coupled with expected genetic advance for these

traits, indicated that more emphasis should be given to these characters while selection for further improvement in yield.

- Seed yield per plant exhibited highly significant and positive correlations with plant height, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod. Correlation between days to 50 per cent flowering and days to maturity, plant height with number of clusters per plant and number of pods per cluster, number of clusters per plant with number of pods per plant were also highly significant and positive.

- Considering the above relationships an ideal plant type in green gram can be considered having more number of clusters, pods per cluster, seeds per pod and pods per plant with increased plant height.

- Path coefficient analysis revealed the highest positive direct effect of number of clusters per plant followed by plant height, 100-seed weight, number of pods per plant, number of seeds per pod and days to 50 per cent flowering, while number of pods per cluster and protein content showed low direct effect. Days to maturity exhibited high negative direct effect, while pod length showed negative but low direct effect. Indirect effects through pod length, 100-seed weight and protein content were very low and negligible. Indirect effects of plant height, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod via days to maturity, plant height, number of clusters per plant and number of pods per plant were high and positive. Indirect effect of above characters via days to flowering, pod length and 100-seed weight were low and negative or positive.

- Based on these findings it could be concluded that in breeding programme aiming to improve seed yield in green gram, more weightage should be given mainly to plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100-seed weight.

- D^2 analysis indicated wider genetic variability among the eighty six genotypes which were grouped in eight clusters, cluster-III showed much genetic divergence with cluster-VIII, VI and V and cluster-IV with V.

- The clustering pattern did not show any relationship between geographic distribution and genetic divergence, as genotypes from the same area scattered in different clusters and the genotypes of different areas were grouped in the same clusters. Therefore, the breeder must evaluate their material for genetic diversity and should not merely depend on their geographical diversity.

- The characters number of pods per plant, seed yield per plant, number of clusters per plant, number of pods per cluster and plant height showed considerably high genetic divergence.

- Cluster-VIII was superior for the character seed yield per plant, plant height and number of pods per plant, cluster-VII, VI, IV and II for 100-seed weight, number of seeds per pod , number of pods per cluster and protein content whereas, cluster-III was superior for number of clusters per plant, pod length, days to flowering and days to maturity.

- As the characters number of clusters per plant, plant height, number of pods per plant, number of seeds per pod and number of pods per cluster possessed significant positive correlations with seed yield along with high

direct effects, it will be effective to inter cross the genotypes of cluster-III, VI, V and VIII for creating wide spectrum of variability and improving seed yield in green gram.

REFERENCES

Allard, R.W. (1960). 'Principles of Plant Breeding'. John Willy and Sons, Inc., New York, pp. 89 and 93.

Ali, M.S. and Shaikh, M.A.Q. (1987). 'Variability and correlation studies in summer mungbean (*Vigna radiata* (L.) Wilczek). Bangladesh J. Agric. Sci., **12** : 63 - 67.

Anonymous (1994 - 95). District wise area, production and yield per hectare of important food and non-food crops in Gujarat State. Directorate of Agriculture, Gujarat State, Ahmedabad.

Anonymous (1994 - 95). Season and crop report. Dept. of Agriculture, Gujarat State, Ahmedabad.

Arunachalam, A.S. (1979). Genetic variability and correlation studies in field bean (*Dolichos lablab* L.). Mysore J. Agric. Sci., **8(3)** : 369.

Birari, S.P. and Ghanekar, S.L. (1992). Genetic diversity in lablab bean. J. Maharashtra Agric. Uni., **17(2)** : 257 - 260.

Boomikumaren, P. and Rathinam, M. (1981). Correlation and path analysis in green gram (*Vigna radiata* (L.) Wilczek). Madras Agric. J., **68** : 643 - 647.

Borah, H.K. and Hazarika, M.H. (1995). Genetic variability and character association in some exotic collection of green gram. Madras Agric. J., **82(4)** : 268 - 271.

*Burton, G.W. (1952). Quantitative inheritance in grasses. Proc. 6th Int. Grassland Congr., **1** : 227 - 283.

Burton, G.W. and De Vane, S.H. (1953). Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. Agron. J., **45** : 478 - 481.

