STUDIES ON VARIABILITY, GENETIC DIVERGENCE AND METROGLYPH ANALYSIS IN MUNG BEAN (*Vigna radiata* (L.) Wilczek)

By

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CERTIFICATE

Ms. Sankavaram Haritha has satisfactorily prosecuted the course of research and that the thesis entitled Studies on Variability, Genetic Divergence and Metroglyph Analysis in Mung bean (*Vigna radiata* (L.) Wilczek) submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that the thesis or part thereof has not been previously submitted by her for a degree of any university.

Date: 5.11.95

Major Advisor

CERTIFICATE

This is to certify that the thesis entitled **Studies on Variability, Genetic Divergence and Metroglyph Analysis in Mung bean (Vigna radiata (L.) Wilczek)** submitted in partial fulfilment of the requirements for the degree of *Master of Science in Agriculture* of the Acharya N. G. Ranga Agricultural University, Hyderabad is a record of the bonafide research work carried out by **Ms. Sankavaram Haritha** under our guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee.

No part of the thesis has been submitted by the student for any other Degree or Diploma. The published part has been fully acknowledged. All assistance and help received during the course of the investigation has been duly acknowledged by the author of the thesis.

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Place:
Date:

SANKAVARAM HARITHA

SYMBOLS AND ABBRIEVIATIONS

Centimeter	Cm
Coefficient of variation	CV
Genetic Advance	GA
Genetic advance as per cent of Mean	GAM
Genotypic	g
Genotypic Coefficient of Variation	GCV
Genotypic Correlation Coefficient	r_g
Gram	g
Harvest Index	HI
Heritability in broad sense	$h^2{}_{(b)}$
Hectare	ha
Kilogram	Kg
Number	no.
Per cent	%
Phenotypic	p
Phenotypic Coefficient of Variation	PCV
Phenotypic Correlation Coefficient	r_p
Similarity Correlation Coefficient	r_{cs}
Standard error of mean	SEm
Standard error of difference	SEd

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DECLARATION

I, **Miss Sankavaram Haritha**, hereby declare that the thesis entitled Studies on Variability, Genetic Divergence and Metroglyph Analysis in Mung bean (*Vigna radiata* (L.) Wilczeck) submitted to Acharya N.G. Ranga Agricultural University for the degree of ***Master of Science in Agriculture*** is the result of the original work done by me. I also declare that the material contained in this thesis has not been published earlier.

Date:

Haritha

Sankavaram Haritha

ABSTRACT

Author	**SANKAVARAM HARITHA**
Title of thesis	**STUDIES ON VARIABILITY, GENETIC DIVERGENCE AND METROGLYPH ANALYSIS IN MUNG BEAN(*Vigna radiata* (L.) wilczek).**
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The present investigation consisting of fifty diverse genotypes of mung bean (*Vigna radiata* (L.) wilczek) was carried-out to study genetic divergence, variability, heritability, and genetic advance as per cent of mean, character association and path coefficient analysis of thirteen quantitative characters. The experiment was laid-out at wetland farm, S.V. Agricultural College, Tirupati in a randomized block design with three replications during *rabi* 1998- '99. The data were recorded on thirteen quantitative characters viz., plant height, days to 50% flowering, days to maturity, branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, 100-seed weight, grain yield per plant, biological yield per plant and harvest index.

Genetic divergence studies revealed that the geographic diversity might not always be related to genetic diversity. Therefore, geographic diversity might not be an index of genetic diversity. A comparison of D^2 analysis with Metroglyph analysis revealed that clustering pattern in both the cases were different. In Metroglyph analysis only two most variable characters viz., 100-seed weight and grain yield per plant were considered whereas in D^2analysis consideration was given for all the characters and the D^2 values were based on pooled means of all the values representing the actual divergence. Hence, Mahalanobis's D^2statistic would be a powerful tool in measuring the genetic divergence.

For selection of genetically divergent desirable parental genotypes, the draw backs of Tocher's method of grouping of genotypes should be managed by comparing with one of the hierarchical method (Complete linkage dendrogram) for effective grouping of genotypes. Canonical root analysis is a confirmation tool available for graphical representation of divergence studies for effective visualization of clusters formed by both the above methods of grouping of genotypes. The genotypes STV 2674, EC 337105, EC 337112, EC 337105, RMG 406, ML 611, LGG 462 and STV 2762 were identified as the best genotypes.

The analysis of genetic parameters revealed higher genotypic coefficient of variation, heritability and genetic advance as per cent of mean for pods per plant, harvest index, plant height, branches per plant and grain yield per plant indicating that simple selection could be practiced for improving these characters.

Character association studies indicated the strong positive correlation of pods per plant, harvest index, biological yield per plant, clusters per plant and pods per cluster with

grain yield and also among themselves. Path coefficient analysis revealed the importance of clusters per plant, pods per cluster, biological yield per plant, days to maturity and seeds per pod in formulating selection criterion for effective improvement of seed yield.

INTRODUCTION

CHAPTER I

1 INTRODUCTION

Pulses form an essential component of vegetarian diet as they contain high protein content. Mung bean (*Vigna radiata* (L.) wilczek) has a good potential to meet the rising demand of pulses and forms an important constituent of Indian diet by providing less expensive source of vegetable dietary protein. It plays an important role in Indian agriculture due to its amenability to various cropping systems, nitrogen fixing ability and high nutritive value. Mungbean is known for its easy digestibility and low flatulence production compared to other pulses. It can also be grown as green manure as well as fodder crop.

India occupies first place with 24.380 million hectares in pulse harvesting area in the world with a production of 14.520 million tonnes against the world's average of 67.667 million hectares and 55.250 million tonnes respectively. Andhra Pradesh is one of the major mung bean growing states in India with an area of 4.719 lakh hectares producing nearly 2.052 lakh tonnes. The productivity of pulses in India is as less as 596 kg/hectare whereas productivity of pulses in the world averaged at 816 kg/hectare (FAO 1998). The per capita availability of pulses has declined from 64 gm/day (1951-1956) to less than 35 gm/day as against FAO/WHO's recommendation of 80gm/day. Since the growth in Pulse production did not keep up pace with an increase in population, the per capita availability of pulses has progressively declined.

It is estimated that the country's population will touch nearly 1350 million by 2020 AD. The country would then need a minimum of 30.3 million tonnes of pulses. The critical position of pulse production, particularly mung bean against the increased population cautioned a need-based research for improvement of sustainable productivity for achieving self-sufficiency in pulse production requirement. To meet the protein requirement of the entire population, there is an urgent need for evolving varieties having shorter duration, bold grain, and high yield potential and disease resistant to increase production.

Mung bean is a short duration legume maturing in about 60 to 75 days, therefore, fits well in various cropping systems involving cereals and commercial crops under rain-fed as well as irrigated conditions. However, the problem of low and uncertain productivity still persists in different agro-climatic niches. Borlaug (1973) rightly called pulse crops as 'slow runners', since, they failed to take the advantage of Green revolution. The constraints for low productivity have been analyzed and some of the factors limiting the break-through in mungbean are:

- Low yield potential of the present day cultivated types.
- Lack of yield stability and narrow adaptability.
- Susceptibility to major diseases like Yellow Mosaic virus and Powdery mildew.
- *Susceptibility* to abiotic stresses like drought, heat and salinity.
- Non-synchronous pod maturity and pod shattering.

Mung bean, a predominantly self-pollinated crop is genetically under-exploited. Improvement made in this crop from the variation created through hybridization or mutation followed by traditional breeding technique of selection has exhausted all the available variability for yield. This has necessitated to formulate an efficient breeding programme to develop stable high yielding cultivars. To accomplish this, an understanding of genetics of yield and yield component characters is essential. The breeding strategy for this crop also involves creation of variability, selection of stable and desirable genotypes from the germ plasm and utilization of selected lines in crop improvement programmes to develop a superior cultivar.

The success of hybridization in self-pollinated crops like mung bean is mainly dependent on the genetic divergence of the parents involved. This diversity not only results in inducing genetic variation but also provides new recombination of genes in the gene pool. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains. In addition to aiding in the selection of divergent parents for hybridization, D^2 statistic measures the degree of diversification and determines the relative contribution of each component character to the total divergence. Metroglyph analysis is a tool, which will eventually help to choose desirable parents for hybridization by classifying a collection of varieties into morphological complex and thus evolving superior varieties.

Generation of variability and selection of superior recombinants among the variants is the major objective of any plant breeding programme. One of the major constraints observed for the lack of break-through in the mungbean productivity has been the lack of genetic variability for high yield potential (Ramanujam, 1978). However, all the studies reported so far indicated considerable variability for yield component traits. Classification of available variability and selection of diverse parents belonging to distinct groups might lead to a wide spectrum of recombinants for quantitatively inherited traits. Hence, studies on genetic diversity are of considerable importance to classify the available genotypes into discrete classes so that parents belonging to diverse groups could be selected. However, it has not been adequately utilized in mungbean improvement programmes.

Seed yield, being a complex entity, is subjected to environmental fluctuations and is largely dependent on inter-relationships of various components. The knowledge of genotypic and phenotypic correlation among yield components and their relationship with yield is of paramount importance in selecting the superior genotypes. Besides, path analysis helps in determining the direct and indirect causes of association and permits to examine the specific forces acting to produce a given correlation. Path analysis also helps in formulating an effective breeding strategy to develop elite genotypes.

Realizing the importance and need for such a comprehensive study in mung bean, the present investigation involving 50 genotypes was carried-out with the following objectives:

- To estimate genetic divergence among 50 genotypes of mung bean by utilizing D^2 statistics and Metroglyph analysis.
- To analyse the findings of D^2 statistics and Metroglyph analysis.
- To study the variability parameters for yield and yield contributing characters.
- To assess the extent of association existing among different yield components with yield and among themselves.
- To reveal the direct and indirect contribution of each component character towards yield.

REVIEW OF LITERATURE

CHAPTER II

2 REVIEW OF LITERATURE

An attempt was made to critically review the literature of past research work done in relevance to the objectives of research programme in mung bean (*vigna radiata* (L.) wilczek) under the following headings.

- Genetic Divergence
- Genetic Parameters
- Character Association
- Path Coefficient Analysis

2.1 GENETIC DIVERGENCE

Mungbean, like other pulse crops was reported that it might have lost variability for high yield potential during the process of its domestication, as a result of its continued cultivation on marginal lands and neglected management conditions (Jain, 1981). Hence, it was suggested that variability thus lost needs to be regenerated by organizing massive hybridization programme using genetically diverse parents. Multivariate D^2 analysis was found to be the best technique to classify the genotypes on the basis of genetic distance between the characters.

Recent developments in quantitative genetics had a substantial contribution in the development of techniques to identify the genetically diverse parents for hybridization programme aimed at combining desirable genes from several sources. The importance of genetic diversity in crop plants was first realized by Darwin (1857) and the term “morphism” employing genetic morphs was given by Huxley (1955) which means the existence of distinct genetic forms in balance in a population. Selection of diverse parents belonging to distant groups leads to a wide spectrum of gene combinations for quantitatively inherited traits.

2.1.1 Mahalanobis's D^2 Analysis

Mahalanobis's D^2 analysis is an effective tool in quantifying the degree of divergence at genetic level and provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936) Gupta and Singh (1969) studied genetic divergence analysis using Mahalanobis's D^2 technique. They noticed the maximum contribution of seed weight and pod length towards the total divergence and grouped all the genotypes into ten clusters. They also reported that the parentage had definite effect on clustering pattern and it was suggested that locally adopted diverse parents might be exploited more successfully through hybridization.

The nature and magnitude of the genetic diversity was studied in 60 indigenous and exotic strains of mung bean by Malhotra *et al* (1974) on 7 characters by multivariate analysis using D^2 statistics. They grouped all the genotypes into 14 different clusters and noticed the presence of wide genetic diversity. It was indicated that geographic diversity didn't have a direct association with genetic diversity. They observed that days to flowering, seed size and primary branches contributed maximum towards genetic divergence.

Shanmugam and Rangaswamy (1982) reported a wide genetic variability among the 45 genotypes of mung bean as revealed by D^2 analysis and grouped them into sixteen clusters. It was found that the genotypes chosen from the same eco-geographic region were scattered into different clusters and the clustering together of genotypes of the same eco-geographic region into one cluster was also observed. They reported that yield per plant followed by number of clusters and pods per cluster contributed maximum towards genetic divergence.

Misra (1986) observed highly significant differences among 30 genotypes of mung bean for yield and seven related characters. He grouped all the 30 genotypes into ten groups and stated that genetic diversity was not related to geographic diversity.

Ramana and Singh (1987) grouped a total of 39 genotypes of mung bean grown in two seasons into 8 clusters using Mahalanobis's D^2 statistics. A total of 21 genotypes occurred in cluster I in the spring and 28 in cluster I in *kharif*. Days to flowering and 100-seed weight contributed most to genetic divergence in *kharif* and spring respectively.

Singh and Pathak (1987) calculated genetic divergence using Mahalanobis D^2 analysis in 20 genotypes of diverse origin in mung bean and grouped them into six clusters. It was found that the members of each cluster were geographically unrelated.

Tawar *et al* (1988) carried out genetic divergence using D^2 analysis in 34 diverse genotypes of mung bean and grouped all the genotypes into five clusters in which cluster I and cluster II had eight genotypes each, while cluster III had six genotypes. Cluster IV and V had five and seven genotypes respectively. Natarajan *et al* (1988) in their genetic diversity studies grouped forty-five genotypes of diverse origin of mung bean into four clusters for eight characters. They observed maximum inter cluster distance was between cluster III and IV and indicated that highly divergent types existed in these clusters. They also revealed that seed weight (57.81 per cent) contributed maximum towards genetic divergence followed by days to flowering (27.67per cent).

Naidu (1989) from his investigation with 49 diverse genotypes of mung bean for 13 quantitative and physiological characters reported the presence of considerable genetic diversity in the genotypes. The environments influenced clustering pattern with 14 clusters during *kharif* followed by 11 in *rabi* uplands and 8 in *rabi* rice fallows. The pattern of distribution into clusters was random irrespective of the parentage. Relation between geographic diversity and genetic diversity was not observed.

Nagaraja Rao (1990) tested for genetic divergence in 77 genotypes of mung bean and grouped all the genotypes into 12 clusters. The number of genotypes in different clusters varied from one in cluster IX, X, XI and XII to twenty-nine in cluster IV. It was also indicated the presence of substantial variability in the material under study. He also stated that there was no relationship between genetic diversity and geographical distribution.

Prasanna Rajesh(1995) carried out genetic divergence studies in seventy diverse genotypes of mung bean and grouped them into 8 clusters with 63 in cluster I and one genotype in the remaining clusters. The contribution of days to maturity and grain yield to maximum divergence was observed.

In a genetic divergence study involving 21 genotypes of mung bean, Veerabadhiran *et al* (1996) revealed that the genotypes chosen from the same eco-geographic region were found scattered in different clusters and clustering together of the genotypes from the same eco-geographic region was also observed.

Appalaswamy (1997) carried-out genetic divergence studies in fifty diverse genotypes of mung bean and grouped all the genotypes into 12 clusters in summer, 6 in winter season and 6 in rainy season respectively. It was also observed that the genotypes from different eco-geographic regions were clustered together indicating that the geographic diversity was not related to genetic diversity.

Manivannan *et al* (1998) from his investigation on genetic divergence in 30 genotypes of mung bean reported that the genotypes were grouped into eight clusters. The maximum contribution of plant height and pod length towards divergence was observed.

2.1.2 Metroglyph Analysis

Metroglyph analysis is a semi-graphic method of studying variability in large number of germ plasm series at the same time. This technique was developed by Anderson (1957) to investigate the pattern of morphological variation in crop species. Such analysis will eventually help to choose desirable parents for hybridization thus, in evolution of superior varieties. It can be used in a two-tier evaluation programme of germ plasm along with D^2 statistic.

Review of literature regarding metroglyph analysis on mungbean is meager; hence literature available on others is presented hereunder.

Singh and Choudary (1974) carried-out metroglyph and index score analysis for 33 varieties of mungbean and recognized four distinct morphological complexes on the basis of flowering time and yielding ability.

Ashok Chhabra *et al* (1985) studied the metroglyph analysis in ninety-three lines of broad bean and classified them into low, moderate and high yielding groups. Moreover, they reported that selection of parental lines from the different groups was suggested as a means of ensuring genetic divergence for most of the traits measured.

Hazarika *et al* (1986) evaluated 67 Pigeonpea lines of three field environments and reported that the grouping patterns of the lines differed between environments. Mishra *et al* (1987) studied seventy-five Soybean genotypes for genetic divergence through D^2 and metroglyph analysis and reported similar kind of results both in metroglyph analysis and index scoring to D^2 analysis.

Divergence analysis through metroglyph and D^2 techniques in 93 faba bean lines was studied by Chhabra *et al* (1988) and grouped them into six clusters. They found 56% congruence between the metroglyph and D^2 techniques.

Mishra and Rao (1990) carried-out a comparative study of D^2 and metroglyph analysis in 117 genotypes of Chickpea. They observed differences in clustering pattern obtained by metroglyph analysis as well as in D^2 analysis. Further they reported that geographic diversity was not associated with genetic diversity.

Borah and Hazarika (1991) studied metroglyph analysis for nine quantitative characters in 30 genotypes of mungbean and grouped them into 8 clusters based on seed yield and number of secondary branches per plant. Satyan *et al* (1991) using metroglyph analysis reported genetic divergence in 121 genotypes of mungbean and grouped them into nine clusters. It was also revealed that 100-seed weight and pod length contributed greatly for divergence. Further, they reported that there is no perfect correlation between geographic origin and genetic diversity. Singh *et al* (1991) while studying the morphological variations in Chickpea, observed no specific pattern of variability in metroglyph and index score analysis. They observed five distinct morphological complexes on the basis of flowering time and yielding ability.

Thiyagarajan and Rajasekaran (1993) studied seven *Vigna Unguiculata* cultivars and their 12 F_1 hybrids using metroglyph analysis and divided genotypes into low, medium and high yielding groups.

Mishra *et al* (1994) evaluated 30 genotypes of bengal gram using metroglyph analysis and grouped them into three categories – high, medium and low yielding groups. They revealed that metroglyph technique could be useful in scoring a large number of genotypes in early generation tests.

While studying metroglyph analysis for the morphological variations in 40 genotypes of Pigeonpea, Roy and Sharma (1994) grouped them into three categories based on yield per plant and plant height. Out of the 9 possible interacting groups, they noticed the distribution of varieties into seven groups.

Ramesh Babu (1998) carried-out metroglyph analysis in 40 genotypes of blackgram and reported that grain yield per plant and plant height exhibited maximum variability and classified the genotypes into eight sub groups.

2.1.3 Complete Linkage Dendrogram

Sorenson (1948) first developed complete linkage dendrogram or the "Farthest Neighbor" method, one of the agglomerative methods of hierarchical clustering approach. In this method, the distances or similarities of each individual are computed with every other individual. A comparison of the similarity coefficients among the pairs of individuals finally leads to a tree diagram, referred to as "Dendrogram". From the dendrogram the clusters of homogenous units can be identified. Several similarity measures have been proposed such as the Euclidean distance and the Mahalanobis distance. This method begins with a pair of similar objects and builds up into clusters. Clustering is done by utilizing the D^2 values and similarity/dissimilarity correlation coefficients by the technique as described by Sneath and Sokal (1973).

The work done regarding complete linkage dendrogram in mung bean is very meager. Hence, available literature on other crops was also summarized hereunder.

Forty genotypes of rice comprising 34 mutants of Kalakeri with five standard varieties were evaluated in two seasons by Mahapatra *et al* (1995) with a view to classify the entries into different clusters following D^2 analysis, canonical analysis, metroglyph analysis and numerical classificatory (dendrogram) analysis. Clustering pattern in different methods indicated that all the genotypes were grouped into three clusters in D^2 analysis, six clusters in metroglyph analysis and seven clusters in dendrogram method (at 0.8 similarity coefficient) of numerical taxonomic approach. This study revealed that the dendrogram approach was more potent for classificatory analysis of biological populations compared to other methods.

Seetaramaiah *et al* (1996) evaluated 17 pairs of CMS (A) and maintainer (B) lines for outcrossing influencing traits in rice. They reported that seven clusters were formed at 40% dissimilarity coefficient, indicated the presence of considerable amount of diversity in the population studied.

Genetic divergence 51 genotypes of spring-wheat was assessed using D^2 analysis by Gupta *et al* (1996) and they revealed that complete linkage dendrogram exhibited conformity with the clustering pattern of D^2 statistic (Tocher's method) at lower similarity coefficient level.

Shoeeb (1997) compared the Tocher's method of clustering with linkage dendrogram in 76 genotypes of coffee, confirmed the existence of differentiation in the clusters formed by these two methods of clustering. It was also concluded that both the methods in combination could be compared for selecting genetically diverse parents for effective breeding programme.

Appalaswamy (1997) compared the Tocher's method of clustering with linkage dendrogram in 50 genotypes of mungbean and concluded that the genotypes were grouped proportionately in case of complete linkage dendrogram. There were little differences in case of inter cluster D^2 values in both the methods.

Ramesh Babu (1998) carried-out genetic divergence studies in 40 diverse genotypes of blackgram and grouped them into 8 clusters. The difference in clustering by both methods was reported in which clusters with single genotypes were more in Tocher's method of clustering when compared to complete linkage dendrogram.

2.2 GENETIC PARAMETERS

The exploitation of genetic variability of quantitative traits generated through hybridization is the sole cause of improvement in any plant-breeding programme. Knowledge on the magnitude of genotypic and phenotypic variability present in any crop species plays a vital role in formulating a successful breeding programme. Estimation of genetic variability alone cannot indicate the possible improvement achieved through selection, but it should be used in conjunction with heritability and genetic advance.

The magnitude of heritability, the most important aspect of genetic constitution of breeding material, determines the degree of success in a selection programme. Heritability measures the relative amount of heritable portion of variability. Genetic advance under selection gives an idea about how much of the genetic gain could be obtained with the selection for a character. High heritability for the character is not always an indication of high genetic gain (Vishnuswarup and Chagle, 1962) but the character with high heritability coupled with high genetic advance could successfully be improved by direct selection (Paul, 1978). Therefore, the estimates of genetic variability, heritability and genetic advance had an immense value in identifying the superior genotypes.

A brief review of literature on genetic parameters is furnished here under.

2.2.1 VARIABILITY

S.No.	Character	Range	Reference
1	Plant height (cm.)	High	Bhargava *et al* (1966) Chowdhury *et al* (1971) Giriraj (1973) Veeraswamy *et al* (1973) Paramasivam and Rajasekharan (1980) Ramana and Singh (1987) Rosaiah (1987) Siddaraju (1987) Kalpana Pandey *et al* (1988) Natarajan *et al* (1988) Lakshmaiah *et al* (1989) Reddy *et al* (1991) Naidu *et al* (1991) Pundir *et al* (1992) Patil and Shinde (1995) Veerabadhiran *et al* (1996) Appalaswamy (1997) Ganesh Ram *et al* (1997)
		Low	Patil and Deshmukh (1988a)
2.	Days to 50% flowering (no.)	High	Singh and Malhotra (1970b) Giriraj (1973) Veeraswamy *et al* (1973) Sandhu *et al* (1979) Tickoo *et al* (1988)
		Low	Medhi *et al* (1980) Paramasivam and Rajasekharan (1980) Ramana and Singh (1987) Patil and Deshmukh (1988a) Borah and Hazarika (1995) Patil and Shinde (1995) Appalaswamy (1997) Shanti priya (1997) Sreedevi (1998)

3.	Days to maturity (no.)	High	Singh and Malhotra (1970b) Sandhu *et al* (1979) Tickoo *et al* (1988) Xianghuai He *et al* (1988)
		Low	Bhargava *et al* (1966) Joshi and Kabaria (1973) Veeraswamy *et al* (1973) Medhi *et al* (1980) Ramana and Singh (1987) Rosaiah *et al* (1987) Patil and Deshmukh (1988a) Borah and Hazarika (1995) Patil and Shinde (1995) Appalaswamy (1997) Shanti priya (1997) Sreedevi (1998)
4.	Branches per plant (no.)	High	Bhargava *et al* (1966) Gupta and Singh (1969) Krishnaswamy *et al* (1973) Veeraswamy *et al* (1973) Sandhu *et al* (1979) Siddaraju (1987) Sandhu *et al* (1988) Reddy *et al* (1991) Naidu *et al* (1991b) Pundir (1992) Borah and Hazarika (1995) Appalaswamy (1997)
		Low	Veerabadhiran *et al* (1996)
5.	Clusters per plant (no.)	High	Bhargava *et al* (1966) Singh and Malhotra (1970b) Veeraswamy *et al* (1973) Pandey *et al* (1978) Sandhu *et al* (1979) Medhi *et al* (1980) Paramasivam and Rajasekharan (1980) Singh and Sharma (1981) Ramana and Singh (1987) Rosaiah *et al* (1987) Siddaraju (1987) Sandhu *et al* (1988) Baisakhi *et al* (1989) Lakshmaiah (1989) Naidu *et al* (1991b) Borah and Hazarika (1995) Prasanna Rajesh(1995) Veerabadhiran and Jehangir (1995) Hiran Kumar (1996) Shanti priya (1997)
6.	Pods per cluster (no.)	High	Vijayabharathi (1993) Prasanna Rajesh(1995) Hiran Kumar (1996) Shanti priya (1997) Madhavilatha (1998)

7.	Pods per plant (no.)	High	Bhargava *et al* (1966) Gupta and Singh (1969) Singh and Malhotra (1970b) Chowdhury *et al* (1971) Giriraj (1973) Joshi and Kabaria (1973) Veeraswamy *et al* (1973b) Rathnaswamy *et al* (1978) Paramasivam and Rajasekharan (1980) Singh and Sharma (1981) Liu *et al* (1984) Ramana and Singh (1987) Rosaiah *et al* (1987) Siddaraju (1987) Kalpana Pandey *et al* (1988) Natarajan *et al* (1988) Sandhu *et al* (1988) Tickoo *et al* (1988) Baisakhi *et al* (1989) Reddy *et al* (1991) Naidu *et al* (1991b) Renganayaki and Sreerangaswamy (1993) Borah and Hazarika (1995) Khorgade (1995) Veerabadhiran and Jehangir (1995) Shanti priya (1997) Sreedevi (1998)
8.	Pod length (cm.)	High	Gupta and Singh (1970) Giriraj (1973) Sandhu *et al* (1979) Paramasivam and Rajasekharan (1980) Ganesh Ram (1997)
		Low	Bhargava *et al* (1966) Singh and Malhotra (1970b) Chowdhury *et al* (1971) Rosaiah *et al* (1987) Natarajan *et al* (1988) Patil and Deshmukh (1988a) Pundir *et al* (1992) Borah and Hazarika (1995) Patil and Shinde (1995) Appalaswamy (1997) Shanti priya (1997)
9.	Seeds per pod (no.)	High	Gupta and Singh (1969) Veeraswamy *et al* (1973) Sandhu *et al* (1979) Virmani *et al* (1983) Siddaraju (1987) Tickoo *et al* (1988)
		Low	Singh and Malhotra (1969) Giriraj (1973) Joshi and Kabaria (1973) Paramasivam and Rajasekharan (1980) Ali and Shaikh (1987) Rosaiah *et al* (1987) Natarajan *et al* (1988) Patil and Deshmukh (1988a) Pundir *et al* (1992) Borah and Hazarika (1995) Appalaswamy (1997)

10.	100- Seed weight (g)	High	Gupta and Singh (1969) Singh and Malhotra (1970b) Giriraj (1973) Sandhu *et al* (1979) Medhi *et al* (1980) Virmani *et al* (1983) Liu *et al* (1984) Mishra and Sahu (1985) Bhadra etal (1987) Tickoo etal (1988) Naidu *et al* (1991a) Pundir *et al* (1991) Reddy *et al* (1991) Madhavilatha (1998)
		Low	Bhargava *et al* (1966) Ramana and Singh (1987) Veerabadhiran and Jehangir (1995) Manivannan *et al* (1996) Appalaswamy (1997) Shanti priya (1997) Sreedevi (1998)
11.	Grain yield per plant (g)	High	Bhargava *et al* (1966) Singh and Malhotra (1970b) Chowdhury *et al* (1971) Giriraj (1973) Pandey *et al* (1978) Sandhu *et al* (1979) Tickoo *et al* (1988) Baisakh *et al* (1989) Naidu *et al* (1991a) Naidu *et al* (1991b) Pundir *et al* (1992) Renganayaki and Sreerangaswamy (1993) Vijayabharathi (1993) Khorgade (1995) Patil and Shinde (1995) Prasanna Rajesh(1995) Veerabadhiran *et al* (1996) Appalaswamy (1997) Ganesh Ram (1997) Shanti priya (1997) Madhavilatha (1998) Sreedevi (1998)
		Low	Patil and Deshmukh (1988) Reddy *et al* (1991)
12	Biological yield per plant	High	Thandapani (1985) Rathnaswamy *et al* (1986) Nijahawan (1988)
13	Harvest Index (%)	High	Madhavilatha (1998)

2.2.2 Heritability and Genetic Advance

S.No.	Character	Range	Reference
1.	Plant Height (cm.)	High Heritability and High GA	Bhargava *et al* (1966) Chowdhury *et al* (1971) Giriraj (1973) Veeraswamy *et al* (1973) Medhi *et al* (1980) Shah and Patel (1981) Ramana and Singh (1987) Siddaraju (1987) Kalpana Pandey *et al* (1988) Tickoo *et al* (1988) Lakshmaiah *et al* (1989) Naidu *et al* (1991a) Patil and Shinde (1995) Manivannan *et al* (1996) Ganesh Ram *et al* (1997)
		High Heritability and Low GA	Paramasivam and Rajasekharan (1980) Borah and Hazarika(1995)
		Low Heritability and Low GA	Singh and Pathak (1986) Rosaiah *et al* (1987)
2.	Days to 50% flowering (no.)	High Heritability and High GA	Chowdhury *et al* (1971) Giriraj (1973)
		High Heritability and Low GA	Singh and Malhotra (1970b) Medhi *et al* (1980) Singh and Pathak (1986) Ramana and Singh (1987) Naidu *et al* (1991a) Patil and Shinde (1995) Manivannan *et al* (1996) Appalaswamy (1997)
		Low Heritability and Low GA	Luthra and Singh (1978)
3.	Days to maturity (no.)	High Heritability and High GA	Empig *et al* (1970) Patil and Shinde (1995)
		High Heritability and Low GA	Singh and Malhotra (1970b) Joshi and Kabaria (1973) Medhi *et al* (1980) Shah and Patel (1981) Patil and Deshmukh (1988) Naidu *et al* (1991)
		Low Heritability and Low GA	Singh and Pathak (1986) Ramana and Singh (1987) Rosaiah *et al* (1987)

4.	Branches per plant (no.)	High Heritability and High GA	Krishnaswamy *et al* (1973) Siddaraju (1987) Naidu *et al* (1991) Borah and Hazarika (1995)
		High Heritability and Low GA	Paramasivam and Rajasekharan (1980) Naidu *et al* (1991a) Appalaswamy (1997)
		Low Heritability and Low GA	Manivannan *et al* (1996) Veerabadhiran *et al* (1996)
5.	Clusters per plant (no.)	High Heritability and High GA	Bhargava *et al* (1966) Chowdhury *et al* (1971) Veeraswamy *et al* (1973) Reddy and Krishnaiah (1977) Medhi *et al* (1980) Shah and Patel (1981) Mishra and Sahu (1985) Ramana and Singh (1987) Rosaiah *et al* (1987) Siddaraju (1987) Lakshmaiah *et al* (1989) Naidu *et al* (1991a) Khorgade (1995) Appalaswamy (1997)
		High Heritability and Low GA	Paramasivam and Rajasekharan (1980) Borah and Hazarika (1995)
		Low Heritability and High GA	Singh and Malhotra (1970b)
		Low Heritability and Low GA	Tickoo *et al* (1988)
6.	Pods per cluster (no.)	High Heritability and Low GA	Prasannarajesh (1995) Appalaswamy (1997)
7.	Pods per plant(no.)	High Heritability and High GA	Bhargava *et al* (1966) Giriraj (1973) Reddy and Krishnaiah (1977) Rathnaswamy *et al* (1978) Paramasivam and Rajasekharan (1980) Shah and Patel (1981) Parida (1982) Parida and Singh (1984) Mishra and Sahu (1985) Rosaiah *et al* (1987) Siddaraju (1987) Kalpana Pandey *et al* (1988) Naidu *et al* (1991a) Naidu *et al* (1991b) Yadav *et al* (1994) Khorgade (1995)
		High Heritability and Low GA	Singh and Pathak (1986) Appalaswamy (1997)
		Low Heritability and High GA	Gupta and Singh (1969) Singh and Malhotra (1970b)
		Low Heritability and Low GA	Tickoo *et al* (1988)

8.	Pod Length (cm.)	High Heritability and High GA	Chowdhury *et al* (1971) Rathnaswamy *et al* (1978)
		High Heritability and Low GA	Gupta and Singh (1969) Giriraj(1973) Veeraswamy *et al* (1973) Pokle and Nomulwar (1975) Borah and Hazarika (1995) Appalaswamy *et al* (1997)
		Low heritability and High GA	Paramasivam and Rajasekharan (1980)
		Low Heritability and Low GA	Shah and Patel (1981) Patel (1983) Rosaiah *et al* (1987) Manivannan *et al* (1996)
9.	100-Seed weight (g)	High Heritability and High GA	Bhargava *et al* (1966) Singh and Malhotra (1970b) Chowdhury *et al* (1971) Giriraj (1973) Pokle and Nomulwar (1975) Reddy and Krishnaiah (1977) Rathnaswamy *et al* (1978) Paramasivam and Rajasekharan (1980) Khorgade (1995)
		High Heritability and Low GA	Gupta and Singh (1969) Ramana and Singh (1987) Patil and Shinde (1995) Borah and Hazarika (1995) Appalaswamy (1997)
		Low Heritability and Low GA	Parida and Singh (1984) Patil and Deshmukh (1988) Manivannan *et al* (1996)
10.	Seeds per pod (no.)	High Heritability and High GA	Joshi and Kabaria (1973) Reddy and Krishnaiah (1977) Medhi *et al* (1980) Shah and Patel (1981) Tickoo *et al* (1988) Yadav (1994)
		High Heritability and Low GA	Giriraj (1973) Paramasivam and Rajasekharan (1980) Parida (1982) Naidu *et al* (1991) Borah and Hazarika (1995) Manivannan (1996) Appalaswamy (1997)
		High Heritability and Low GA	Bhargava *et al* (1966) Singh and Malhotra (1970b) Singh and Pathak (1986) Ramana and Singh (1987) Rosaiah *et al* (1987) Siddaraju (1987)

11.	Grain yield per plant (g)	High Heritability and High GA	Giriraj (1973) Ramana and Singh (1987) Rosaiah *et al* (1987) Kalpana Pandey (1988) Naldu *et al* (1991) Patil and Shinde (1995) Khorgade (1995) Ganesh Ram (1997)
		High Heritability and Low GA	Bhargava *et al* (1966) Gupta and Singh (1969) Paramasivam and Rajasekharan (1980) Singh and Pathak (1986) Patil and Deshmukh (1988) Borah and Hazarika (1995) Manivannan *et al* (1996) Veerabadhiran *et al* (1996) Appalaswamy (1997)
		Low Heritability and High GA	Singh and Malhotra (1970b) Parida and Singh (1984)
		Low Heritability and Low GA	Tickoo *et al* (1988)
12.	Harvest Index (%)	High Heritability and Low GA	Appalaswamy (1997)

2.2.3 Genetic Advance as per cent of Mean

S. No.	Character	Range	Reference
1.	Plant Height (cm.)	High	Bhargava *et al* (1966) Chowdhury *et al* (1971) Giriraj (1973) Veeraswamy *et al* (1973) Shah and Patel (1981) Ramana and Singh (1987) Siddaraju (1987) Natarajan *et al* (1988) Lakshmaiah *et al* (1989) Patil and Shinde (1995) Veerabadhiran and Jehangir (1995) Manivannan *et al* (1996) Veerabadhiran *et al* (1996) Madhavilatha (1998)
		Low	Paramasivam and Rajasekharan (1980) Borah and Hazarika (1993)
2.	Days to 50% flowering (no.)	High	Giriraj (1973) Veerabadhiran and Jehangir (1995)
		Low	Ramana and Singh (1987) Borah and Hazarika (1995) Manivannan *et al* (1996) Shanti priya (1997) Sreedevi (1998)
3.	Days to maturity (no.)	High	Empig *et al* (1970) Patil and Shinde (1995)
		Low	Singh and Malhotra (1970b) Joshi and Kabaria (1973) Veeraswamy *et al* (1973) Shah and Patel (1981) Rosaiah *et al* (1987) Patil and Deshmukh (1988) Borah and Hazarika (1995)
4	Branches per plant (no.)	Low	Paramasivam and Rajasekharan (1980) Manivannan *et al* (1996) Madhavilatha (1998)
5.	Clusters per plant (no.)	High	Singh and Malhotra (1970b) Chowdhury *et al* (1971) Veeraswamy *et al* (1973) Reddy and Krishnaiah (1971) Shah and Patel (1981) Misra and Sahu (1985) Ramana and Singh (1987) Siddaraju (1987) Lakshmaiah *et al* (1989) Khorgade (1995) Prasannarajesh (1995) Hiran Kumar (1996) Madhavilatha (1998)
		Low	Paramasivam and Rajasekharan (1980)
6.	Pods per cluster (no.)	High	Vijayabharathi (1993) Prasannarajesh (1995) Hiran Kumar (1996) Shanti priya (1997) Madhavilatha (1998)
7.	Pods per plant (no.)	High	Bhargava *et al* (1966) Gupta and Singh (1969) Singh and Malhotra (1970b) Giriraj (1973)

			Veeraswamy *et al* (1973) Reddy and Krishnaiah (1977) Rathnaswamy *et al* (1978) Shah and Patel (1981) Parida and Singh (1984) Ramana and Singh (1987) Natarajan *et al* (1988) Miahand Bhadra (1989) Vijayabharathi (1993) Borah and Hazarika (1995) Hiran Kumar (1996) Shanti priya (1997) Sreedevi (1998)
8.	Pod length (cm.)	High	Chowdhury *et al* (1971) Paramasivam and Rajasekharan (1980) Borah and Hazarika (1995)
		Low	Giriraj (1973) Veeraswamy *et al* (1973) Shah and Patel (1981) Rosaiah *et al* (1987) Patil and Shinde (1995) Shantipriya (1997) Madhavilatha (1998) Sreedevi (1998)
9.	Seeds per pod (no.)	High	Shah and Patel (1981) Borah and Hazarika (1995)
		Low	Giriraj (1973) Paramasivam and Rajasekharan (1980) Ramana and Singh (1987) Siddaraju (1987) Manivannan *et al* (1996) Madhavilatha (1998)
10.	100-Seed weight (g)	High	Singh and Malhotra (1970b) Chowdhury (1971) Giriraj (1973) Rathnaswamy *et al* (1979) Paramasivam and Rajasekharan (1980) Natarajan *et al* (1988) Khorgade (1995)
		Low	Patil and Deshmukh (1988) Patil and Shinde (1995) Manivannan *et al* (1996) Shanti priya (1997) Sreedevi (1998)

11.	Grain yield per plant (g)	High	Singh and Malhotra (1970b) Giriraj (1973) Joshi and Kabaria (1973) Parida and Singh (1984) Ramana and Singh (1987) Rosaiah *et al* (1987) Natarajan *et al* (1988) Renganayaki and Sreerangaswamy (1993) Vijayabharathi (1993) Borah and Hazarika (1995) Khorgade (1995) Prasannarajesh (1995) Hiran Kumar (1996) Shanti priya (1997) Madhavilatha (1998) Sreedevi (1998)
		Low	Patil and Deshmukh (1988)
12.	Harvest Index (%)	High	Madhavilatha (1998)

11.	Grain yield per plant (g)	High	Singh and Malhotra (1970b) Giriraj (1973) Joshi and Kabaria (1973) Parida and Singh (1984) Ramana and Singh (1987) Rosaiah *et al* (1987) Natarajan *et al* (1988) Renganayaki and Sreerangaswamy (1993) Vijayabharathi (1993) Borah and Hazarika (1995) Khorgade (1995) Prasannarajesh (1995) Hiran Kumar (1996) Shanti priya (1997) Madhavilatha (1998) Sreedevi (1998)
		Low	Patil and Deshmukh (1988)
12.	Harvest Index (%)	High	Madhavilatha (1998)

2.3 CHARACTER ASSOCIATION

2.3.1 Association of Component Characters with Grain yield

Genetic improvement of yield is the primary concern to the plant breeder. Yield is a complex character and is highly influenced by the environment. On the contrary, yield component traits are not only less complex and simply inherited but also influenced much less due to environmental deviations. Thus, selection based on the component characters has been considered to be more effective as compared to direct selection for yield (Grafius, 1956). Knowledge on the association of yield components with yield is of paramount importance while aiming at improvement in yield.