Byregowda, M.; Chandraprakash, J.; Jagadeesh Babu, C.S. and Rudraswamy, P. (1997). Genetic variability and inter-relationships among yield and yield components in green gram (*Vigna radiata* (L.) Wilczek). Crop Res., **13(2)** : 361 - 368.

Chandel, K.P.S.; Joshi, B.S. and Pant, K.C. (1973). Yield in mungbean and its components. Indian J. Genet., **33** : 271 - 276.

Chandra, N.; Mehra, R.B. and Chaturvedi, S.N. (1993). Genetic diversity in mung-bean. Indian J. Pulses Res., **6(2)** : 123 - 126.

*Choi, K.J.; Choi, H.G.; Lim, H.K. and Lee,D.K. (1986). Studies on mung bean varieties-variants in agronomic characteristics of mung bean varieties. Research Reports Rural Development Administration, Korea Republic Crops, **28** : 162 - 167. (Fide-4464. Pl. Breed. Abstr., **57** : 467).

Chopra, D.P. and Gupta, B.S. (1978). A study on genotypic and phenotypic variability in mung under rainfed conditions for western Rajasthan. Curr. Agric., **2** : 61 - 64.

Chowdhury, J.B.; Chowdhury, R.K. and Kakar, S.N. (1971). Studies on the genetic variability in moong (*Phaseolus aureus* Roxb.). J. Res., P.A.U., **8** : 169 - 172.

Das, P.K. and Gupta, T.D. (1984). Multivariate analysis in black gram (*Vigna mungo* (L.) Hepper). Indian J. Genet. Pl. Breed. **44(2)** : 243 - 247.

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

Falconer, D.S. (1960). "Introduction to quantitative genetics." Ronald Press Co., New York.

Falconer, D.S. (1981). "Introduction to quantitative genetics (II Ed.)." Ronald Press Co., New York.

Fisher, R.A. (1918). The correlation among relatives on the supposition of Mendelian inheritance. Trans. Royal Soc. of Edinburgh, **52** : 399 - 433.

*Fisher, R.A. (1936). The use of multiple measurement in taxonomic problems. Ann. Eugen., London, 7 : 179.

*Galton, F. (1989). "Natural Inheritance." Mac Millan, London.

Gayen, P.; Roychaudhury, P.; Dasgupta, T. and Dana, S. (1991). variability and correlation studies of some characters of pod and seed in mungbean (*Vigna radiata* (L.) Wilczek). Ann. Agric. Res., **12(3)** : 255 - 258.

Golsangi, B.S.; Parameswarppa, R. and Biradar, B.D. (1996). Studies on inter-character association and cause-effect relationship among quantitative characters at different plant densities in cowpea. Ann. Agric. Res., **17(3)** : 217 - 222.

Goulden, C.H. (1962). "Methods of Statistical Analysis." Asia Publ. House, New Delhi.

Griffing, B. and Lindston, E.W. (1954). A study of combining abilities of corn inbreds having varying proportions of corn belt and non-corn belt germplasm. Agron. J., **46** : 545 - 552.

Gupta, M.P. and Singh, R.B. (1970). Variability and correlation studies in greengram (*Vigna radiata* (L.) Wilczek). Indian J. Agric. Sci., **39** : 482 - 493.

Gupta, S.N.; Lal, S.; Rai, L. and Tomar, Y.S. (1982). Correlation and path analysis in mung bean (*Vigna radiata* (L.) Wilczek). H.A.U. J. Res., **12** : 287 - 291.

Holkar, S. and Yadava, H.S. (1995). Divergence analysis in F_2 mung bean (*Vigna radiata* (L.) Wilczek). Crop Res., **9(1)** : 81 - 84.

Hotelling, H. (1936). Relation between two sets of varieties. Biometrics, **28** : 321 - 377.

Ilhamuddin.; Tajammal, M.A. and Inayatullah (1989). Genotypic and phenotypic variability in yield and other quantitative characters in mungbean. Sarhad J. Agric., **5(1)** : 69 - 71.

Jackson, M.L. (1967). "Soil chemical analysis" Prentice Hall of India Pvt., New Delhi.

Jain, H.K. (1975). Development of high yielding varieties of pulses, perspectives, possibilities and experimental approaches. Int. Workshop on Grain Legumes, ICRISAT, Hyderabad, pp. 177 - 185.

Javia, A.L. (1986). Variability and association analysis in greengram. M.Sc. (Agri.) Thesis (Unpublished). Gujarat Agricultural University, Sardar Krushinagar, Dantiwada.

Johnson, H.W.; Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soyabean. Agron. J., **47** : 314 - 318.

*Khan, I.A. (1985). Correlation and path coefficient analysis of yield components in mung-bean. Bot. Bulle. Academia Sinica. **26** : 13 - 20 (Fide - 7389. Pl. Breed. Abstr., **55** : 810).

Krishnaiah, V.V.; Durgaprasad, M.M.K. and Hanumantha Rao, Y. (1979). Inter-relationship between yield and yield components in green gram. Andhra Agric. J., **26** : 1 - 4.

Kumar, S.S.; Sudhrshanam, A.; Vinodkumar, S. and Narshimha Reddy, V. (1995). Correlation and path coefficient analysis in green gram. Madras Agric. J., **82(3)** : 160 - 162.

*Liu, D.J.; Zhou, Y.F.; Liu, C.H. and Wu, B. (1984). Heritability, genetic correlations and path analysis of quantitative characters in local cultivars of *Phaseolus aureus*. Heriditas. **6** : 13 - 14. (Fide - 3375. Pl. Breed. Abstr., **56** : 359).

Mahalanobis, P.C. (1936). On the generalized distance in statistics. Proc. Nat. Inst. Sci., (India)., **2** : 49 - 55.

Malhotra, V.V.; Sukhdev Singh and Singh, K.B. (1974). Relation between genotypic diversity and genetic divergence and the relative role of each character toward maximizing divergence in green-gram. Indian J. Agric. Sci., **44** : 811 - 815.

Marangappanavar, L.R. (1986). Genetic diversity, gene action and character association in cowpea. Mysore J. Agric. Res., **20(3)** : 231.

Malik, B.A.; Tahir, M.; Khan, I.A.; Zubair, M. and Choudhary, A.H. (1987). Genetic variability, character correlation and path analysis of yield component in mung bean (*Vigna radiata* (L.) Wilczek). Pakistan J. Botany, **19(1)** : 88 - 89.

Miah, N.N. and Bhaora, S.K. (1989). Genetic variability in the F_2 generation of mung bean. Bangladesh J. Agric. Res., **14(1)** : 72 - 75.

Miller, A.A.; Williams, J.C.; Robinson, H.F. and Comstock, R.E. (1958). Estimates of genotypic and environmental variance and co-variance in upland cotton and their implications in selections. Agron. J., **50** : 126 - 131.

Misra, R.C. (1985). Criteria for choice of characters for construction of selection indices in green gram. Madras Agric. J., **72** : 265 - 271.

Misra, R.C. (1986). Genetic divergence in green gram (*Vigna radiata* (L.) Wilczek). G.A.U. Res. J., **12(1)** : 56 - 58.

Naidu, N.V. and Satyanarayana, A. (1991). Association between mean performance in green gram. Indian J. Agric. Sci., **61(6)** : 420 - 421.

Naidu, N.V. and Rosaiah, G. (1993). Association analysis in segregating and non-segregating population of mung bean (*Vigna radiata* (L.) Wilczek). Ann. Agric. Res., **14(1)** : 25 - 29.

Naidu, N.V.; Satyanarayana, A. and Raja Rajeshwar, V. (1994). Path analysis of yield and yield attributes in different environment in mung bean. Indian J. Agric. Sci., **28(1)** : 74 - 78.

Narsinghani, V.G.; Kanwal, K.S. and Singh, S.P. (1978). Genetic divergence in pea. Indian J. Genet., **28** : 375 - 379.

Natarajan, C.; Thiyagarajan, K. and Rathinaswamy, R. (1988). Association and genetic diversity studies in green gram. Madras Agric. J., **75(7)** : 238 - 245.

Natharajan, M. and Palaniswamy, (1990). Genetic divergence and realized heterosis based on dry matter components in mung bean (*Vigna radiata* (L.) Wilczek). Indian J. Genet., **50(3)** : 248 - 252.

Patel, H.S. (1989). Genetic variability, correlation and path coefficient analysis in green gram (*Vigna radiata* (L.) Wilczek). M.Sc. (Agri.) Thesis (Unpublished). Gujarat Agricultural University. Sardar Krushinagar, Dantiwada.