It is essential to have knowledge of genetic correlation among the factors contributing to the yield in order to affect selection of yieldcomponent characters. This leads to most effective method of selection by the use of favourable contribution of characters and to minimize the retarding effect of antagonistic correlation (Singh and Bains, 1967).

Several workers have studied the correlation coefficients in mung bean and contradictory associations have been reported for almost all the character pairs. This may be attributed to the different experimental material handled by them.

A brief review of literature on association of component characters with grain yield is presented here under:

S.No.	Character	Type of association	Reference
1.	plant height	Positive and Significant	Giriraj and Vijay Kumar (1974) Yohe and Poehlman (1975) Upadhya *et al* (1980) Raghuram Reddy (1980) Boomikumaran and Rathinam (1981) Lill *et al* (1985) Misra and Sahu (1985) Rosaiah (1985) Natarajan *et al* (1985) Khan (1988) Sandhu *et al* (1988) Singh *et al* (1988) Lakshmaiah *et al* (1989) Satyan *et al* (1989) Khorgade *et al* (1990) Nagaraja Rao (1990) Reddy *et al* (1991) Reddy sekhar (1992) Renganayaki and Sreerangaswamy (1993) Singh and Pathak (1993) Borah and Hazarika (1995) Sarma and Talukdar (1996) Manivannan and Nadarajan (1996) Shanti Priya (1997)
		Positive and Non-significant	Naidu *et al* (1991) Hiran Kumar (1996)
		Significant and Negative	Bhaumik and Jha (1976) Xianghuai He *et al* (1988) Ahuja and Chowdhury (1991) Veerabadhiran and Jehangir (1995)
		Negative and Non-significant	Holkar and Raut (1992) Pundir *et al* (1992) Madhavilatha (1998)
2.	Days to 50% flowering	Positive and Significant	Chandel *et al* (1973) Joshi and Kabaria (1973) Malhotra *et al* (1974) Giriraj and Vijayakumar (1974) Raghuram Reddy (1980) Lill *et al* (1984) Patil and Deshmukh (1988) Lakshmaiah *et al* (1989) Reddy *et al* (1991)
		Positive and Non-significant	Naidu (1989) Kumar *et al* (1995) Hiran Kumar (1996)
		Negative and Significant	Gupta and Singh (1969) Xianghuai He *et al* (1988) Holkar and Raut (1992) Patak and Patel (1993) Veerabadhiran and Jehangir (1995)
		Negative and Non-significant	Natarajan *et al* (1988) Babu Rao (1994) Veerabadhiran and Jehangir (1995)

3.	Days to maturity	Positive and Significant	Singh *et al* (1968) Joshi and Kabaria (1973) Gupta *et al* (1982) Patil and Deshmukh (1988) Lakshmaiah *et al* (1989) Satyan *et al* (1989) Naidu *et al* (1991) Singh and Pathak (1993) Reddy *et al* (1994) Kumar *et al* (1995) Sarma and Talukdar (1996) Hirankumar (1996)
		No correlation	Singh and Malhotra (1970 a) Shah and Patel (1981) Pathak and Patel (1993)
		Negative and Significant	Muntgomery *et al* (1972) Lawn (1979) Malik *et al* (1982) Holkar and Raut (1992)
		Negative and Non-significant	Sandhu *et al* (1980) Babu Rao (1994)
4.	Branches per plant	Positive and Significant	Singh and Malhotra (1970) Malhotra (1974 a) Pokle and Patil (1974) Upadhya *et al* (1980) Nagaraja Rao (1981) Shamsuzzaman *et al* (1983) Khan (1988) Rao (1990) Pundir *et al* (1992) Borah and Hazarika (1995)
		Negative and Significant	Sandhu *et al* (1978) Naidu (1989)
5.	Clusters per plant	Positive and Significant	Krishnaswamy *et al* (1973) Malhotra *et al* (1974) Raghuram Reddy (1980) Boomikumaran and Rathinam (1981) Nagaraja Rao (1981) Thandapani and Rao (1984) Vidhyadhar *et al* (1984) Ramana and Singh (1987) Malik *et al* (1987) Raut *et al* (1988) Singh (1988) Lakshmaiah *et al* (1989) Satyan *et al* (1989) Naidu (1989) Khorgade *et al* (1990) Naidu *et al* (1991) Patel (1991) Pundir *et al* (1992) Borah and Hazarika (1995) Poornachandra Rao (1995) Prasanna Rajesh(1995) Veerabadhiran and Jehangir (1995) Manivannan and Nadarajan (1996) Shantipriya (1997)
		Positive and Non-significant	Singh and Singh (1973 a) Sandhu *et al* (1979) Parida and Singh (1984) Mishra and Sahu (1985) Rosaiah *et al* (1987) Sandhu *et al* (1988) Reddy sekhar (1992) Reddy *et al* (1994)
		Negative and Significant	Khan (1988)

			Khan and Ahmed (1989) Sarma and Talukdar (1996)
6.	Pods per cluster	Positive and Significant	Satyan *et al* (1989) Patel (1991) Reddy sekhar (1992) Vijayabharathi (1993) Reddy *et al* (1994) Poornachandra Rao (1995) Prasanna Rajesh(1995) Sarma and Talukdar (1996) Manivannan and Nadarajan (1996) Appalaswamy (1997) Shantipriya (1997) Madhavilatha (1998) Sreedevi (1998)
		Positive and Non-significant	Gupta *et al* (1982)
7.	Pods per plant	Positive and Significant	Singh *et al* (1968) Gupta and Singh (1969) Singh and Malhotra (1970) Krishnaswamy *et al* (1973) Chandel *et al* (1973) Singh and Singh (1973 a) Giriraj and Vijay Kumar (1974) Malhotra *et al* (1974) Bhaumik and Jha (1976) Rathnaswamy *et al* (1978) Raghuram Reddy (1980) Nagaraja Rao (1981) Singh and Sarma (1981) Chowdhury *et al* (1982) Gupta *et al* (1982) Shamsuzzaman *et al* (1983) Lill *et al* (1985) Mishra and Sahu (1985) Malik *et al* (1987) Ramana and Singh (1987) Khan (1988) Natarajan *et al* (1988) Patil and Deshmukh (1988) Xianghuai He *et al* (1988) Sandhu *et al* (1988) Singh *et al* (1988) Lakshmaiah *et al* (1989) Satyan *et al* (1989) Khorgade *et al* (1990) Ahuja and Chowdhury (1991) Naidu *et al* (1991) Holkar and Raut (1992) Pundir *et al* (1992) Reddy sekhar (1992) Renganayaki and Sreerangaswamy (1993) Singh and Pathak (1993) Vijayabharathi (1993) Borah and Hazarika (1995) Poornachandra Rao (1995) Prasanna Rajesh(1995) Veerabadhiran and Jehangir (1995) Sreedevi (1998)
		Positive and Non-significant	Singh and Singh (1970) Tomar *et al* (1973) Shakoor *et al* (1978) Parida and Singh (1984) Reddy *et al* (1991)

8.	Pod length	Positive and Significant	Gupta and Singh (1969) Singh and Malhotra (1970 a) Joshi and Kabaria (1973) Singh *et al* (1980) Chowdhury *et al* (1982) Mishra and Sahu (1985) Singh *et al* (1988) Sandhu *et al* (1988) Xianghuai He *et al* (1988) Patil and Deshmukh (1988 a) Satyan *et al* (1989) Holkar and Raut (1992) Pundir *et al* (1992) Singh and Pathak (1993) Reddy *et al* (1994) Poornachandra Rao (1995) Prasanna Rajesh(1995) Veerabadhiran and Jehangir (1995) Hirankumar (1996) Manivannan and Nadarajan (1996)
		Positive and Non-significant	Tomar *et al* (1973) Sandhu *et al* (1979) Shakoor *et al* (1979) Raghuram Reddy (1980) Khan and Ahmed (1989) Naidu *et al* (1991b) Reddy sekhar (1992) Borah and Hazarika (1995)
		Negative and Significant	Kumar (1995)
		Negative and Non -significant	Giriraj and Vijaya Kumar (1974) Pathak and Patel (1993) Madhavilatha (1998)
9.	Seeds per pod	Positive and Significant	Singh *et al* (1968) Malhotra *et al* (1970) Joshi and Kabaria (1973) Giriraj and Vijaya Kumar (1974) Pokle and Patil (1974) Bhaumik and Jha (1976) Sandhu *et al* (1979) Parida (1982) Parida and Singh (1984) Ramana and Singh (1987) Sandhu *et al* (1988) Khan (1988) Natarajan *et al* (1988) Raut *et al* (1988) Xianghuai He *et al* (1988) Satyan *et al* (1989) Hari babu (1990) Naidu *et al* (1991) Pundir *et al* (1992) Reddy sekhar (1992) Singh and Pathak (1993) Reddy *et al* (1994) Borah and Hazarika (1995) Veerabadhiran and Jehangir (1995) Hiran Kumar (1996) Patil *et al* (1996) Sreedevi (1998)
		Positive and Non-significant	Singh and Singh (1970) Tomar *et al* (1973) Shakoor *et al* (1979) Raghuram Reddy (1980) Lakshmaiah *et al* (1989)
		Negative and Significant	Pathak and Patel (1993)

		Negative and Non-significant	Mishra and Sahu (1985) Madhavilatha (1998)
10.	100-seed weight	Positive and Significant	Singh *et al* (1968) Gupta and Singh (1969) Malhotra (1970) Bhaumik and Jha (1976) Parida (1982) Kumari and George (1985) Rosaiah (1985) Sandhu (1988) Raut *et al* (1988) Xianghuai He *et al* (1988) Naidu (1989) Ahuja and Chowdhury (1991) Holkar and Raut (1992) Pundir *et al* (1992) Singh and Pathak (1993) Reddy *et al* (1994) Kumar *et al* (1995) Borah and Hazarika (1995) Prasanna Rajesh(1995) Veerabadhiran and Jehangir (1995) Sarma and Talukdar (1996) Appalaswamy (1997) Madhavilatha (1998)
		Positive and Non-significant	Singh and Singh (1970) Singh and Malhotra (1970 a) Tomar *et al* (1973) Singh *et al* (1976) Sandhu *et al* (1979)
		Negative and Significant	Chandel *et al* (1973) Giriraj and Vijayakumar (1974) Rathnaswamy *et al* (1978) Raghuram Reddy (1980) Nagaraja Rao (1981) Reddy sekhar (1992) Vijayabharathi (1993) Hirankumar (1996)
		Negative and Non-significant	Upadhya *et al* (1980) Natarajan *et al* (1988)
11.	Biological yield per plant (g)	Positive and significant	Malik *et al* (1987) Natarajan *et al* (1988) Lampang *et al* (1987)
12.	Harvest index	Positive and Significant	Patil *et al* (1996) Applaswamy (1997) Madhavilatha (1998)

2.3.2 Association among yield component traits

Character pairs	Nature of association	Reference
Plant height with		
Branches per plant	Positive and significant	Manivannan and Nadarajan (1996)
	Negative and significant	Naidu (1989)
Clusters per plant	Positive and Significant	Natarajan (1988) Khorgade (1990) Naidu *et al* (1991) Reddy sekhar (1992) Borah and Hazarika (1995) Veerabadhiran and Jehangir (1995)

	Negative and significant	Misra and Sahu (1985)
Pods per cluster	Positive and significant	Khorgade *et al* (1990) Naidu *et al* (1991)
Pods per plant	Positive and significant	Reddy sekhar (1992) Borah and Hazarika (1995)
	Negative and significant	Veerbadhiran and Jehangir (1995)
Pod length	Positive	Saraswathy *et al* (1979) Sandhu (1979) Raghuram Reddy (1980) Singh and Sharma (1981) Manivannan and Nadarajan (1996)
	Negative and non significant	Pundir *et al* (1992)
Seeds per pod	Positive and significant	Natarajan *et al* (1988) Xianghuai He *et al* (1988) Lakshmaiah *et al* (1989) Satyan *et al* (1989) Naidu *et al* (1991) Pathak and Patel (1992) Reddisekar (1992) Sharma and Talukdar (1996)
	Negative and non significant	Pundir *et al* (1992)
100 Seed weight	Positive	Singh *et al* (1989) Naidu *et al* (1991) Sarma and Talukdar (1996)
	Negative and Significant	Raghuram Reddy (1980) Nagaraja Rao (1980) Pundir *et al* (1992) Reddisekar (1992) Veerabadhiran and Jahangir (1995)
Harvest index	Negative and Significant	Babu Rao (1994)
Days to 50% flowering with		
Days to maturity	Positive and significant	Singh and Malhotra (1970a) Malhotra *et al* (1974) Gupta *et al* (1982) Patil and Deshmukh (1988b) Naidu (1989) Kumar *et al* (l1995) Hiran kumar (1996) Madhavilatha (1998)
Plant height	Positive and significant	Singh and Malhotra (1970a) Raghuram Reddy (1980) Ramana and Singh (1987) Patil and Deshmukh (1988b) Naidu (1989) Kumar *et al* (1995) Veerabadhiran and Jehangir (1995)
	Negative and significant	Holkar and Raut (1992)
	Negative and non significant	Naidu (1989)
Branches per plant	Positive and Significant	Malhotra *et al* (1974) Raghuram Reddy (1980) Appalaswamy (1997)
Clusters per plant	Negative and significant	Sandhu *et al* (1979)

		Veerabadhiran and Jehangir (1995)
	Positive and significant	Malhotra *et al* (1974) Raghuram Reddy (1980)
Pods per plant	Positive and significant	Kumar *et al* (1995)
	Negative	Gupta and Singh (1969) Singh and Malhotra (1970a) Malhotra *et al* (1974) Sandhu *et al* (1974)
Pod length	Positive and significant	Singh and Malhotra (1970a) Malhotra *et al* (1974) Upadhya *et al* (1980) Ramana and Singh (1987)
	Negative	Sandhu *et al* (1979)
Seeds per pod	Positive and non-significant	Patil and Deshmukh (1988b)
100-Seed weight	Negative	Gupta and Singh (1969) Sandhu *et al* (1979) Raghuram Reddy (1980) Nagaraja Rao (1981)
Harvest Index	Negative and non-significant	Babu Rao (1994)
Days to maturity with		
Plant height	Positive and significant	Malhotra *et al* (1974) Lakshmaiah 91989) Patel and Narkheded (1989) Satyan *et al* (1989) Khorgade *et al* (1990) Naidu *et al* (1991) Kumar *et al* (1995) Sarma and Talukdar (1996)
Branches per plant	Positive and significant	Appalaswamy (1997)
	Negative and non-significant	Upadhya *et al* (1980) Naidu (1989)
Clusters per plant	Positive and significant	Naidu (1989) Satyan *et al* (1989) Khorgade *et al* (1990) Naidu *et al* (1991) Hiran kumar (1996) Sarma and Talukdar (1996)
Pods per plant	Positive and significant	Hiran kumar (1996)
	Negative	Pathak and Patel (1993)
Pod length	Positive and significant	Patil and Narkhede (1989) Kumar (1995)
	Negative and non-significant	Naidu *et al* (1989) Reddy *et al* (1994)
Seeds per pod	Positive and significant	Patil and Narkhede (1989) Pathak and Patel (1993)
	Negative	Sandhu *et al* (1979) Sarma and Talukdar (1996)
100-Seed weight	Positive and significant	Misra and Sahu (1985) Khorgade *et al* (1990) Naidu *et al* (1991) Sarma and Talukdar (1996)

	Negative and significant	Singh and Malhotra (1970a) Malhotra *et al* (1974) Reddy sekhar (1992)
Harvest index	Negative and non significant	Babu Rao (1994)
Branches per plant with		
Clusters per plant	Positive and significant	Manivannan and Nadarajan (1996)
Pods per cluster	Positive and non-significant	Manivannan and Nadarajan (1996) Appalaswamy (1997)
Pod length	Positive and non-significant	Manivannan and Nadarajan (1996)
Seeds per pod	Positive and significant	Upadhya *et al* (1980)
	Positive and non-significant	Manivannan and Nadarajan (1996)
100-Seed weight	Negative and non-significant	Pundir *et al* (1992)
Clusters per plant with		
Pods per cluster	Positive and significant	Satyan *et al* (1989) Manivannan and Nadarajan (1996)
	Negative and non-significant	Reddy *et al* (1994)
Pods per plant	Positive and significant	Malhotra *et al* (1974) Singh *et al* (1976) Sandhu *et al* (1979) Raghuram Reddy (1980) Nagaraja Rao (1981) Natarajan *et al* (1988) Lakshamaiah *et al* 91989) Satyan *et al* (1989) Khorgade *et al* (1990) Borah and Hazarika (1995) Veerabadhiran and Jehangir (1995) Hirankumar (1996)
Pod length	Positive and significant	Singh *et al* (1988) Singh *et al* (1989) Khorgade *et al* (1990) Naidu *et al* (1991)
	Positive and non-significant	Naidu (1989) Reddy *et al* (1994)
	Negative	Singh *et al* (1976) Satyan *et al* (1989)
Seeds per pod	Positive and significant	Singh and Malhotra (1970a) Singh *et al* (1988) Satyan *et al* (1989) Veerabadhiran and Jehangir (1995)
	Positive and non-significant	Natarajan *et al* (1988) Pundir *et al* (1992)
	Negative	Singh *et al* (1976) Sarma and Talukdar (1996)
100-Seed weight	Positive and significant	Singh *et al* (1988) Singh *et al* (1989) Khorgade *et al* (1990) Naidu *et al* (1991)

		Reddy *et al* (1994)
	Negative	Singh and Malhotra (1970a) Raghuram Reddy (1980) Natarajan *et al* (1988) Satyan *et al* (1989) Sarma and Talukdar (1996)
Harvest Index	Negative and significant	Babu Rao (1994)
Pods per plant with		
Pod length	Positive and significant	Singh and Singh (1970) Malhotra *et al* (1974) Singh *et al* (1988) Naidu *et al* (1991) Poornachandra Rao (1995)
	Negative	Singh *et al* (1968) Pokle and Patil (1974) Sandhu *et al* (1979), (1988) Satyan *et al* (1989)
Seeds per pod	Positive and significant	Singh and Singh (1970) Malhotra *et al* (1974) Singh *et al* (1988) Naidu *et al* (1991) Veerabadhiran and Jehangir (1995)
	Negative	Singh (1980)
100-Seed weight	Positive and significant	Singh and Singh (1970) Malhotra *et al* (1974) Singh *et al* (1988) Naidu *et al* (1991)
	Negative	Malhotra *et al* (1974) Raghuram Reddy (1980) Nagaraja Rao (1981) Liu *et al* (1984) Siddaraju (1987) Natarajan *et al* (1988) Satyan *et al* (1989) Reddiseakhar (1992)
Pods per cluster with		
Plant height	Positive and significant	Singh *et al* (1989)
Clusters per plant	Positive and significant	Singh *et al* (1989)
Pods per plant	Positive and significant	Gupta *et al* (1982) Singh et ai (1989) Reddy sekhar (1992) Vijayabhararthi (1993)
Pod length	Positive and non-significant	Reddy *et al* (1994)
	Negative	Gupta *et al* (1982) Singh *et al* (1989)
Seeds per pod	Positive and significant	Singh *et al* (1989) Reddy sekhar (1992) Reddy *et al* (1994)
	Negative and non-significant	Gupta *et al* (1982) Manivannan and Nadarajan (1996)
100-Seed weight	Negative and non-significant	Singh *et al* (1989) Reddy *et al* (1994)

Pod length with		
Seeds per pod	Positive and significant	Malhotra *et al* (1974) Bhaumik and Jha (1976) Nagaraja Rao (1981) Parida and Singh (1984) Misra and Singh (1985) Ramana and Singh (1987) Sandhu *et al* (1988) Reddy sekhar (1992) Borah and Hazarika (1995) Poornachandra Rao (1995) Veerabadhiran and Jehangir (1995) Patil *et al* (1996) Madhavilatha (1998)
	Positive and non-significant	Singh and Malhotra (1970a) Giriraj and Vijayakumar (1974) Raghuram Reddy 91980) Boomikumaran and Rathinam (1981)
Seed weight	Positive and significant	Misra and Sahu (1985) Patil *et al* (1996)
	Positive and non-significant	Malhotra *et al* (1974) Boomikumaran and Rathinam (1981) Sandhu *et al* (1988) Gayen *et al* (1991) Naidu *et al* (1991) Borah and Hazarika (1995)
Harvest Index	Positive and non-significant	Patil *et al* (1996)
Seeds per pod with		
100-Seed weight	Positive and significant	Patil and Deshmukh (1988b) Satyan *et al* (1989) Kumar *et al* (1995)
	Negative and significant	Malhotra *et al* (1974) Raghuram Reddy (1980) Natarajan *et al* (1988) Lakshmaiah *et al* (1989) Reddy sekhar (1992) Reddy *et al* (1994)
100-Seed weight with		
Pod length	Positive and significant	Shanti priya (1997)
Harvest index	Positive and significant	Patil *et al* (1996)
Harvest Index with		
Pod weight	Positive and significant	Patil *et al* (1996) Madhavilatha (1998)

2.4 PATH COEFFICIENT ANALYSIS

Path coefficient analysis, a statistical device developed by Wright (1934) helps in partitioning of the correlation coefficients into direct and indirect effects of independent variable on dependent variable. As yield is influenced by several factors, selection based on simple correlation without taking into consideration between the component characters is not effective. Hence, path analysis is of much importance in any plant breeding programme. Correlation in combination with path analysis would give a better insight into cause and effect relationship between different pairs of characters. Dewey and Lu (1959) and Frakes (1961) demonstrated the utility of path coefficient analysis in plant selection and since then its application has been extended to almost to every crop.

The available literature on path coefficient analysis is furnished here in a tabular form.

2.4.1 Direct Effects

Character	Positive direct effect on yield	Negative direct effect on yield
Plant height	Giriraj and Vijayakumar (1973) Malhotra *et al* (1974) Pokle and Patil (1974) Boomikumaran and Rathinam (1981) Malik *et al* (1987) Khan *et al* (1988) Patil and Deshmukh (1988) Patil and Narkhede (1989) Khorgade *et al* (1990) Renganayaki and Sreerangaswamy (1993) Kumar *et al* (1995) Sarma and Talukdar(1996) Manivannan and Nadarajan (1996) Madhavilatha (1998)	Gupta *et al* (1982) Malik *et al* (1982) Malik *et al* (1987) Ahuja and Chowdhury (1991) Holkar and Raut (1992) Reddy *et al* (1994) Appalaswamy (1997)
Days to 50% flowering	Patil and Deshmukh (1988) Naidu (1989)	Malik *et al* (1987) Natarajan *et al* (1988) Holkar and Raut (1992) Babu Rao (1994) Kumar *et al* 91995) Shantipriya (1997)
Days to maturity	Upadhya and Singh (1981) Misra and Sahu (1985) Patel (1991) Pathak and Patel (1993) Reddy *et al* (1994) Babu Rao (1994) Hiran Kumar (1996)	Malik *et al* (1987) Khan *et al*(1988) Patil and Deshmukh (1988) Appalaswamy (1997)

Branches per plant	Upadhya and Singh (1981) Satyan *et al* (1986) Khan *et al* (1988) Nagaraja Rao (1990) Kalpande (1997) Madhavilatha (1998)	Sandhu *et al* (1980) Naidu *et al* (1989) Pundir *et al* (1991)
Clusters per plant	Pokle and Patil (1974) Saraswathy *et al* (1979) Boomikumaran and Rathinam (1981) Gupta *et al* (1982) Thandapani and Rao (1984) Vidhyadhar *et al* (19840 Raut *et al* (1988) Nagaraja Rao (1990) Pundir *et al* (1992) Reddy sekhar (1992) Poornachandra Rao (1995) Veerabadhiran and Jehangir (1995) Hiran Kumar (1996) Appalaswamy(1997)	Malhotra (1974) Malik *et al* (1987) Khan (1988) Babu Rao (1994) Naidu *et al* (1994) Shantipriya (1997)
Pods per cluster	Boomikumaran and Rathinam (1981) Gupta *et al* (1982) Vijayabharathi (1993) Hirankumar (1996) Sarma and Talukdar (1996) Appalaswamy (1997)	Reddy *et al* (1994) Shantipriya (1997)
Pods per plant	Singh *et al* (1968) Singh and Malhotra (1970) Chandel *et al* (1973) Tomar *et al* (1973) Malhotra *et al* (1974) Meshram (1978) Rathnaswamy *et al* (1978) Saraswathy *et al* (1979) Shakoor *et al* (1979) Malik *et al* (1982) Thulasidas (1984) Kumari and George (1985) Misra and Sahu (1985) Siddaraju (1987) Natarajan *et al* (1988) Raut *et al* (1988) Singh *et al* (1988) Patil and Narkhede (1989) Khorgade *et al* (1990) Naidu *et al* (1991) Holkar and Raut (1992) Reddy sekhar (1992) Vijayabharathi (1993) Naidu *et al* (1994) Prasanna Rajesh(1995) Poornachandra Rao (1995) Veerabadhiran and Jehangir (1995) Kumar *et al* (1995) Manivannan and Nadarajan (1996) Byre gouda (1997) Kalpande (1997) Shantipriya (1997)	Pokle and Patil (1974) Gupta *et al* (1982) Vidhyadhar *et al* (1984) Pun and Villareal (1989)

Pod length	Tomar *et al* (1973) Giriraj and Vijaya Kumar (1974) Shakoor *et al* (1977) Gupta *et al* (1982) Thandapani and Rao (1984) Thulasidas (1984) Khan (1988) Misra and Sahu (1985) Patil and Narkhede (1989) Pundir *et al* (1992) Manivannan and Nadarajan (1996) Appalaswamy (1997)	Chandel *et al* (1973) Rathnaswamy (1978) Malik *et al* (1987) Holkar and Raut (1992) Kumar *et al* (1995)
100-Seed weight	Singh and Malhotra (1970) Chandel *et al* (1973) Saraswathy *et al* (1979) Thandapani and Rao (1984) Thulasidas (1984) Vidhyadhar *et al* (1984) Raut *et al* (1988) Patil and Deshmukh (1988b) Patil and Narkhede (1989) Pun and Villareal (1989) Khorgade *et al* (1990) Pundir *et al* (1992) Geetha *et al* (1993) Kumar *et al* (1995) Shantipriya (1997) Appalaswamy (1997) Byre gowda (1997) Madhavilatha (1998)	Giriraj and Vijayakumar (1973) Holkar and Raut (1992) Reddy *et al* (1994)
Seeds per pod	*Singh et al* (1968) Singh and Malhotra (1970) Malhotra *et al* (1974) Pokle and Patil (1974) Rathnaswamy (1978) Gupta *et al* (1982) Vidhyadhar *et al* (1984) Kumari and George (1985) Misra and Sahu (1985) Siddaraju (1987) Natarajan (1988) Raut *et al* (1988) Pun and Villareal (1989) Khorgade *et al* (1990) Geetha *et al* (1993) Prasanna Rajesh(1995) Shantipriya (1997) Byregowda (1997) Madhavilatha (1998)	Malik *et al* (1982) Malik *et al* (1987) Khan *et al* (1988) Patil and Deshmukh (1988) Naidu (1989) Pundir *et al* (1992) Renganayaki and Sreerangaswamy (1993)
Harvest index	Babu Rao (1994) Appalaswamy (1997) Madhavilatha (1998)	Patil *et al* (1996)

2.4.2 Indirect Effects:

2.4.2.1 Indirect effect of Plant height on yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50% flowering	Pathak and Patel (1993)	Kumar *et al* (1995)
Days to maturity	-	Kumar *et al* (1995) Sarma and Talukdar (1996)
Clusters per plant	Gupta *et al* (1982)	Sarma and Talukdar (1996)
Pods per plant	Malhotra *et al* (1974) Malik *et al* (1982) Khan (1988) Natarajan *et al* 91988) Singh *et al* (1989) Khorgade *et al* (1990) Holkar and Raut (1992)	Veerabadhiran and Jehangir (1995)
Pods per cluster	-	Sarma and Talukdar (1996)
Pod length	Pathak and Patel (1993)	Pundir *et al* (1992)
Seeds per pod	Malhotra *et al* (1974) Malik *et al* (1982) Khan (1988) Natarajan *et al* (1988) Khan and Ahmed (1989)	Pundir *et al* (1992) Sarma and Talukdar (1996)
100-Seed weight	-	Sarma and Talukdar (1996)

2.4.2.2 Indirect effects of Days to 50% flowering through

Character	Positive indirect effect	Negative indirect effect
Plant height	Natarajan *et al* (1988) Kumar *et al* (1995) Veerabadhiran and Jehangir (1995)	Patil and Deshmukh (1988)
Days to maturity	-	Patil and Deshmukh (1988)
Clusters per plant	Veerabadhiran and Jehangir (1995)	Natarajan *et al* (1988)
Pods per plant	Natarajan *et al* (1988) Kumar *et al* (1995)	Veerabadhiran and Jehangir (1995)
Pod length	Natarajan *et al* (1988) Pathak and Patel (1993) Veerabadhiran and Jehangir (1995)	Kumar *et al* (1995)
Seeds per pod	-	Natarajan *et al* (1988)
100-Seed weight	Kumar *et al* (1995)	Natarajan *et ai* (1988)

2.4.2.3 Indirect effect of days to maturity on yield through

Character	Positive indirect effect	Negative indirect effect
Plant height	Patil and Narkhede (1989) Kumar *et al* (1995) Sarma and Talukdar (1996)	Patil and Deshmukh (1988)
Pods per plant	Patil and Narkhede (1989) Khorgade *et al* (1990) Kumar *et al* (1995) Shantipriya (1997)	-
Seeds per pod	Patil and Deshmukh (1988)	-
Pod length	Patil and Deshmukh (1988) Pathak and Patel (1993)	Kumar *et al* (1995)

100-Seed weight	Kumar *et al* (1995)	Patil and Deshmukh (1988)

2.4.2.4 *Indirect effect of branches per plant on yield through*

Character	Positive indirect effect	Negative indirect effect
Plant height	Pundir *et al* (1992)	-
Clusters per plant	Pundir *et al* (1992)	-
Seeds per pod	Pundir *et al* (1992)	-

2.4.2.5 *Indirect effect of clusters per plant through*

Character	Positive indirect effect	Negative indirect effect
Plant height	Misra and Sahu (1985) Khan and Ahmed (1989)	Gupta *et al* (1982) Pundir *et al* (1992) Veerabadhiran and Jehangir (1995)
Days to 50% flowering	Misra and Sahu (1985)	-
Days to maturity	-	Veerabadhiran and Jehangir (1995)
Branches per plant	-	Pundir *et al* (1992)
Pods per cluster	Gupta *et al* (1982) Sarma and Talukdar (1996)	-
Pods per plant	Gupta *et al* (1982) Misra and Sahu (1985) Khan (1988) Natarajan *et al* (1988) Singh *et al* (1989) Khorgade *et al* (1990) Reddy sekhar (1992) Prasanna Rajesh(1995) Veerabadhiran and Jehangir (1995) Shantipriya (1997)	Pokle and Patil (1974)
Pod length	-	Pundir *et al* (1992)
100-Seed weight	-	Pundir *et al* (1992) Veerabadhiran and Jehangir (1995)

2.4.2.6 *Indirect effect of pods per cluster on yield through*

Character	Positive indirect effect	Negative indirect effect
Pods per plant	Reddy sekhar (1992) Prasanna Rajesh(1995) Shantipriya (1997)	-
100-Seed weight	Madhavilatha (1998)	

2.4.2.7 *Indirect effect of pods per plant on yield through*

Character	Positive indirect effect	Negative indirect effect
Plant height	Pokle and Patil (1974) Patil and Narkhede (1989) Kumar *et al*(1995)	Malik *et al* (1982)
Clusters per plant	Pokle and Patil (1974) Gupta eta l (1982) Vidhyadhar *et al* (1984)	-
Pods per cluster	Gupta *et al* (1982)	-
Pod length	Rathnaswamy *et al* (1978) Patil and Narkhede (1989)	-
Seeds per pod	Pokle and Patil (1974) Rathnaswamy *et al* (1978) Gupta *et al* (1982) Thulasidas (1984) Khan and Ahmed (1989) Holkar and Raut (1992) Reddy sekhar (1992)	-
100-Seed weight	Thulasidas (1984)	-

2.4.2.8 Indirect effect of pod length on yield through

Character	Positive indirect effect	Negative indirect effect
Plant height	Gupta *et al* (1982)	Misra and Sahu (1985)
Days to maturity	Patil and Narkhede (1989)	-
Clusters per plant	Vidhyadhar *et al* (1984)	Gupta *et al* (1982) Misra and Sahu (1985)
Pods per plant	Khan (1988) Natarajan *et al* (1988) Patil and Narkhede (1989) Holkar and Raut (1992) Kumar *et al* (1995) Veerabadhiran and Jehangir (1995)	Gupta *et al* (1982) Misra and Sahu (1985)
Pods per cluster	Kumar *et al* (1995)	Gupta *et al* (1982)
Seeds per pod	Rathnaswamy *et al* (1978) Gupta *et al* (1982) Vidhyadhar *et al* (1984) Khan (1988) Natarajan *et al* (1988) Khan and Ahmed (1989)	-
100-Seed weight	Patil and Narkhede (1989) Kumar *et al* (1995)	

2.4.2.9 Indirect effect of number of seeds per pod on yield through

Character	Positive indirect effect	Negative indirect effect
Plant height	Pokle and Patil (1974) Patil and Narkhede (1989) Sarma and Talukdar (1996)	Pundir *et al* (1992)
Clusters per plant	Gupta *et al* (1982) Thandapani and Rao (1984) Vidhyadhar *et al* (1984)	Malhotra *et al* (1974) Pundir *et al* (1992)
Pods per plant	Chandel *et al* (1973) Malhotra *et al* (1974) Rathnaswamy *et al* (1978) Gupta *et al* (1982) Patil and Narkhede (1989) Khorgade *et al* (1992) Holkar and Raut (1992) Reddy sekhar (1992) Pundir *et al* (1992) Veerabadhiran and Jehangir (1995)	Pokle and Patil (1974)
Pods per cluster	Gupta *et al* (1982)	-
Pod length	Gupta *et al* (1982) Thandapani and Rao (1984) Pathak and Patel (1993)	-
100-Seed weight	-	Thandapani and Rao (1984)

2.4.2.10 Indirect effect of 100-Seed weight on yield through

Character	Positive indirect effect	Negative indirect effect
Plant height	Kumar *et al* (1995) Sarma and Talukdar (1996)	Patil and Deshmukh (1988)
Days to 50% flowering	Veerabadhiran and Jehangir (1995)	-
Days to maturity	Patil and Narkhede (1989)	Patil and Deshmukh (1988) Misra and Sahu (1985)
Clusters per plant	Thandapani and Rao (1984) Veerabadhiran and Jehangir (1995)	Misra and Sahu (1985) Pundir *et al* (1992)
Pods per plant	Patil and Narkhede (1989) Singh *et al* (1989) Pundir *et al* (1992)	-
Pod length	Thandapani and Rao (1984) Veerabadhiran and Jehangir (1995)	–
Seeds per pod	Veerabadhiran and Jehangir (1995)	Thandapani and Rao (1984) Misra and Sahu (1985)

MATERIALS AND METHODS

CHAPTER III

3 MATERIALS AND METHODS

The present investigation was carried-out during *rabi* 1998-'99 at Wetland farm of Sri Venkateswara Agricultural College, Tirupati, situated at an altitude of 182.90m above mean sea level, 13°N latitude and 79°E longitude. The soil was sandy loam with medium fertility. The materials used and methods followed pertaining to the present investigation are presented here under.

3.1 MATERIALS

The experimental material consisted of fifty diverse genotypes of mung bean obtained from various zonal coordinating centers of India. The material was made available for the study by the Associate Director of Research (ADR), Regional Agricultural Research Station, Lam, Guntur (A.P.). The details of genotypes and the geographical region to which they are adapted are furnished in Table 1.

3.2 METHODS

3.2.1 Field Layout

The experiment was laid-out in a randomized block design replicated thrice. The crop was sown on 23rd December 1998 and each genotype was sown in single row of 4.5m length with a spacing of 30cm between rows and 15cm between plants within rows. Two seeds per hill were planted and later thinned to obtain the required level of 30 plants per row. Border rows were sown to avoid border effect and tresspass damage.

3.2.2 Crop Husbandry

The field was ploughed and harrowed twice until a fine tilth of soil was obtained. The crop was raised under irrigated conditions during *rabi* 1998 and was fertilized at the rate of 20 kgN, 50 kg P_2O_5 and 40kg K_2O per hectare in the form of Urea, Single super phosphate and Muriate of potash respectively. Irrigation, weeding and plant protection operations were taken up as and when needed during the crop growth uniformly to all genotypes.