Patel, S.T. and Shah, R.M. (1982). Genetic parameters, association and path analysis in black gram (*Vigna mungo* (L.) Hepper). Madras Agric. J., **69** : 535 - 539.

Pandey, K.; Raghuvanshi, S.S. and Sing, S.P. (1988). Selection of parameters for different traits in mung bean (*Vigna radiata* (L.) Wilczek). Narendra Deva J. Agric. Res., **3(1)** : 69 - 72.

Panse, V.G. and Sukhatme, P.V. (1978). "Statistical Methods for Agricultural Workers II Ed." I.C.A.R. Publication, New Delhi.

Paramasivam, J. and Rajasekaran, S. (1980). Genetic variability in green gram (*Vigna radiata* (L.) Wilczek). Madras Agric. J., **67** : 421 - 424.

Parida, D. and Singh, D.P. (1984). Association, heritability and genetic advance in the F_2 generation of wide and varietal crosses of green gram. Madras Agric. J., **71** : 351 - 356.

Patil, H.S.; Deshmukh, R.B. and Deokar, A.B. (1987). Variability studies in some quantitative characters of mung bean. J. Maharashtra Agric. Uni., **12** : 132 - 134.

Patil, H.S. and Deshmukh, R.B. (1988). Correlation and path coefficient analysis in mung bean. J. Maharashtra Agric. Uni., **13(2)** : 183 - 185.

Pokle, V.S. and Patil, V.N. (1975). Path coefficient analysis in green gram. Sci. Cul., **41** : 265 - 266.

Pokle, V.S. and Nomulwar, M.T. (1977). Correlation and discriminant function in mung. Nagpur Agric. College Magazine, **50** : 29 - 31.

Pundir, S.R.; Singh, V.P. and Gupta, K.R. (1992). Genetic variability for some quantitative traits in mung bean (*Vigna radiata* (L.) Wilczek). Haryana Agric. Uni. J. Res., **22** : 109 - 112.

Ramana, M.V. and Singh, D.P. (1987). Genetic parameters and character association in green gram. Indian J. Agric. Sci., **57** : 661 - 663.

Ramanujam, S. and Tirumalachar, D.K. (1967). Genetic variability of certain characters in red pepper (*Capsicum annum* L.). Mysore J. Agric. Sci., **1** : 30 - 36.

Rao, C.R. (1952). "Advanced Statistical Methods in Biometrical Research", John Willy and Sons, Inc., New York, pp. 390.

Raut, S.K.; Chaudhari, M.S. and Khorgade, P.W. (1988). Character association and path analysis in green gram (*Vigna radiata* (L.) Wilczek). Annal. Pl. Physio., **2(1)** : 37 - 42.

Reddy, S.R. (1977). Study of genetic variability for yield and yield components and certain other characters in the germplasm of *Phaseolus aureus* Roxb. and *Phaseolus mungo* L. Thesis Abstr., **3** : 299.

Reddy, C.R.; Sekhar, M.R. and Reddy, K.R. (1994). Character association and path coefficient analysis in green gram (*Vigna radiata* (L.) Wilczek). Annal. Agric. Res., **15(4)** : 423 - 427.

Roquib, M.A. and Patnaik, R.K. (1990). Genetic variability in grain yield and its components in cowpea (*Vigna unguiculata*). Environ. Ecol., **8(1A)** : 197 - 200.

Sandhu, T.S.; Bhullar, B.S.; Cheema, H.S. and Brar, J.S. (1980). Path coefficient analysis for grain yield and its attributes in green gram. Indian J. Agric. Sci., **50** : 541 - 544.

Shanmugam, A.S. and Rangaswami, S.R. (1982). Genetic diversity for quantitative characters in green gram (*Vigna radiata* (L.) Wilczek). Madras Agric. J. **69(10)** : 631 - 636.

Sharma, J.D. and Gupta, V.P. (1994). Selection parameters in inter-specific derivatives of urdbean x mungbean. Indian J. Pulses Res., **7(2)** : 174 - 176.

Satyan, B.A.; Amarnath, K.C.N. and Siddaraju, I. (1989). Phenotypic and genotypic correlation coefficients of some quantitative characters in green gram. Current Res. Uni. Agric. Sci., **18(12)** : 170 - 172.