Table 1 : Details of 50 genotypes of Mung bean

S. NO.	GENOTYPE	GEOGRAPHICAL REGION TO WHICH ADAPTED
1	STV 2662	Lam (A.P.)
2	STV 2667	Lam (A.P.)
3	STV 2669	Lam (A.P.)
4	STV 2674	Lam (A.P.)
5	STV 2762	Lam (A.P.)
6	STV 2705	Lam (A.P.)
7	STV 2724	Lam (A.P.)
8	STV 2731	Lam (A.P.)
9	STV 2781	Lam (A.P.)
10	STV 2442	Lam (A.P.)
11	STV 2810	Lam (A.P.)
12	STV 2789	Lam (A.P.)
13	STV 2790	Lam (A.P.)
14	Pusa 9131	New Delhi
15	Pusa 16	New Delhi
16	Jonnalagadd local	Lam (A.P.)
17	Pant M3	Pant Nagar (U.P.)
18	V 1628	Taiwan (Thailand)
19	MGG 221	Madhira (A.P.)
20	MGG 329	Madhira (A.P.)
21	STV 2774	Lam (A.P.)
22	STV 2773	Lam (A.P.)
23	EC 337108	New Delhi
24	COGG 901	Coimbatore (T.N.)
25	MGG 316	Madhira (A.P.)
26	MGG 318	Madhira (A.P.)
27	CO 4	Coimbatore (T.N.)
28	EC 337103	New Delhi
29	EC 337105	New Delhi
30	EC 337111	New Delhi
31	EC 337112	New Delhi
32	EC 337104	New Delhi
33	MGG 320	Madhira (A.P.)
34	ML 5	Ludhiana
35	MGG 295	Madhira (A.P.)
36	LGG 423	Lam (A.P.)
37	LGG 440	Lam (A.P.)
38	LGG 458	Lam (A.P.)
39	LGG 463	Lam (A.P.)
40	LGG 470	Lam (A.P.)
41	LGG 468	Lam (A.P.)
42	RMG 406	M.P.
43	RMG 475	M.P.
44	LGG 462	Lam (A.P.)
45	ML 611	Ludhiana
46	ML 515	Ludhiana
47	Ganga 6	Sri Ganga Nagar
48	RMG 452	M.P.
49	LGG 460	Lam (A.P.)
50	ML 682	Ludhiana

3.2.3 Data Recording

Observations were recorded on randomly chosen ten competitive plants in each genotype in each replication. The data were recorded on individual plants for the following quantitative characters except days to 50% flowering and days to maturity and their means were used for statistical analysis. The data on days to 50% flowering and days to maturity were recorded on plot basis.

3.2.3.1 Plant height (cm)

Length of main stem from ground level to the tip of the main raceme was measured in centimeters at maturity.

3.2.3.2 Days to 50 per cent flowering

Number of days taken from sowing to the attainment of flowering by 50 per cent of the plants in each plot and in each replication.

3.2.3.3 Days to Maturity

The number of days taken from the date of sowing to pod maturity by 50 per cent of the plants in each plot was taken as the number of days to maturity.

3.2.3.4 Number of branches per plant

Number of all branches at maturity was recorded as number of branches per plant.

3.2.3.5 Number of clusters per plant

Number of pod bearing clusters was counted on each sample plant at the time of harvest.

3.2.3.6 Number of pods per cluster

Number of pods from the effective clusters of each random sample plant were averaged and expressed as number of pods per cluster.

3.2.3.7 Number of pods per plant

Number of pods from all clusters on each plant was counted and was recorded as the number of pods per plant.

3.2.3.8 Pod length (cm)

Length of pods was measured in centimeters from the base of the pod to the tip excluding the beak. Ten randomly selected pods from each sample plant were measured and the average of all the pods length was expressed as the pod length in centimeters for that sample plant.

3.2.3.9 Number of seeds per pod

The seeds of ten randomly selected pods from each plant were counted and averaged to obtain the number of seeds per pod.

3.2.3.10 100-seed weight (g)

At random from each sample plant, one hundred well-filled seeds were counted and weighed in grams.

3.2.3.11 Grain yield per plant (g)

The seeds from each sample plant were dried and weighed in grams to obtain grain yield per plant.

3.2.3.12 Biological yield per plant (g)

The mean dry weight of the each of sample plants was expressed as Biological yield per plant in grams.

3.2.3.13 Harvest Index (%)

Harvest Index was calculated by using the formula,

$$\frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

3.3 STATISTICAL ANALYSIS

The treatment means obtained for each character was subjected to the following statistical analysis:

1. Analysis of Variance.
2. Estimation of genetic divergence using Mahalanobis's D^2 analysis, Metroglyph Analysis, Canonical root analysis and Complete linkage dendrogram (Hierarchical method).
3. Estimation of genotypic coefficient of variation, phenotypic coefficient of variation, heritability (broad sense) and genetic advance.
4. Estimation of phenotypic and genotypic correlations.
5. Path coefficient analysis.

3.3.1 Analysis of Variance

The data for different characters were statistically analyzed on the basis of the technique as propounded by Panse and Sukhatme (1957),

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where

Y_{ij} = Phenotypic observation in i^th^ genotype and j^th^ replication

μ = General Mean

g_i = Effect of i^{th} genotype

r_j = Effect of j^{th} replication

e_{ij} = Random error associated with i^{th} genotype and j^{th} replication

The analysis of variance of each character was carried out as indicated

Source of Variation	Degrees of Freedom	Sum of Squares	Mean Squares	F ratio
Replication	(r -1)	RSS	M_r	M_r/M_e
Genotypes	(t -1)	VSS	M_v	M_v/M_e
Error	(r -1)(t -1)	ESS	M_e	
Total	(rt – 1)	TSS		

Where

r = Number of Replications

t = Number of Genotypes

M_r = Mean Sum of Squares due to replications

M_v = Mean Sum of Squares due to genotypes

M_e = Mean Sum of Squares due to Error

The significance test was carried-out by referring to 'F' table value given by Fisher and Yates (1967).

3.3.2 Genetic Divergence

The data collected on different characters were analyzed through Mahalanobis's generalized distance (D^2), Metroglyph Method, Canonical root analysis and complete linkage dendrogram (Hierarchical Method).

3.3.2.1 Mahalanobis's generalized distance (D^2)

Genetic diversity between genotypes can be well estimated using D^2 analysis given by Mahalanobis (1936).

The D^2 value between i^{th} and j^{th} genotypes for p characters was calculated as

$$D^2_{ij} = P \sum_{t=1} (Y_{it} - Y_{jt})$$

where

Y_{it} = Uncorrelated mean value of i^{th} genotype for t character

Y_{jt} = Uncorrelated mean value of j^{th} genotype for t character

D^2_{ij} = D^2 value between i^{th} and j^{th} genotype

3.3.2.1.1 Test of Significance

Variances were calculated from all the 13 characters investigated and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1957). A dispersion table was prepared from the estimates. After testing the differences between genotypes for each of the characters, a simultaneous test of significance of differences between the mean values of a number of correlated variables was done (Rao, 1952) by using 'V' statistic, which in turn utilizes Wilk's λ criterion (Wilk, 1932). The sum of squares and sum of products of error and error plus variety variance – covariance matrix were used for this purpose.

The estimates of λ (Wilk's criterion) were done using the following formula:

$$\lambda = \frac{(E)}{(E + V)}$$

where

(E) = Determinant of error matrix

(E + V) = Determinant of error + Varieties matrix

The significance of 'λ' was tested by

$$X^2_{pq} = V = - m \log_e \lambda$$

where

m = $n - (p + q + 1) / 2$ with pq degrees of freedom

n = degrees of freedom of error + varieties

p = number of characters

q = number of genotypes – 1

$\log_e \lambda = 2.3407 \log_{10} \lambda$

3.3.2.1.2 Transformation of Correlated Variables

Transformation was done using pivotal condensation method. Transformation of correlated variables into standardised uncorrelated ones was done before working out the D^2 values because computation of D^2 values was reduced to simple enumeration of differences in mean values of various characters of the two genotypes i.e., Σdi^2.

3.3.2.1.3 Computation of D^2 values

The D^2 value between i^{th} and j^{th} genotypes for p characters was calculated as

$$D^2_{ij} = P \sum_{t=1} (Y_{it} - Y_{jt})^2$$

where

Y_{it} = Uncorrelated mean value of i^{th} genotype for 't' character

Y_{jt} = Uncorrected mean value of i^{th} genotype for 't' character

D^2_{ij} = D^2 value between i^{th} and j^{th} genotype

3.3.2.1.4 Testing the significance of D^2 values

The D^2 values obtained for a pair of genotypes was taken as the calculated value of 'χ^2' and tested against tabulated χ^2 at 'p' degrees of freedom where 'p' is the number of characters considered.

3.3.2.1.5 Determination of group constellations /clusters

Grouping of the genotypes into different clusters was done by using Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that any two variables belonging to the same cluster should at least on an average show a smaller D^2 value among themselves than those belonging to two different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes into order to know their relative distance from each other. For this purpose D^2 values of all the possible combinations in each genotype was arranged in increasing order of the magnitude in a tabular form as described by Singh and Chowdhury (1977). To start with, the genotypes having the smallest distance from each other are considered first to which third population having the smallest average D^2 value from the first two genotypes were added. Then comes the nearest fourth genotype and so it goes on. At certain stage, when it was felt that after adding a particular variety, there was an abrupt increase in the average D^2 value, then that variety was not considered for inclusion in that cluster. Thus, the process was continued till all the genotypes are included in one or the other cluster.

3.3.2.1.6 Average intra-cluster distance

For the measurement of intra cluster distances, the formula used was

$$\sum D_i^2/n$$

where

$\sum D_i^2$ = the sum of distances between all possible combinations (n) of the population included in a cluster.

3.3.2.1.7 Average inter-cluster distance

Clusters are taken one by one and their distance from other clusters was calculated. The distance between two clusters was the sum of the D^2 values between the members of other clusters divided by the product of number of genotypes in both the clusters under consideration.

Category	D values
Closely related	Below 22
Moderately divergent	Between 22 and 30
Highly divergent	Above 30

3.3.2.1.8 Cluster Diagram

The clusters and their mutual relationship were presented diagrammatically. The square root of average D^2, which was an approximate measure of divergence between groups, had been used to denote the distance.

3.3.2.1.9 Contribution of individual characters towards divergence

In all the combinations, each cluster was ranked on the basis of its contribution towards divergence between two entries ($d_i = Y_{it} - Y_{jt}$). Rank 1 is given to the highest mean difference and rank 'p' to the lowest difference, where 'p' is the total number of characters. Percentage contribution of each character (X) towards genetic divergence is calculated using the formula

$$X = (N \times 100) / M,$$

Where

N = number of genotype combinations where the character was ranked first

M = All possible combinations of number of genotypes

3.3.2.2 Metroglyph Analysis

Preliminary grouping of genotypes was done according to metroglyph analysis given by Anderson (1957). Replication means of characters were used for this purpose.

Two highly variable characters were selected. One of them was plotted on the X-axis and the other on Y-axis. Means of Y values were plotted against the means of X values for each genotype. A circle (glyph) on the graph thus represented a particular genotype. Besides, the two characters which were taken on X and Y-axes, all the other were represented by rays on the glyph. Each ray represents a particular character and occupies the same position on each glyph. The range of variation for each character was depicted by three grades of ray length, viz., very short ray, short ray and long ray. The grades low (L), medium (M) and high (H) for each character were obtained by dividing the range of variation into three equal classes.

3.3.2.3 Canonical Analysis

Canonical analysis was used to verify the clustering pattern obtained by Mahanalobis's D^2 statistics. The canonical vectors or roots were calculated to represent genotypes in two-dimensional graphical form (Rao, 1952). Various steps involved are:

3.3.2.3.1 Calculation of sum of squares and sum of products

The correlated standard means were transformed into the uncorrelated standardized variables. For each character and character combinations, sum of squares and sum of products were computed using the transformed variables to obtain the matrix of variances and covariances (Matrix A). From Matrix A, Matrix $(A)^p$ was derived where 'p' is the number of characters.

3.3.2.3.2 Calculation of the first vector

The first approximate trial vector was obtained by first getting the column totals of matrix $(A)^p$ and then by dividing each of the column totals by the highest quantity among them. The canonical variates were determined by interaction starting with the trial vector, each column of $(A)^p$ matrix was multiplied by this vector to get another column vector. The highest element in this vector was found and the vector elements were divided by this element. This new vector was then used as a trial vector and the procedure was repeated till the elements of the two approximation vectors were same. The vectors were then standardized by dividing them by the correlated sum of squares of these vectors. The first root λ, was calculated as the p^{th} root of the highest column total of the last approximation.

3.3.2.3.3 Calculation of the second vector

For getting the second vector λ_2, the original $(A)^p$ matrix was transformed and represented as $(B)^p$. In $(B)^p$, each $(i, j)^{th}$ element was calculated as follows

$(i, j)^{th}$ element = $(A)^p - \lambda_1 X_i{}^{th}$ element $X_j{}^{th}$ element of the first vector

The procedure followed in case of matrix A was repeated to obtain the second canonical root.

3.3.2.3.4 Estimation of Z values

From the values of $Y_1, Y_2, \ldots\ldots, Y_{ij}$ the mean values of characters considered Z_1, Z_2 and Z_3 were calculated as

$Z_1 = (Y)(V_1);\; Z_2 = (Y)(V_2)$

where (Y) was mean transformed values and V_1, V_2 were the first and second vectors respectively. The mean values Z_1 and Z_2 for each genotype were represented in a two-dimensional diagram.

3.3.2.3.5 Contribution of vectors towards divergence

Total contribution of all vectors was given by sum of diagonal elements in matrix A.

Per cent of vector1 (λ_1) = $(\lambda_1 \times 100)$ / (Total contribution of all vectors)

Per cent of vector1 (λ_2) = (λ_2 x 100) / (Total contribution of all vectors)

3.3.2.4 Complete linkage Dendrogram

This was one of the hierarchical methods as classified by Everitt (1974), starts with the computation of the 'distance' or similarities of each individual with every other individual. A comparison of such similarity coefficients among the pairs of individuals or objects finally leads to a tree diagram, referred as 'Dendrogram'. For the dendrogram, the clusters of homogeneous units can be identified.

Sorenson (1948) first developed the method, Complete linkage dendrogram. Johnson (1967) called this method as 'Maximum' method. This method was based on the distance matrix D. Computation of a similarity measurement between all possible pairs of D^2 values would result in an 'n' x symmetrical matrix (where n is the number of genotypes). Similarity measurement was nothing but correlation coefficient between the variables. Any coefficient C_{ij} in the matrix gives the resemblance between i and j. The next step is to arrange the objects into a hierarchy. So objects (genotypes) were associated with other groups which they most closely resemble and so on until all the objects had been placed into a complete classification scheme (Sneath and Sokal, 1973).

The essential features of this particular method of cluster analysis could be summarized as,

1. The correlation coefficient was used as a similarity measure.
2. Highest similarities were clustered or linked first
3. Two objects (genotypes) could be connected only if they had mutually highest correlation with each other.
4. After two objects (genotypes) were clustered, their correlations with all other objects were averaged.

3.3.3 Estimation of Genetic parameters

The data obtained from the analysis of variance were used to estimate the following parameters.

3.3.3.1 Phenotypic and Genotypic Variance

The phenotypic and genotypic variances were estimated according to the method of Lush (1940).

$$\text{Genotypic variance } (\sigma^2{}_g) = \frac{\text{Mean squares due to treatments} - \text{Mean squares due to error}}{\text{Number of replications}}$$

Phenotypic variance $(\sigma^2{}_p) = (\sigma^2{}_g)$ + variance due to error

3.3.3.2 Phenotypic and Genotypic coefficients of variation (PCV and GCV)

These were computed according to Burton (1952)

$$\text{Phenotypic coefficient of variation (\%)} = \frac{(\text{Phenotypic standard deviation x 100})}{(\text{General Mean})}$$

$$\text{Genotypic coefficient of variation (\%)} = \frac{(\text{Genotypic standard deviation x 100})}{(\text{General Mean})}$$

Categorization of the range of variation was affected as proposed by Sivasubramanian and Menon (1973)

Less than 10%	- Low
10 - 20%	- Moderate
More than 20%	- High

3.3.3.3 Heritability in broad sense ($h^2{}_{(b)}$)

Heritability in broad sense was estimated using the formula of Allard (1960)

$$\text{Heritability } h^2{}_{(b)} = \frac{\text{Genotypic variance}(\sigma^2{}_g)}{\text{Phenotypic variance } (\sigma^2{}_p)} \times 100$$

As suggested by Johnson *et al* (1955), $h^2_{(b)}$ estimates were categorized as

Low	0 - 30%
Medium	30 - 60%
High	61% and above

3.3.3.4 *Genetic Advance (GA)*

This was estimated as per the formula proposed by Lush (1949) and Johnson *et al* (1955)

$$GA = K.\ \sigma_{p.}\ h^2_{(b)}$$

where

K = selection differential at 5 per cent selection intensity which accounts to a constant value 2.06 (Lush, 1949)

$h^2_{(b)}$= heritability in broad sense

σ_p = phenotypic standard deviation

3.3.3.5 *Genetic Advance as per cent of Mean (GAM)*

$$GAM = GA\ /\ \text{Grand Mean} \times 100$$

The range of Genetic Advance as per cent of Mean was classified as suggested by Johnson *et al* (1955)

Low	less than 10%
Moderate	0 - 20%
High	more than 20%

3.3.4 Character Association

Genotypic and phenotypic correlation coefficients were calculated using the method given by Johnson *et al* (1955)

3.3.4.1 Genotypic Coefficient of Correlation (r_g)

$$r_g\,(x_i\,x_j) = \frac{\mathrm{Cov}_g(x_i\,x_j)}{\sqrt{v_g(x_i)\,.\,v_g(x_j)}}$$

where $r_g(x_i\,x_j)$ = Genotypic correlation between i^{th} and j^{th} characters

$v_g(x_i)$ = Genotypic variance of i^{th} character

$v_g(x_j)$ = Genotypic variance of j^{th} character

$\mathrm{Cov}_g\,(x_i\,x_j)$ = Genotypic covariance between i^{th} and j^{th} characters

3.3.4.2 Phenotypic Coefficient of Correlation (r_p)

$$r_p\,(x_i\,x_j) = \frac{\mathrm{Cov}_p\,(x_i\,x_j)}{\sqrt{v_p(x_i)\,.\,v_p(x_j)}}$$

where $r_p(x_i\,x_j)$ = Phenotypic correlation between i^{th} and j^{th} characters

$v_p(x_i)$ = Phenotypic variance of i^{th} character

$v_p(x_j)$ = Phenotypic variance of j^{th} character

$\mathrm{Cov}_p\,(x_i\,x_j)$ = Phenotypic covariance between i^{th} and j^{th} characters

The significance of correlation coefficients were tested by comparing genotypic and phenotypic correlation coefficients with the table value (Fisher and Yates,1963) at (n–2) degrees of freedom at 5% and 1% level of significance, where 'n' denotes the number of treatments used in the calculations.

3.3.5 Path Coefficient Analysis

The direct and indirect effects of the yield components on the yield were estimated by Path coefficient analysis as illustrated by Dewey and Lu (1959).

The path coefficients were obtained by solving the 'p' normal equation following the matrix method given by Singh and Chowdhury (1985).

The following set of simultaneous equations were formed and solved for estimating various direct and indirect effects.

$$
\begin{array}{l}
r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots\ldots\ldots\ldots\ldots +r_{1i}P_{iy} \\
r_{2y} = r_{21}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots\ldots\ldots\ldots\ldots +r_{2i}P_{iy} \\
\quad . \qquad . \qquad . \qquad . \qquad\qquad\qquad\qquad . \\
\quad . \qquad . \qquad . \qquad . \qquad\qquad\qquad\qquad . \\
\quad . \qquad . \qquad . \qquad . \qquad\qquad\qquad\qquad . \\
r_{iy} = r_{i1}P_{1y} + r_{i2}P_{2y} + r_{i3}P_{3y} + \ldots\ldots\ldots\ldots\ldots +P_{iy}
\end{array}
$$

where r_{12} to r_{i-1} = coefficient of correlation among causal factors.

P_{1y} to P_{iy} = direct effects of characters 1 to i on character y.

The above equations were written in a matrix form as under

$$
\begin{array}{cccc}
A & & C & B \\
\begin{bmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ . \\ . \\ r_{iy} \end{bmatrix}
& =
& \begin{bmatrix}
1 & r_{12} & r_{13} \;\ldots\ldots\ldots & r \\
r_{21} & 1 & r_{23} \;\ldots\ldots\ldots & r_{2i} \\
r_{31} & r_{32} & 1 \;\ldots\ldots\ldots & r_{3i} \\
. & . & . & . \\
. & . & . & . \\
r_{i1} & r_{i2} & r_{i3} \;\ldots\ldots\ldots & r_{i3}
\end{bmatrix}
& \begin{bmatrix} P_{1y} \\ P_{2y} \\ P_{3y} \\ . \\ . \\ P_{iy} \end{bmatrix}
\end{array}
$$

Then

$$B = [\,C\,]^{-1} A$$

where [C] = $\begin{bmatrix} C_{11} & C_{12} & C_{13} \;\ldots\ldots & C_{1i} \\ C_{21} & C_{22} & C_{23} \;\ldots\ldots & C_{2i} \\ C_{i1} & C_{i2} & C_{i3} \;\ldots\ldots & C_{ii} \end{bmatrix}$

Then direct effects were calculated as follows

$$P_{1y} = {}^{i}\Sigma_{i=1}\, C_{1i}\, r_{1y}$$

$$P_{2y} = {}^{i}\Sigma_{i=2}\, C_{2i}\, r_{2y}$$

$P_{ly} = {}^{l}\Sigma_{i=l}\ C_{ii}\ r_{iy}$

Besides the direct and indirect effects, the residual effect which measures the contribution of the characters not considered in the causal scheme was obtained as,

Residual effect (P_{RY}) = $1 - (P_{1y}r_{1y} + P_{2y}r_{2y} + \ldots\ \ldots\ \ldots\ \ldots)$

where P_{RY} = residual effect

P_{iy} = direct effect of x_i on y

r_{iy} = correlation coefficient of x_i on y.

RESULTS

CHAPTER IV

4 RESULTS

Fifty genotypes of mung bean were evaluated for variability, genetic divergence, mean performance, character association and path analysis for thirteen characters viz., plant height, days to 50% flowering, days to maturity, branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, 100-seed weight, grain yield per plant, biological yield per plant and harvest index. The data collected on these characters were used for biometrical studies. The results obtained from these investigations are furnished in this chapter.

4.1 MEAN PERFORMANCE

The data recorded on thirteen characters was subjected to analysis of variance. (Table: 2) The treatment differences among the fifty genotypes were significant for all the characters studied and the mean performance of these genotypes is presented in Table: 3.

4.1.1 Plant height

The mean of genotypes for plant height ranged from 27.33 to 49.20 cm with a general mean of 36.80 cm. Among all the genotypes STV 2773 was the shortest and LGG 468 was the tallest. Nineteen genotypes were taller than their general mean height value.

Table 2: Analysis of variance for thirteen characters for fifty genotypes of Mung bean.

S.No	Character	Replication df = 2	Treatment df = 49	Error df = 98
1	Plant Height (cm.)	0.02	71.77**	1.22
2	Days to 50% flowering	0.05	6.41**	0.51
3	Days to maturity	0.08	44.57**	1.79
4	Branches per plant	0.03	1.33**	0.03
5	Clusters per plant	0.01	9.40**	0.25
6	Pods per cluster	0.02	0.47**	0.03
7	Pods per plant	0.14	253.32**	4.34
8	Pod length (cm.)	0.02	0.66**	0.03
9	Seeds per pod	0.21	1.94**	0.15
10	100-Seed Weight (g)	0.00	0.27**	0.00
11	Grain yield per plant (g)	0.15	38.51**	0.75
12	Biological yield per plant (g)	0.12	44.77**	0.80
13	Harvest Index (%)	1.03	130.06**	3.53

** Significant at 1% level

Table 3: Mean performance of fifty genotypes for thirteen quantitative characters in Mung bean

S.No	Genotype	Plant height (cm.)	Days to 50% flowering	Days to maturity	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm.)	Seeds per pod (no.)	100-seed weight (g)	Grain yield per plant (g)	Biological yield per plant (g)	Harvest index (%)
1	LGG468	49.20	44.66	75.66	0.93	7.60	4.40	32.33	6.21	8.73	4.03	11.40	38.12	29.91
2	COGG901	34.00	42.33	68.33	1.80	7.00	3.33	23.00	7.20	10.46	3.35	8.07	30.88	26.15
3	LGG463	32.93	41.66	67.33	1.40	8.40	3.13	25.33	7.10	9.46	3.47	8.33	33.15	25.12
4	LGG470	39.00	42.00	67.33	0.86	7.06	3.66	27.46	7.02	10.40	3.07	8.43	35.31	23.87
5	LGG440	30.93	43.66	71.33	0.73	7.53	3.33	22.00	6.00	9.73	3.48	8.34	29.52	28.22
6	EC337104	40.66	43.00	71.33	1.60	7.00	3.13	21.53	5.47	8.46	3.28	5.98	29.74	20.10
7	LGG423	33.86	44.33	75.00	1.33	8.20	3.53	27.33	6.17	8.73	3.83	8.82	31.77	27.76
8	LGG458	47.00	43.33	69.33	2.53	9.60	4.20	38.60	5.79	8.53	3.41	10.90	37.55	29.05
9	Co 4	33.53	41.00	65.33	1.46	7.20	3.13	23.80	6.77	10.46	3.65	8.64	31.17	27.73
10	MGG319	32.40	45.00	74.00	2.53	8.73	3.66	31.06	6.20	8.64	3.15	8.36	30.96	27.01
11	STV2731	37.66	45.33	76.00	1.93	9.13	3.46	31.60	5.79	8.46	3.09	8.27	30.68	26.96
12	MGG320	46.66	42.33	66.00	1.73	9.60	3.73	34.93	6.13	10.53	3.60	12.92	36.10	35.78
13	MGG316	27.76	42.33	69.00	1.53	9.40	3.40	28.53	6.21	10.33	3.78	11.21	33.80	33.05
14	STV2790	31.73	44.00	73.33	0.80	7.33	3.73	26.60	6.52	10.40	3.82	10.57	32.73	32.29
15	EC337108	39.40	42.00	67.66	1.13	11.13	3.80	40.73	7.16	10.73	3.64	15.94	39.77	40.06

S.No	Genotype	Plant height (cm.)	Days to 50% flowering	Days to maturity	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm.)	Seeds per pod	100-seed weight (g)	Grain yield per plant (g)	Biological yield per plant (g)	Harvest index (%)
16	MGG329	34.46	41.00	64.66	3.06	9.26	3.46	31.46	6.04	8.80	3.71	9.65	31.85	30.28
17	Pusa9131	32.73	43.33	69.33	2.73	9.93	3.53	34.66	6.06	9.86	2.99	10.22	32.87	31.08
18	ML5	38.73	44.00	70.33	3.26	11.13	3.60	39.13	6.73	9.66	3.15	12.12	33.61	36.04
19	Pusa16	41.93	41.66	65.66	0.66	11.26	3.66	41.73	6.73	10.06	3.48	14.62	36.71	39.82
20	MGG 295	35.93	41.00	63.66	0.86	8.60	3.66	30.73	6.22	8.86	2.92	7.97	29.75	26.79
21	STV 2773	27.33	43.00	69.33	1.66	7.00	3.33	22.46	5.50	8.60	3.21	6.22	28.96	21.45
22	STV 2774	35.06	41.00	64.33	2.66	8.73	4.13	34.06	6.80	9.13	3.23	10.43	31.21	33.30
23	Pant M 3	33.53	41.66	66.00	2.40	10.93	3.66	38.33	6.71	10.46	2.96	11.88	32.43	36.61
24	MGG 221	37.86	43.33	67.66	1.73	11.46	3.80	42.60	6.77	9.66	3.44	12.18	34.63	35.17
25	Jonnalagadd local	39.60	43.33	70.66	2.33	12.40	3.93	48.80	6.96	10.46	3.30	15.15	40.16	37.71
26	V 1628	38.26	41.33	63.66	2.40	10.66	3.40	42.73	5.82	8.86	2.95	10.34	35.99	28.67
27	RMG 452	35.20	44.00	69.66	3.06	9.00	4.06	32.46	6.35	9.93	3.89	9.54	30.67	31.11
28	ML 682	39.33	42.33	67.00	2.60	9.60	3.93	35.40	6.29	9.26	3.15	10.33	31.25	33.06
29	ML 515	33.33	42.00	71.00	1.66	8.80	3.53	30.20	6.26	8.66	3.37	8.92	30.55	29.21
30	EC337103	42.40	42.00	72.33	1.66	12.13	4.26	50.66	6.96	10.47	3.70	18.30	40.82	44.84
31	RMG 406	46.86	43.66	75.33	2.60	13.66	4.66	58.06	6.78	9.06	3.31	17.44	40.13	43.45
32	Ganga 6	33.33	45.66	75.00	2.53	9.13	3.86	35.13	5.68	8.60	3.40	10.30	31.45	32.74
33	LGG 462	41.80	43.66	74.00	1.53	11.66	4.13	47.06	5.78	8.73	4.06	16.73	39.73	42.08
34	ML 611	43.46	45.00	74.66	2.33	11.67	4.20	48.40	6.59	9.06	3.41	15.02	38.38	39.05
35	STV 2662	35.13	47.00	77.33	1.53	9.20	4.26	37.53	6.28	8.53	2.71	8.68	31.10	27.92

S.No	Genotype	Plant height (cm.)	Days to 50% flowering	Days to maturity	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm.)	Seeds per pod	100-seed weight (g)	Grain yield per plant (g)	Biological yield per plant (g)	Harvest index (%)
36	STV 2781	40.00	41.33	61.66	2.06	9.06	3.46	31.00	6.22	9.86	3.04	9.28	31.66	29.33
37	LGG 475	33.13	42.66	67.33	1.93	10.73	3.66	39.00	6.24	9.66	3.69	13.61	36.49	37.29
38	EC337112	35.80	44.00	70.33	2.46	12.80	4.40	55.06	7.17	10.00	3.58	19.06	41.61	45.79
39	STV 2810	34.40	41.66	65.00	2.33	8.66	4.13	35.53	6.56	10.40	3.29	12.71	35.91	33.90
40	STV 2667	35.66	45.66	72.66	2.20	10.60	4.40	39.60	6.28	9.06	3.53	12.69	37.02	34.30
41	EC337111	38.26	40.33	68.33	1.60	12.33	4.53	52.52	7.18	8.40	3.49	15.97	37.24	42.89
42	STV 2669	31.80	44.00	67.66	1.66	9.53	3.66	33.13	6.17	8.53	3.38	9.57	31.76	30.12
43	STV 2724	33.33	42.00	67.33	1.33	9.46	3.66	33.06	6.48	10.73	3.41	12.12	36.54	33.162
44	STV 2762	36.60	41.00	64.66	2.60	10.87	4.06	42.40	6.20	10.26	3.44	14.98	37.28	40.15
45	STV 2789	35.26	42.66	66.33	0.800	9.40	3.93	34.00	6.20	10.06	3.23	10.72	36.20	29.601
46	EC337105	40.13	43.00	69.33	1.60	11.73	4.26	49.13	7.27	10.93	3.83	20.59	42.67	48.23
47	STV 2674	43.66	41.66	66.00	2.53	12.80	4.40	55.13	6.58	10.40	3.68	21.40	44.72	47.87
48	STV 2705	35.40	43.00	65.66	1.93	11.26	3.600	40.33	6.74	8.66	3.63	12.72	36.16	35.16
49	STV 2442	32.13	41.66	64.00	2.06	8.40	3.53	29.20	5.82	10.40	3.43	10.60	33.89	31.30
50	LGG 460	31.60	43.000	71.00	2.33	7.23	4.26	31.267	6.29	10.53	3.54	11.94	35.50	33.58
	Range	27.33 - 49.20	41.00 - 47.00	61.67 – 77.33	0.67– 3.27	7.00 – 13.67	3.13 – 4.00	21.53 – 58.67	5.47 – 7.27	8.40 – 10.93	2.71 – 4.07	5.99 – 21.41	28.96 – 44.73	20.11 – 48.24
	SEd	0.90	0.58	1.09	0.14	0.41	0.13	1.70	0.13	0.31	0.02	0.71	0.73	1.54
	CD 5%	1.79	1.16	2.17	0.28	0.81	0.26	3.37	0.26	0.62	0.04	1.40	1.45	3.05
	CD 1%	2.37	1.53	2.88	0.36	1.07	0.35	4.47	0.34	0.82	0.05	1.85	1.92	4.03
	CV %	3.01	1.66	1.93	8.95	5.15	4.31	5.73	2.48	4.01	0.75	7.33	2.57	5.64

4.1.2 Days to 50% flowering

The range for days to 50% flowering varied from 41.00 days to 47.00 days with a general mean of 42.89 days. The genotypes Co 4, MGG 329, STV 2774 and STV 2762 were earlier in flowering while STV 2662 showed delayed flowering.

4.1.3 Days to Maturity

The number of days to maturity ranged from 61.67 to 77.33 days with a general mean of 69.12 days. The earliest maturity was recorded by STV 2781 where as STV 2662 showed late maturity. Twenty-four genotypes were earlier in maturity when compared to mean maturity of genotypes.

4.1.4 No. of branches per plant

Highest number of branches per plant was recorded by the genotype ML 5 (3.27) where as the lowest number was registered by Pusa 16 (0.67). Twenty-four genotypes showed more number of branches per plant than the general mean of the genotypes (1.90).

4.1.5 No. of clusters per plant

The genotype RMG 406 recorded maximum number of clusters per plant (13.67), while three genotypes viz., COGG 901, EC 337104 and STV 2773 recorded the lowest (7.00). Twenty genotypes surpassed the general mean number of clusters per plant (9.72).

4.1.6 No. of Pods per cluster

The number of pods per cluster ranged from 3.13 to 4.66. The maximum number of pods per cluster was recorded in RMG 406 whereas the minimum in LGG 463 and EC

337104. Twenty-one genotypes exceeded the general mean number of pods per cluster (3.82).

4.1.7 No. of Pods per plant

The genotypes RMG 406 recorded the highest number of pods per plant (58.06) while LGG 440 registered the lowest number of pods per plant (21.53). Twenty-one genotypes showed more number of pods per plant than the general mean (36.33).

4.1.8 Pod length

The genotype EC 337105 had longest pods (7.27 cm) while EC 337104 had the shortest pods (5.47 cm). Twenty-two genotypes recorded greater pod length than the general mean value of the genotypes (6.41cm).

4.1.9 Number of seeds per pod

The mean number of seeds per pod ranged from 8.40 (EC 337111) to 10.93 (EC 337105) with a general mean of 9.58 seeds per pod. Twenty-six genotypes showed higher number of seeds per pod when compared to the general mean.

4.1.10 Hundred seed weight

The genotype LGG 462 recorded maximum seed weight (4.07g) whereas STV 2662 registered minimum seed weight (2.71g). Twenty-five genotypes showed more seed weight than the mean (3.43 g).

4.1.11 Grain yield per plant

This character mean ranged from 5.99 g to 21.41 g. The genotype RMG 406 recorded the highest grain yield whereas EC 337104 registered the lowest grain yield per plant. Twenty-two genotypes displayed more grain yield per plant than the general mean-seed yield (11.80 g).

4.1.12 Biological yield per plant

The maximum and minimum biological yield per plant was recorded in STV 2674 (44.73g) and STV 2773 (28.97g) respectively. Twenty-three genotypes had high biological yield when compared to general mean of genotypes (34.77g).

4.1.13 Harvest Index

The character mean ranged from 20.11% to 48.24% being the lowest harvest index recorded in EC 337104 and the maximum in EC 337105. Twenty-one genotypes surpassed their mean value for harvest index (33.33%).

4.2 GENETIC DIVERGENCE

Fifty genotypes of mung bean were quantitatively assessed by adopting Mahalanobis's D^2 statistic, Metroglyph analysis, Canonical analysis and Complete linkage dendrogram using yield and its component characters.

4.2.1 Test with Wilk's criterion and analysis of variance for dispersion of genotypes

Wilk's 'V' (statistic) criterion was used to test the significant differences between the genotypes based on the pooled effects of all the characters. The significance of 'V' (statistic) values was tested by $\chi 2$ at 637 degrees of freedom. The 'V' statistic value (4708.11**) was highly significant indicating that the genotypes differed significantly when all the characters were considered simultaneously.

The analysis of variance of dispersion of fifty genotypes is presented in Table: 4. The significance of genotypes clearly indicated the significant pooled effect of all the

Table 4: Analysis of Variance for dispersion in fifty genotypes of Mung bean

Source of variance	Degrees of Freedom	Mean Sum of Squares
Genotypes	49	124.23D + 03**
Error	97	0.087D-12
Total	146	416.94D+02

** Significant at 1% level

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** Significant at 1% level

characters studied between different genotypes. Hence, further analysis was made to estimate D^2 values.

4.2.1.1 Mahalanobis's D^2 values

The mean values of fifty genotypes [(X_1)-(X_2)] were transformed into standardized uncorrelated mean values [(Y_1)-(Y_2)]. The D^2 values were computed for all the possible 50(50 – 1)/2 = 1225 pairs of genotypes. The highest D^2 value of 3164.56 was observed between the genotypes LGG 468 and STV 2662 whereas the lowest D^2 value of 31.85 was recorded between the genotypes LGG 475 and STV 2705.

4.2.1.2 Grouping of genotypes

All the fifty genotypes of mung bean were grouped into ten clusters using the Tocher's method (Rao, 1952). The distribution of the genotypes into clusters along with the geographic area of adaption is presented in Table 5. Cluster I had the maximum number of 22 genotypes representing different eco-geographical regions of the country. Cluster III had 9 genotypes and clusters V, IV and IX had 8, 4 and 2 genotypes respectively, while the remaining clusters included one genotype each.

4.2.1.3 Intra and Inter-cluster average distance

The average intra and inter-cluster D^2 and D values among the clusters formed are given in Table 6 and fig. 1. The maximum intra-cluster D^2 (237.89) and D (15.42) distance were recorded by cluster V, while the clusters II, VI, VIII, and X recorded minimum intra cluster distance of 0.00 as they include single genotype in each cluster.