Searle, S.R. (1965). The value of indirect selection. Biometrics, **21** : 582 - 707.

Singh, K.B. and Malhotra, R.S. (1970 a). Estimates of genetic and environmental variability in mung (*Phaseolus aureus* Roxb.). Madras Agric. J., **57** : 155 - 159.

Singh, K.B. and Malhotra, R.S. (1970 b). Inter-relationships between yield and yield components in mung bean. Indian J. Genet., **30** : 244 - 250.

Singh, K.B.; Malhotra, R.S. and Singh, H. (1978). Correlation and path coefficient analysis in green gram. Indian J. Agric. Sci., **12** : 44 - 46.

Singh, R.P. and Pathak, M.M. (1987). Multivariate analysis of divergence in mungbean (*Vigna radiata* (L.) Wilczek). Farm Sci. J., **2(2)** : 182 - 183.

Singh, R.P.; Singh, M.L.; Singh, U. and Singh, I.P. (1977). Path analysis in green gram. Madras Agric. J., **64** : 296 - 297.

Singh, S.B. and Tripathi, B.K. (1985). Genetic divergence in pea. Indian J. Genet. Pl. Breed., **45(2)** : 389 - 393.

Singh, V.P.; Malik, B.P.S.; Yadava, R.K. and Chowdhury, J.B. (1980). Component analysis of yield in mung bean. Crop Improv., 7 : 97 - 101.

Sonawane, M.N. and Patil, F.B. (1991). Genetic divergence in forage cowpea. J. Maharashtra Agric. Uni., **16(2)** : 167 - 169.

Steel, G.D. and Torrie, J.H. (1960). "Principles and Procedures of Statistics." Mac Graw Hill Book Co. Inc., New York, pp - 481.

Thakur, C. (1979). "Scientific Crop Production Vol. 1." Metropolitan Book Co. Pvt. Ltd., New Delhi.

Thiagarajan, K.; Rathinaswamy, P. and Rajasekaran, S. (1988). Genetic divergence in cow pea. Madras Agric. J., **75(3)** : 125 - 128.

Tomar, G.S.; Singh, L. and Mishra, P.K. (1973). Correlation and path coefficient analysis of yield characters in mung bean. Genet. Abstr., **6** : 113 (Fide. Sabrao Newsletter, **5** : 125 - 127).

*Vavilov, N.Z. (1926). Studies on the origin of cultivated plants. Chronica Botanica, **13** : 116.

Veerabadhiran, P. and Jehangir, K.S. (1995). Genetic variability, correlation and path analysis in green gram. Madras Agric. J., **82(5)** : 365 - 367.

Veerabadhiran, P.; Ramamorthi, N. and Nadarajan, N. (1996). Genetic variation and diversity in green gram. Madras Agric. J., **83(10)** : 633 - 635.

Veeraswamy, R.; Rathanaswamy, R. and Palaniswamy, G.A. (1973). Genetic variability in some quantitative characters of *Phaseolus aureus* Roxb. Madras Agric. J., **60** : 1320 - 1322.

Vidyadhar; Sharma, G.S. and Gupta, S.C. (1984). Path analysis in green gram. Indian J. Agric. Sci., **54** : 144 - 145.

*Wilk's, S.S. (1932). Criterion of generalization in the analysis of variance. Biometrics, **24** : 471 - 484.

Wright, S. (1921). Correlation and causation. J. Agric. Res., **20** : 557 - 585.

Yohe, J.M. and Poehlman, J.M. (1975). Regression, correlations and combining ability in mung bean (*Vigna radiata* (L.) Wilczek). Tropical Agric., **52** : 343 - 352.