Table 5: Cluster composition of fifty genotypes of Mung bean(Tocher's method)

Cluster	No. of genotypes	Genotypes	Geographic area of adaptation
I	22	LGG-475, LGG-440, LGG-460, LGG-463	Lam (A.P.)
		STV-2705,STV-2667,STV-2762, STV-2669, STV-2724, STV-2442, STV-2810, STV-2774, STV-2789	Lam (A.P.)
		MGG-221, MGG-320, MGG-329	Madhira (A.P.)
		ML-515	Ludhiana (Punjab)
		Pusa-16	New Delhi
		COGG-901 CO-4	Coimbatore (T.N.)
		EC-337108	New Delhi
		Ganga 6	Sri Ganganagar
II	1	ML 682	Ludhiana (Punjab)
III	9	Pusa 9131	New Delhi
		Pant M 3	Pant nagar (U.P.)
		STV-2871, STV-2731	Lam (A.P.)
		ML 5	Ludhiana (Punjab)
		V 1628	Taiwan (Thailand)
		MGG-319, MGG-295	Madhira (A.P.)
		LGG-470	Lam (A.P.)
IV	4	LGG-423	Lam (A.P.)
		STV-2790	Lam (A.P.)
		MGG-316	Madhira (A.P.)
		RMG-452	M.P.
V	8	EC-337103, EC-337105, EC-337112, EC-3337111	New Delhi
		STV-2674	Lam (A.P.)
		ML-611	Ludhiana (Punjab)
		RMG-406	M.P.
		Jonnalagadd local	Lam (A.P.)
VI	1	LGG-458	Lam (A.P.)
VII	1	EC-337104	New Delhi
VIII	1	STV-2773	Lam (A.P.)
IX	2	LGG-468 LGG-462	Lam (A.P.)
X	1	STV-2662	Lam (A.P.)

Table 6: Inter Cluster and Intra Cluster(diagonal) average of D^2 and D values (parentheses) of fifty genotypes of Mung bean (Tocher's Method)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	218.50 (14.78)	313.78 (17.71)	651.88 (25.53)	421.64 (20.53)	459.84 (21.44)	338.37 (18.39)	341.47 (18.47)	439.61 (20.96)	1000.07 (31.62)	1055.86 (32.49)
II		0.00 (0.00)	153.78 (12.40)	912.88 (30.21)	578.35 (24.04)	295.46 (17.18)	241.49 (15.54)	340.77 (18.46)	1669.70 (40.86)	453.30 (21.29)
III			209.64 (14.47)	1243.06 (35.25)	879.30 (29.65)	565.39 (23.77)	365.00 (19.10)	367.64 (19.17)	2164.48 (46.52)	370.21 (19.24)
IV				166.79 (12.91)	651.78 (25.53)	663.98 (25.76)	716.25 (26.76)	848.49 (29.12)	500.14 (22.36)	2025.90 (45.01)
V					237.89 (15.42)	343.99 (18.54)	691.90 (26.30)	1008.19 (31.75)	773.00 (27.80)	1438.30 (37.92)
VI						0.00 (0.00)	386.63 (19.66)	777.51 (27.88)	835.03 (28.89)	1119.83 (33.46)
VII							0.00 (0.00)	185.91 (13.63)	1354.68 (36.80)	681.31 (26.10)
VIII								0.00 (0.00)	1917.03 (43.78)	549.66 (23.44)
IX									199.82 (14.13)	3113.41 (55.79)
X										0.00 (0.00)

Fig. 1: Statistical Distance among 10 clusters of Mung Bean

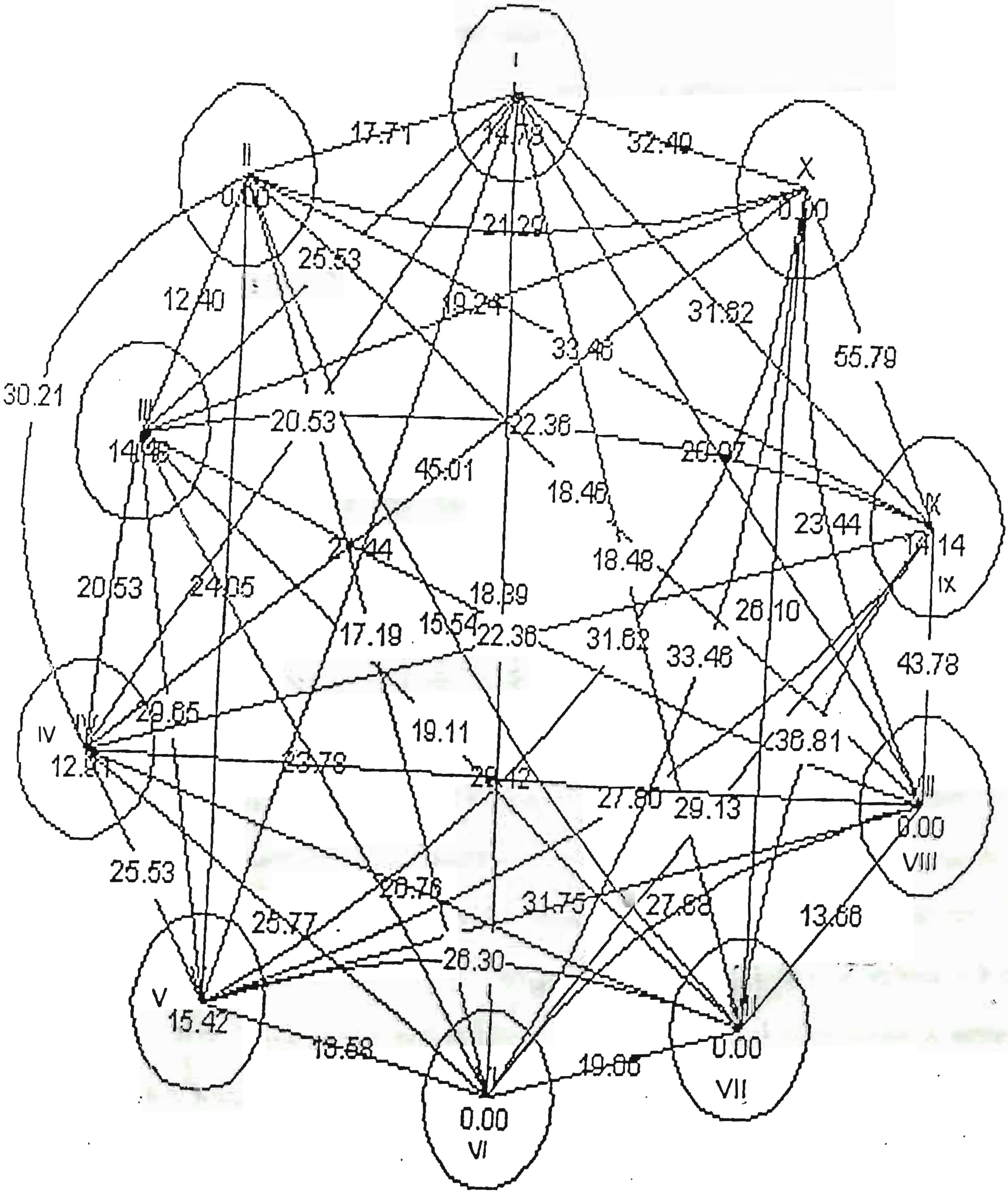
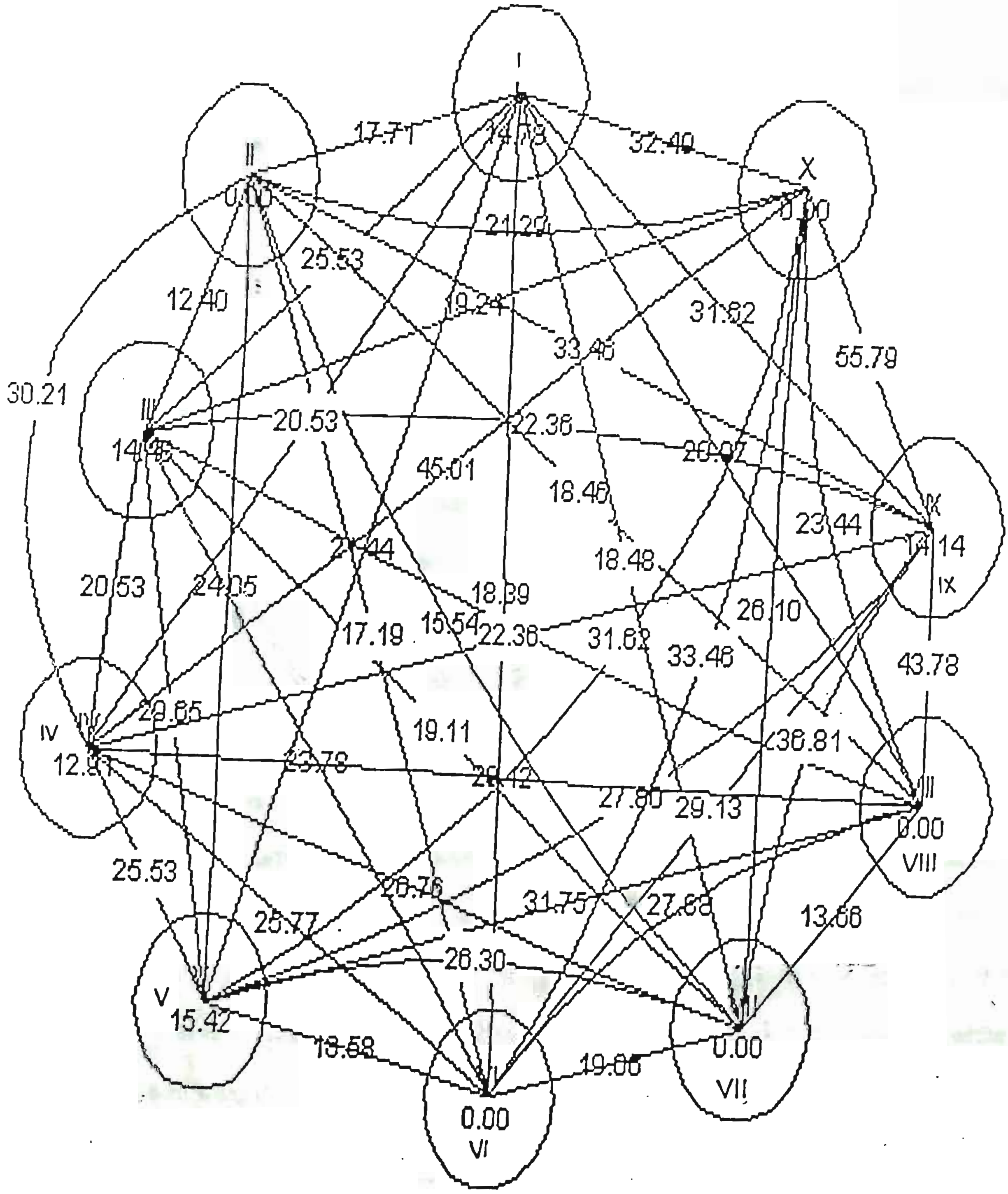


Fig. 1: Statistical Distance among 10 clusters of Mung Bean



4.2.1.4 Clustering pattern in relation to geographic diversity

The genotypes were distributed at random in all the clusters. There was no relationship between geographic diversity and genetic diversity as the genotypes from different geographic regions were included in the same cluster.

4.2.1.5 Cluster means for various characters

The cluster means for each of the thirteen characters were presented in Table7. Considerable differences between the clusters were observed for most of the characters studied. The cluster mean for plant height ranged from 27.33 cm to 45.50 cm. Cluster VIII recorded shorter plant height, while cluster IX had taller plant height. The genotypes in cluster II took minimum of 42.33 days to attain 50% flowering while the genotypes in cluster X attained 50% flowering in 47.00 days. Cluster II recorded the earliest maturity (67.00days) and the genotypes in cluster X had taken 77.33 days to attain maturity. Lowest number of branches per plant (1.23) was recorded in cluster x and the highest number of branches per plant (2.60). The number of clusters per plant ranged from 7.00 to 12.42 with clusters VI and VIII being the lowest and highest number was recorded in cluster VI . The number of pods per cluster ranged from 3.13 (cluster VII) to 4.33(cluster V).

The genotypes in cluster VII the recorded lowest number of pods per plant (21.53) whereas highest number was observed in cluster V (52.18). The genotypes in cluster VII had shortest pods (5.47cm.), while those in cluster V had the longest pods (6.93 cm.) The number of seeds per pod ranged from a lowest of 8.46 in cluster VII to a highest of 9.85 in clusters IV and V. The lowest test-weight of 2.71 g was recorded in cluster X while the highest seed weight of 4.05 g

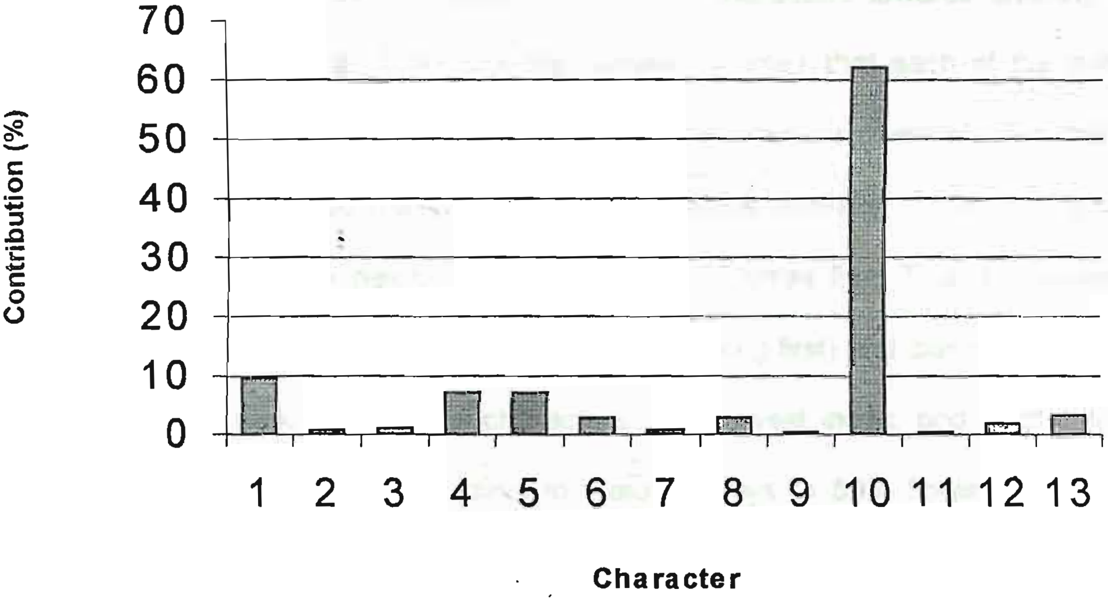
Table 7: Cluster means for thirteen characters in fifty genotypes of Mung bean (Tocher's Method)

Cluster	Plant Height (cm.)	Days to 50 % flowering	Days to maturity	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm.)	Seeds per pod	100-Seed weight (g)	Grain yield per plant (g)	Biological yield per plant (g)	Harvest Index (%)
I	35.12	42.50	67.54	1.80	9.35	3.72	33.75	6.44	9.75	3.47	11.34	34.26	32.82
II	39.33	42.33	67.00	2.60	9.60	3.93	35.40	6.29	9.26	3.15	10.33	31.25	33.06
III	36.47	42.77	68.00	2.11	9.47	3.57	34.08	6.31	9.48	3.03	9.65	32.58	29.60
IV	32.14	43.66	71.75	1.68	8.48	3.68	28.73	6.31	9.85	3.83	10.04	32.25	31.05
V	41.26	42.87	70.87	2.14	12.42	4.33	52.18	6.93	9.85	3.54	17.87	40.72	43.73
VI	47.00	43.33	69.33	2.53	9.60	4.20	38.60	5.79	8.53	3.41	10.90	37.55	29.05
VII	40.66	43.00	71.33	1.60	7.00	3.13	21.53	5.47	8.46	3.28	5.98	29.74	20.11
VIII	27.33	43.00	69.33	1.66	7.00	3.33	22.46	5.50	8.60	3.22	6.22	28.96	21.45
IX	45.50	44.16	74.83	1.23	9.63	4.26	39.70	6.00	8.73	4.05	14.07	38.93	35.99
X	35.13	47.00	77.33	1.53	9.20	4.26	37.53	6.28	8.53	2.71	8.68	31.10	27.92

Table 8: Contribution of different quantitative characters to diversity in Mung bean

S.No.	Character	Times ranked first	Contribution (%)
1	Plant height	116	9.47
2	Days to 50% flowering	9	0.73
3	Days to maturity	11	0.90
4	Branches per plant	89	7.27
5	Clusters per plant	87	7.10
6	Pods per cluster	35	2.86
7	Pods per plant	7	0.57
8	Pod length	36	2.94
9	Seeds per pod	5	0.41
10	100-Seed weight	763	62.29
11	Grain yield per plant	3	0.24
12	Biological yield per plant	23	1.88
13	Harvest Index	41	3.35

Fig. 2: Contribution of different quantitative characters to diversity in Mungbean



1. Plant height
2. Days to 50% flowering
3. Days to maturity
4. Branches per plant
5. clusters per plant
6. Pods per cluster
7. Pods per plant
8. Pod length
9. Seeds per pod
10. 100-seed weight
11. Grain yield per plant
12. Biological yield per plant
13. Harvest index.

was registered in cluster IX. The highest grain yield per plant was recorded for cluster V (17.87) and lowest for cluster VII (5.98). The cluster mean for biological yield per plant was the highest in cluster V (40.72) and the lowest in cluster VIII (28.96g). The genotypes in cluster V recorded the highest harvest index (43.73) and those in cluster VII recorded the lowest harvest index (20.11).

4.2.1.6 Relative contribution of characters towards diversity:

The relative contribution of thirteen characters towards diversity is presented in Table 8 and fig. 2. The more the number of times that each of the thirteen characters appeared in first rank, the more it contributes towards diversity. The character 100-seed weight contributed maximum (62.29%) towards diversity by taking first rank 763 times, followed by plant height (9.47%) ranking 116 times first. This is followed by number of branches per plant (7.27%) with 89 times ranking first) and clusters per plant (7.10%) with 87 times ranking first. The characters viz., harvest index. pod length, pods per cluster, biological yield per plant, days to maturity, days to 50% flowering, pods per plant and seeds per pod contributed 3.35%, 2.94%, 2.86%, 1.88%, 0.9%, 0.73%, 0.57% and 0.41% respectively to the total genetic divergence.

4.2.1.7 Cluster diagram

With the help of D^2 values, a cluster diagram was constructed (fig.1) showing the relationship between the different populations. The greatest distance between two clusters existed between cluster X and IX (3113.41) indicating greatest divergence. The least distance was recorded between clusters II and III (153.78) indicating least genetic divergence among the ten clusters formed.

4.2.2 Metroglyph Analysis

Metroglyph analysis was carried-out for fifty genotypes of mung bean using the replicated means. The scattered diagram of the metroglyph plot is presented in fig. 3. A small circle or glyph represented the position of each genotype. The genotypes were plotted taking grain yield per plant on X–axis and 100–seed weight on Y–axis as these two characters exhibited maximum variability. The remaining yield contributing characters have been represented on the respective glyph by rays. The length of the ray depicted the variation for each character. The variation for each character was divided into three groups i.e., low, medium and high. The genotypes with low, medium and high values were given the index score 1, 2 and 3 respectively.

The fifty genotypes were divided into eight groups or clusters mainly on the basis of two important characters viz., grain yield per plant and 100-seed weight, which had a wide range of variability. Clusters I to VIII were found to be discrete with remarkable differences and referred to as

low yielding with less seed weight,
    with medium seed weight and
    with high seed weight.
medium yielding with less seed weight,
    with medium seed weight and
    with high seed weight.

high yielding with less seed weight,
    with medium seed weight and
    with high seed weight.