*** Original not seen**

Appendix - I : Meterological observations for the year 1996 at the Regional Pulse Research Station, Navsari

Months	Temperature (°C)		Humidity (%)	
	Max.	Min.	Max.	Min.
Feb - 96	33.1	23.5	58	42
Mar - 96	35.8	21.0	79	40
April - 96	34.7	23.1	81	43
May - 96	33.9	29.0	88	54
June - 96	33.2	27.4	82	68

Appendix-II : Mean performance of eighty six genotypes of green gram for various characters

Sr. No.	Genotypes	Seed yield per plant (g)	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100-seed weight (g)	Protein content (%)
1.	GM-9018	3.42	39.32	71.67	25.47	3.43	4.33	12.00	6.23	10.43	4.25	23.30
2.	GM-9110	4.59	38.33	70.68	38.87	7.30	6.03	42.63	8.17	11.90	4.52	25.71
3.	GM-9321	7.52	36.33	73.66	42.90	7.70	4.83	32.90	6.93	11.80	4.01	24.27
4.	GM-9307	6.24	37.00	69.00	47.23	6.20	5.07	31.83	7.43	10.23	4.44	21.84
5.	GM-9208	7.81	35.67	69.68	43.27	8.10	8.73	79.97	6.90	11.17	3.89	25.14
6.	GM-9411	4.32	38.33	73.00	43.77	5.57	5.16	33.06	5.80	8.20	4.13	23.68
7.	GM-84-13	5.13	34.67	71.98	35.30	6.78	5.17	32.20	5.83	11.90	4.65	24.62
8.	GM-9206	4.35	38.21	70.67	41.30	6.97	5.97	40.86	4.37	8.53	4.66	22.23
9.	GM-9023	7.93	37.66	69.67	41.67	4.53	5.30	21.50	5.30	10.56	4.51	25.33
10.	GM-9406	4.41	38.33	69.35	42.13	6.63	6.33	37.30	8.17	8.96	4.96	24.42
11.	GM-9317	8.86	35.67	71.32	40.57	5.73	6.70	36.00	7.20	9.50	4.03	23.50
12.	GM-88-44	4.52	33.33	74.33	41.06	6.47	7.20	37.27	6.43	11.00	4.72	21.30
13.	HUM-2	7.06	44.66	76.34	26.20	3.40	4.37	16.57	5.46	8.13	4.29	22.77
14.	GM-9315	4.87	36.21	72.68	34.63	5.00	6.83	39.57	4.21	11.26	5.02	23.87
15.	GM-9402	5.91	37.67	72.96	38.03	5.77	5.83	32.33	6.73	10.23	6.01	25.13
16.	GM-8801	5.69	42.67	71.31	34.57	6.83	7.43	50.90	5.10	8.43	4.88	22.61
17.	GM-9403	7.49	38.67	71.95	42.97	6.67	5.43	41.53	8.13	12.67	4.55	24.95
18.	GM-8906	9.76	31.33	55.99	40.87	6.98	6.37	44.20	7.20	12.96	4.52	24.08
19.	GUJ-3	6.31	41.66	70.68	46.37	6.00	4.77	21.60	6.30	9.67	4.66	23.32
20.	GM-86-14	7.90	44.67	72.67	33.03	5.03	6.33	33.73	5.13	11.13	4.98	25.54
21.	GM-9410	5.89	39.00	67.99	18.00	6.17	5.97	37.46	4.26	8.83	4.73	22.40
22.	GM-8213	6.58	38.22	73.00	30.03	8.00	8.27	76.40	6.56	9.23	4.62	23.31
23.	GM-9106	5.27	38.32	72.31	25.13	6.40	4.13	29.96	7.20	8.00	5.52	25.34
24.	GM-9316	5.01	36.99	72.66	34.60	5.73	4.93	27.00	5.10	9.17	4.49	22.23
25.	HUM-7	6.78	34.99	70.67	32.67	5.63	5.07	25.00	7.10	10.53	4.72	24.31
26.	GM-87-16	4.04	37.00	63.00	55.83	8.23	5.97	43.47	6.23	11.40	4.67	23.71
27.	GM-84-4	8.07	37.67	71.98	35.63	8.27	6.43	51.83	4.76	12.23	4.70	23.31
28.	GM-9404	7.75	37.00	74.65	30.03	6.37	5.36	25.50	6.10	13.67	5.27	22.24
29.	GM-9302	6.59	39.33	71.01	51.30	5.37	5.27	30.70	4.40	10.90	4.40	25.70
30.	GM-9006	8.33	37.65	73.00	46.00	7.27	5.26	37.17	7.26	11.80	4.94	21.67
31.	GM-9304	12.62	37.00	69.67	48.17	9.87	5.63	44.43	7.20	11.33	4.72	24.06
32.	PS-16	4.98	36.66	71.68	42.93	4.10	6.13	23.80	4.70	8.50	4.14	22.41

Appendix-II (Contd.)

Sr. No.	Genotypes	Seed yield per plant (g)	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100-seed weight (g)	Protein content (%)
33.	GM-9202	9.17	35.00	69.99	56.13	6.67	7.40	50.03	6.70	12.37	4.36	23.72
34.	GM-84-26	8.60	39.33	72.33	55.16	7.10	5.70	44.73	5.27	9.23	4.32	25.71
35.	GM-88-35	3.76	37.33	74.66	38.90	3.43	3.53	15.73	6.10	8.53	4.61	24.05
36.	GM-9419	10.27	41.67	71.33	57.90	6.97	5.53	47.36	8.67	14.56	5.08	23.32
37.	GM-9008	3.97	37.31	69.00	33.30	4.37	4.33	22.76	4.50	8.30	4.86	22.76
38.	GM-9310	6.10	45.33	72.33	43.23	6.06	5.27	34.33	5.93	8.23	5.25	21.68
39.	GM-9320	10.88	39.66	68.98	46.03	8.33	4.60	43.33	6.43	11.20	4.46	25.53
40.	GM-9408	7.50	41.33	72.33	44.93	5.27	5.13	31.76	4.17	12.20	4.79	24.61
41.	GM-9318	6.45	36.00	68.67	51.63	6.57	4.93	33.36	5.90	9.53	4.42	25.57
42.	GM-9010	8.05	43.00	69.33	53.70	6.06	4.70	33.40	6.50	8.86	4.96	22.61
43.	GM-9415	7.59	38.33	71.00	56.20	7.03	5.50	48.87	6.17	11.70	4.38	23.71
44.	K-851	6.20	37.67	57.44	37.40	5.83	5.33	35.33	5.30	11.60	4.36	22.42
45.	GM-9303	10.77	32.68	76.67	46.50	9.20	6.46	60.13	4.20	8.43	4.72	25.73
46.	GM-9306	4.62	40.68	71.66	44.93	6.67	4.70	35.77	7.37	10.26	4.85	21.85
47.	GM-9104	4.87	38.33	70.33	37.87	6.68	5.10	26.17	5.37	13.00	4.13	23.14
48.	GM-9307	4.41	36.66	70.67	49.33	5.76	5.33	30.26	8.10	8.56	4.37	24.06
49.	GM-9207	7.86	38.65	70.33	51.63	6.03	6.73	38.63	6.53	11.57	4.22	24.79
50.	GM-9409	4.95	38.66	71.00	46.70	10.33	4.13	43.93	7.47	11.26	4.24	25.55
51.	GM-9311	7.24	37.67	73.00	56.40	3.30	4.63	16.63	4.33	7.83	5.15	21.66
52.	GM-9317	6.95	38.34	72.01	40.13	8.37	4.56	33.20	6.00	11.36	3.97	25.72
53.	GM-8904	5.60	34.32	67.66	38.23	5.36	4.73	21.93	7.53	8.53	4.77	23.72
54.	GM-9103	4.04	37.99	72.98	59.80	4.33	3.27	17.10	5.50	11.60	4.15	24.24
55.	GM-9412	6.96	37.99	72.34	34.93	7.97	7.87	35.46	8.23	9.67	3.95	22.78
56.	GM-84-6	2.62	36.67	79.33	36.50	5.63	5.03	21.90	4.40	11.23	4.45	25.33
57.	GM-86-19	5.07	38.32	71.98	34.40	6.37	6.36	40.16	7.50	11.70	4.88	22.59
58.	GM-9420	7.01	32.67	70.56	33.70	4.83	6.20	31.46	5.17	14.27	5.11	25.71
59.	GM-86-17	6.43	39.02	76.00	36.93	6.07	5.36	33.87	5.57	9.53	4.95	24.84
60.	GM-9407	5.93	40.66	76.01	34.87	6.53	4.33	32.77	8.27	10.13	5.42	25.56
61.	GM-9413	3.75	37.68	62.00	31.33	4.73	6.57	27.27	5.60	10.73	5.15	25.55
62.	GM-9401	9.63	37.00	67.01	26.16	6.20	6.93	32.87	6.40	8.33	5.26	24.61
63.	Pusa-9072	3.80	40.66	76.33	28.60	3.80	5.27	21.33	7.57	9.30	4.20	22.77
64.	GM-9111	3.14	36.67	69.68	27.23	3.80	6.43	17.43	8.13	8.76	5.96	23.32

Appendix-II (Contd.)

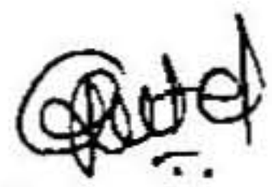
Sr. No.	Genotypes	Seed yield per plant (g)	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100-seed weight (g)	Protein content (%)
65.	GUJ-2	6.85	38.99	68.00	28.83	4.27	5.03	18.10	10.37	13.67	5.84	22.41
66.	GM-9002	4.71	41.33	74.00	19.73	3.37	4.67	13.90	7.50	10.60	5.13	25.91
67.	GM-9305	3.46	36.65	71.66	30.46	4.03	3.60	18.66	6.10	8.03	5.27	22.04
68.	GM-88-10	4.05	35.65	76.00	21.90	6.37	3.46	23.60	5.50	10.43	4.78	23.51
69.	GM-9309	4.86	41.00	73.00	24.33	5.07	3.93	22.57	6.50	9.53	5.20	22.49
70.	GM-9314	5.86	40.33	66.65	24.83	3.00	3.33	12.20	5.33	8.60	4.50	24.44
71.	GM-9001	3.62	34.98	71.00	24.93	3.86	3.97	16.93	7.13	11.33	4.92	21.84
72.	GM-9308	4.54	38.67	72.33	28.80	5.50	4.33	27.36	9.40	9.63	4.40	25.14
73.	GM-9405	2.63	39.66	76.66	13.90	4.13	4.33	17.80	5.07	9.00	5.26	24.06
74.	GM-9301	4.62	37.68	72.00	26.33	5.60	5.37	29.47	6.90	11.63	4.82	25.75
75.	GM-9021	5.93	34.66	67.68	22.73	6.13	3.40	21.50	7.47	9.80	5.67	22.23
76.	GM-3	6.39	38.98	71.66	27.93	4.36	5.07	23.47	6.00	8.20	5.12	25.35
77.	LGG-472	4.93	41.67	69.00	33.90	4.03	3.53	16.48	8.47	8.10	4.93	22.41
78.	RMG-337	3.07	54.22	86.43	21.53	8.60	7.07	15.00	9.23	8.56	5.19	24.26
79.	RUM-120	8.97	54.89	84.77	22.30	9.40	6.66	19.20	7.63	9.16	5.73	24.49
80.	RUM-112	2.73	45.79	80.55	32.30	9.26	6.97	26.20	5.80	8.63	4.33	22.61
81.	RUM-351	3.50	38.12	72.02	23.67	3.66	4.06	15.76	7.33	11.40	4.61	25.17
82.	Pusa-9531	4.50	35.66	75.00	36.60	4.13	3.90	19.36	6.53	12.40	4.42	24.62
83.	Pusa-9532	6.51	35.99	71.98	29.60	5.23	3.53	22.70	7.90	13.60	5.28	22.41
84.	Pusa-9571	3.72	37.98	73.00	26.13	4.40	4.37	24.20	7.97	10.53	4.26	25.38
85.	CO-4	7.85	50.67	85.33	58.43	9.20	7.50	18.77	8.17	12.43	4.15	22.23
86.	TARM-1	2.77	37.65	75.02	36.43	5.20	5.93	30.17	5.23	11.36	3.72	24.94
	Mean	6.002	38.660	71.860	37.405	6.011	5.380	31.210	6.464	10.387	4.721	23.853
	S.Em. ±	0.113	1.932	1.951	1.826	0.465	0.477	1.419	0.160	0.851	0.054	0.060
	C.D. at 5 %	0.314	5.381	5.430	5.082	1.294	1.336	3.954	0.445	2.375	0.150	0.167
	C.V. %	2.313	6.119	3.326	5.980	9.480	10.859	5.569	3.034	10.039	1.391	0.308

CERTIFICATE

This is to certify that I have no objection for supplying to any scientist only one copy or any part of this thesis at a time through reprographic process, if necessary for rendering reference services in a library or documentation centre.

Place : Navsari

Date : December २५, 1997



(C. R. Patel)