Cluster V composed of maximum number of 8 genotypes while the clusters I, IV and VIII had 7 genotypes each, Clusters II and VII of 6 each, cluster VI and cluster III of 5 and 4

Table 9 : Limits, scores and signs used for eight characters for Metroglyph analysis in Mung bean

Character	Mean range	Score < 1	Sign	Score >2	Sign	Score >3	Sign
Plant height (cm.)	27.33 to 49.20	36.81		36.81 to 39.25		39.25	
Pod length (cm.)	5.47 to 7.27	6.41		6.41 to 6.65		6.65	
Days to 50% flowering	41.00 to 49.00	42.89		42.89 to 4 3.62		43.62	
Days to maturity	61.67 to 77.33	69.12		69.12 to 71.05		71.05	
Branches per plant	0.67 to 3.27	1.90		1.90 to 2.23		2.23	
Clusters per plant	7.00 to 13.67	9.72		9.72 to 10.61		10.61	
Pods per cluster	3.13 to 4.67	3.82		3.82 to 4.01		4.01	
Pods per plant	21.53 to 58.07	36.33		36.33 to 4 0.92		40.92	

Table 10: Index scores of 10 quantitative characters for fifty genotypes of Mung bean.

S.NO.	Genotype	Plant height	Days to 50% flowering	Days to maturity	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length	100-Seed weight	Grain yield per plant	Total score
1	LGG 468	3	3	3	1	1	3	1	1	3	2	21
2	COGG 901	1	1	1	1	1	1	1	3	1	1	12
3	LGG 463	1	1	1	1	1	1	1	3	1	1	12
4	LGG 470	2	1	1	1	1	1	1	1	1	1	13
5	LGG 440	1	3	3	1	1	1	1	1	2	1	15
6	EC 337104	3	2	3	1	1	1	1	1	1	1	15
7	LGG 423	1	3	3	1	1	1	1	1	3	1	16
8	LGG 458	3	2	2	3	1	3	2	1	1	2	21
9	CO 4	1	1	1	1	1	1	1	3	3	1	14
10	MGG 319	1	3	3	3	1	1	1	1	1	1	19
11	STV 2731	2	3	3	2	1	1	1	1	1	1	16
12	MGG 320	3	1	1	1	1	1	1	1	2	2	14
13	MGG 316	1	1	1	1	1	1	1	1	3	2	13
14	STV 2790	1	3	3	1	1	1	2	2	3	2	18
15	EC 337108	3	1	1	1	1	1	1	3	3	3	21
16	MGG 329	1	1	1	3	3	1	1	1	3	1	14
17	Pusa 9131	1	2	2	3	2	1	1	1	1	2	16
18	ML 5	2	3	2	3	3	1	2	3	1	2	22
19	Pusa 16	3	1	1	1	3	1	3	3	2	3	21
20	MGG 295	1	1	1	1	1	1	1	1	1	1	10
21	STV 2773	1	2	2	1	1	1	1	1	1	1	12
22	STV 2774	1	1	1	3	1	3	1	3	1	2	17
23	Pant M 3	1	1	1	3	3	1	2	3	1	2	18
24	MGG 221	2	2	1	1	3	1	3	3	1	2	19
25	Jonnalagadd local	3	2	2	3	3	2	3	3	1	3	25

S.NO.	Genotype	Plant height	Days to 50% flowering	Days to maturity	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length	100-Seed weight	Grain yield per plant	Total score
26	V 1628	2	1	1	3	3	1	3	1	1	2	18
27	RMG 452	1	3	2	3	1	3	1	2	3	1	20
28	MR 682	3	1	1	3	1	2	1	1	1	2	16
29	ML 515	1	1	2	1	1	1	1	1	1	1	11
30	EC 337103	3	1	3	1	3	3	3	3	3	3	26
31	RMG 406	3	3	3	3	3	3	3	3	1	3	28
32	Ganga 6	1	3	3	3	1	2	1	1	1	2	18
33	LGG 462	3	3	3	1	3	3	1	1	3	3	26
34	ML 611	3	3	3	3	3	3	3	3	1	3	28
35	STV 2662	1	3	3	1	1	3	2	1	1	1	17
36	STV 2781	3	1	1	2	1	1	1	1	1	1	13
37	LGG 475	1	1	1	2	3	1	2	1	3	2	17
38	EC337112	1	3	2	3	3	3	3	3	2	3	26
39	STV 2810	1	1	1	3	1	3	1	2	1	2	16
40	STV 2667	1	3	3	2	2	3	2	1	2	2	21
41	EC 337111	2	1	1	1	3	3	3	3	2	3	22
42	STV 2669	1	3	1	1	1	1	1	1	1	1	12
43	STV 2724	1	1	1	1	1	1	1	2	1	2	12
44	STV 2762	1	1	1	3	3	3	3	1	1	3	20
45	STV 2789	1	2	1	1	1	2	1	1	1	2	13
46	EC337105	3	2	2	1	3	3	3	3	3	3	26
47	STV 2674	3	1	1	3	3	3	3	2	3	3	25
48	STV 2705	1	1	1	2	3	1	2	3	3	2	20
49	STV 2442	1	1	1	2	1	1	1	1	1	2	12
50	LGG 460	1	2	2	3	1	3	1	1	2	2	18

Fig. 4: Pattern of Distribution of 50 genotypes of Mungbean scored for 10 characters

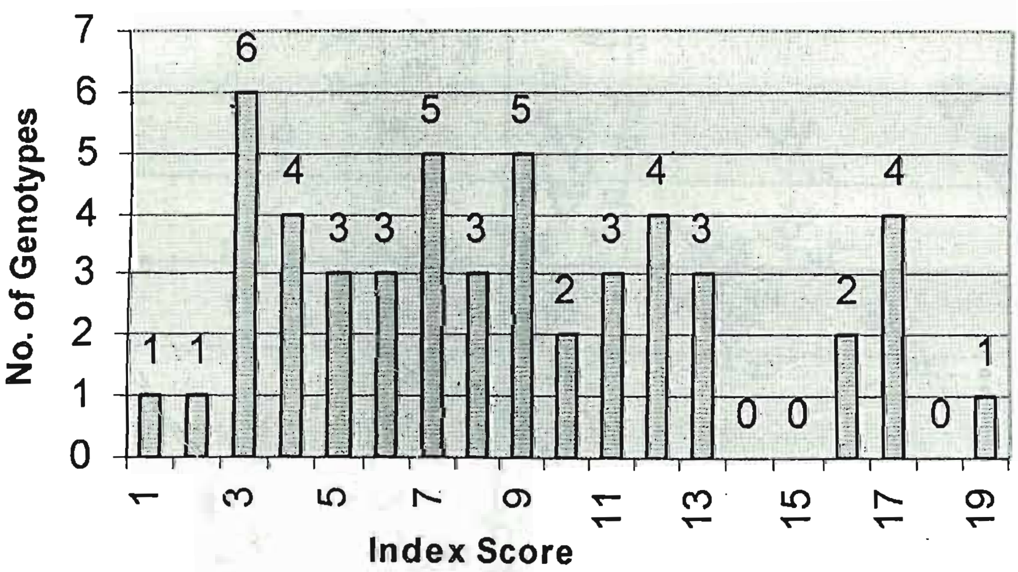
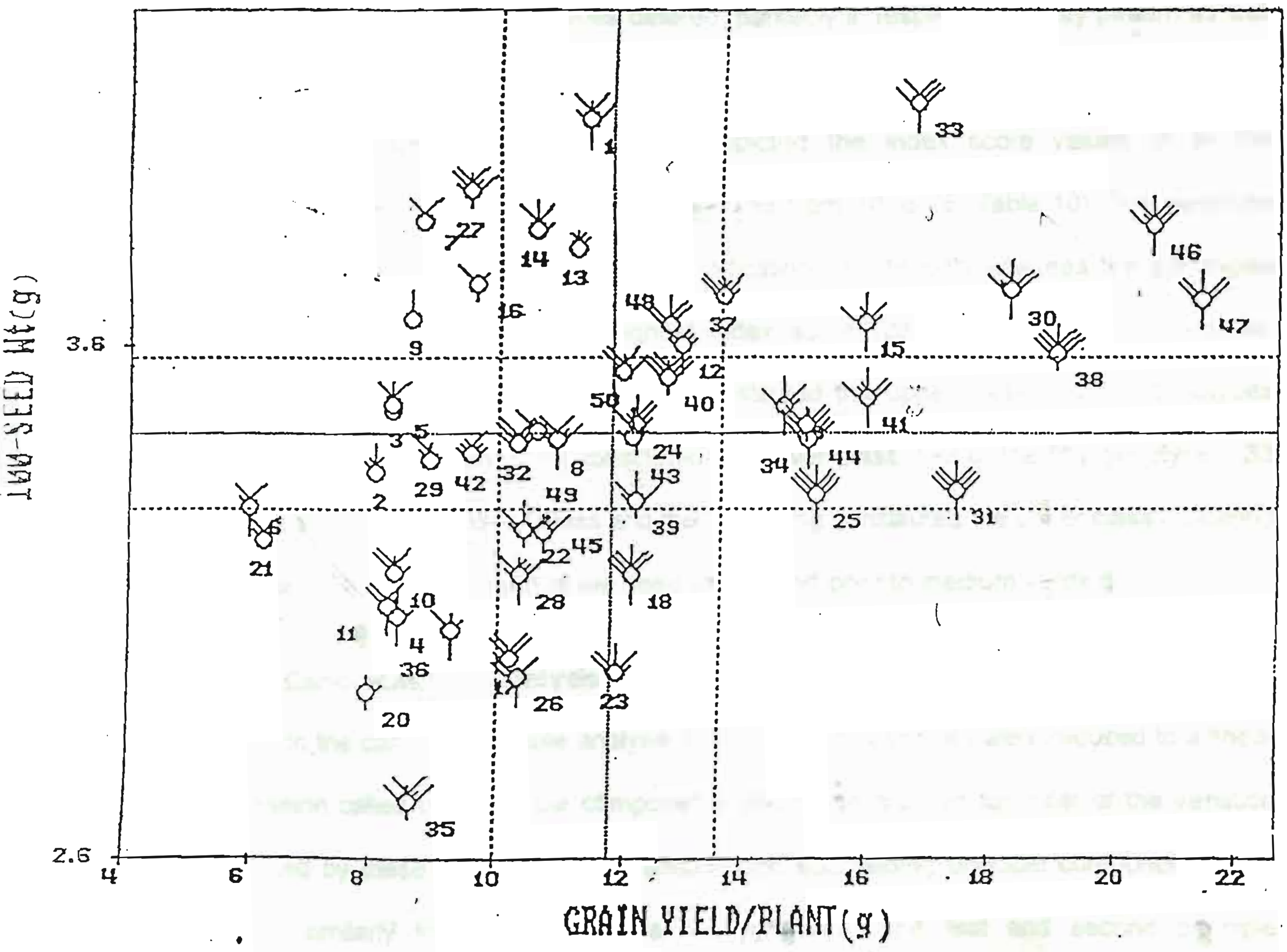


Fig. 3: Scattered diagram of fifty genotypes of Mung bean on the metroglyph plot.



genotypes respectively (fig. 3). The genotypes LGG 463 and LGG 440 in cluster II; LGG 470 and STV 2731 in cluster I; STV 2667 and MGG 221 in cluster V and Pusa 16 and STV 2762 in cluster VII were superimposed over each other. The genotypes MGG 320 and STV 2705; STV 2774 and STV 2789, Pusa 9131 and V 1628 were found in close proximity with each other in clusters VI and IV respectively. The clustering pattern was not in conformity with that obtained in Mahalanobis's D^2 statistic. For the nine characters plotted on the glyph, the genotypes differed markedly in respect of the ray pattern as well as for the pattern of variability.

The frequency diagram (fig. 4) depicted the index score values of all the characters under study. The range of score was from 10 to 28 (Table 10). The genotype MGG 295 scored least index score (10) indicating its inferiority whereas the genotypes RMG 406, ML 611 scored the highest index score (28). The genotypes, which fall between the index score of 19 and 28 constituted the upper class and the genotypes which, fall between 10 and 19 constituted the lower class. Out of the fifty genotypes, 33 genotypes constituted lower class and the remaining constituted the upper class indicating that most of them comprised of low seed weight and poor to medium yielding.

4.2.3 Canonical root analysis

In the canonical variate analysis, the number of variables were reduced to a linear expression called the principle components and these account for most of the variation produced by these characters. The second and succeeding principle components were formed similarly to account for residual variability. The first and second principle components (Z_1 and Z_2) were used to obtain a scattered distribution of the genotypes on a graph. When depicted graphically, considering all the characters together based on genetic divergence the genotypes differed widely.

4.2.3.1 Canonical roots

In the present study, canonical root analysis was carried out for fifty genotypes of mung bean as per the method suggested by Rao, 1952. The first principle accounted for 56.55% of the total variability followed by the second principle for 18.01% and third principle for 6.45%of the total variability (Table 11). The three vectors accounted for 81.02% of total variability. The mean values of the canonical variates for three roots Z_1, Z_2 and Z_3 are presented in Table 12. The first two vectors Z_1 and Z_2 contributed for 74.56% of the total variability. Hence these two components were considered enough to explain the diversity of genotypes. The Z_1 values were plotted against Z_2 values graphically (fig.5).

4.2.3.2 Contribution of vectors towards divergence

The amount of contribution of canonical vectors of all the characters towards genetic diversity is presented in Table 13. The character 100-seed weight contributed maximum (0.979) to the diversity in the vector Z_1. It was followed by pods per cluster (0.101), plant height (0.097), clusters per plant (0.081), days to maturity (0.077) pods per plant (0.052), biological yield per plant (0.034), pod length (0.027) and seeds per pod (0.013). The remaining characters days to 50% flowering, branches per plant, grain yield per plant and harvest index contributed negatively towards genetic divergence.

Clusters per plant contributed maximum to diversity (0.541) in the vector Z_2. It was followed by plant height (0.436), pods per cluster (0.354), branches per plant (0.261), biological yield per plant (0.211), grain yield per plant (0.131), days to maturity (0.086)

Table 11: Canonical root values, per cent of variation absorbed and cumulative total variation for fifty genotypes of Mung bean.

Canonical root	Values of canonical root	Per cent of variation absorbed	Cumulative total per cent variation
Z_1	7463.32	56.55	56.55
Z_2	2376.38	18.01	74.56
Z_3	851.54	6.45	81.02

Table 12: Mean Values of Canonical Variates in fifty genotypes of Mung bean.

S. No.	Genotype	'X' Vector	'Y' Vector	'Z' Vector
1	LGG 468	186.04	10.33	-21.92
2	COGG 901	152.85	3.94	-26.53
3	LGG 463	157.54	4.10	-25.76
4	LGG 470	143.28	9.12	-19.46
5	LGG 440	157.77	-1.31	-25.26
6	EC 337104	151.81	6.94	-24.59
7	LGG 423	173.84	1.70	-28.39
8	LGG 458	160.05	19.15	-30.25
9	CO 4	163.37	0.62	-27.86
10	MGG 319	147.01	9.31	-32.24
11	STV 2731	145.68	11.54	-27.83
12	MGG 320	165.49	13.89	-27.19
13	MGG 316	169.07	0.44	-32.08
14	STV 2790	172.18	-1.35	-26.19
15	EC 337108	167.21	13.60	-23.60
16	MGG 329	167.17	7.48	-38.38
17	Pusa 9131	139.31	12.68	-33.82
18	ML 5	147.66	18.01	-34.79
19	Pusa16	160.70	13.92	-22.29
20	MGG 295	136.70	9.24	-22.77
21	STV 2773	146.55	0.62	-29.53
22	STV 2774	149.42	11.42	-33.19
23	Pant M 3	138.13	14.45	-31.99
24	MGG 221	139.03	13.97	-29.55
25	Jonnalagadd Local	155.35	21.45	-29.14
26	V 1628	138.23	18.08	-31.49
27	RMG 452	175.97	6.54	-39.02
28	MR 682	147.17	14.62	-32.19
29	ML 515	155.01	6.57	-28.57
30	EC 337103	172.41	20.24	-25.19
31	RMG 406	159.86	30.49	-28.06
32	Ganga 6	157.30	8.66	-35.23
33	LGG 462	186.18	14.48	-29.04
34	ML 611	161.41	21.62	-28.94
35	STV 2662	132.06	14.56	-24.89
36	STV 2781	141.14	12.64	-28.78
37	LGG 475	167.30	8.81	-32.89
38	EC 337112	166.56	20.70	-31.19
39	STV 2810	151.37	11.06	-31.63
40	STV 2667	163.84	12.97	-32.22
41	EC 337111	161.33	19.46	-27.06
42	STV 2669	154.83	6.36	-30.98
43	STV 2724	155.94	7.70	-27.71
44	STV 2762	158.03	15.40	-33.98
45	STV 2789	149.54	9.18	-24.12
46	EC 337105	176.35	17.71	-24.71
47	STV 2764	171.43	25.38	-28.62
48	STV 2705	165.69	11.22	-31.66
49	STV 2442	154.83	5.03	-33.04
50	LGG 460	161.52	5.69	-32.76

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S. No.	Genotype	'X' Vector	'Y' Vector	'Z' Vector
1	LGG 468	186.04	10.33	-21.92
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4	LGG 470	143.28	9.12	-19.46
5	LGG 440	157.77	-1.31	-25.26
6	EC 337104	151.81	6.94	-24.59
7	LGG 423	173.84	1.70	-28.39
8	LGG 458	160.05	19.15	-30.25
9	CO 4	163.37	0.62	-27.86
10	MGG 319	147.01	9.31	-32.24
11	STV 2731	145.68	11.54	-27.83
12	MGG 320	165.49	13.89	-27.19
13	MGG 316	169.07	0.44	-32.08
14	STV 2790	172.18	-1.35	-26.19
15	EC 337108	167.21	13.60	-23.60
16	MGG 329	167.17	7.48	-38.38
17	Pusa 9131	139.31	12.68	-33.82
18	ML 5	147.66	18.01	-34.79
19	Pusa16	160.70	13.92	-22.29
20	MGG 295	136.70	9.24	-22.77
21	STV 2773	146.55	0.62	-29.53
22	STV 2774	149.42	11.42	-33.19
23	Pant M 3	138.13	14.45	-31.99
24	MGG 221	139.03	13.97	-29.55
25	Jonnalagadd Local	155.35	21.45	-29.14
26	V 1628	138.23	18.08	-31.49
27	RMG 452	175.97	6.54	-39.02
28	MR 682	147.17	14.62	-32.19
29	ML 515	155.01	6.57	-28.57
30	EC 337103	172.41	20.24	-25.19
31	RMG 406	159.86	30.49	-28.06
32	Ganga 6	157.30	8.66	-35.23
33	LGG 462	186.18	14.48	-29.04
34	ML 611	161.41	21.62	-28.94
35	STV 2662	132.06	14.56	-24.89
36	STV 2781	141.14	12.64	-28.78
37	LGG 475	167.30	8.81	-32.89
38	EC 337112	166.56	20.70	-31.19
39	STV 2810	151.37	11.06	-31.63
40	STV 2667	163.84	12.97	-32.22
41	EC 337111	161.33	19.46	-27.06
42	STV 2669	154.83	6.36	-30.98
43	STV 2724	155.94	7.70	-27.71
44	STV 2762	158.03	15.40	-33.98
45	STV 2789	149.54	9.18	-24.12
46	EC 337105	176.35	17.71	-24.71
47	STV 2764	171.43	25.38	-28.62
48	STV 2705	165.69	11.22	-31.66
49	STV 2442	154.83	5.03	-33.04
50	LGG 460	161.52	5.69	-32.76

Fig. 5: Group constallations of the first (X) and second (Y) canonical variates showing the relative position of 50 genotypes of Mungbean as determined by D^2 cluster composition

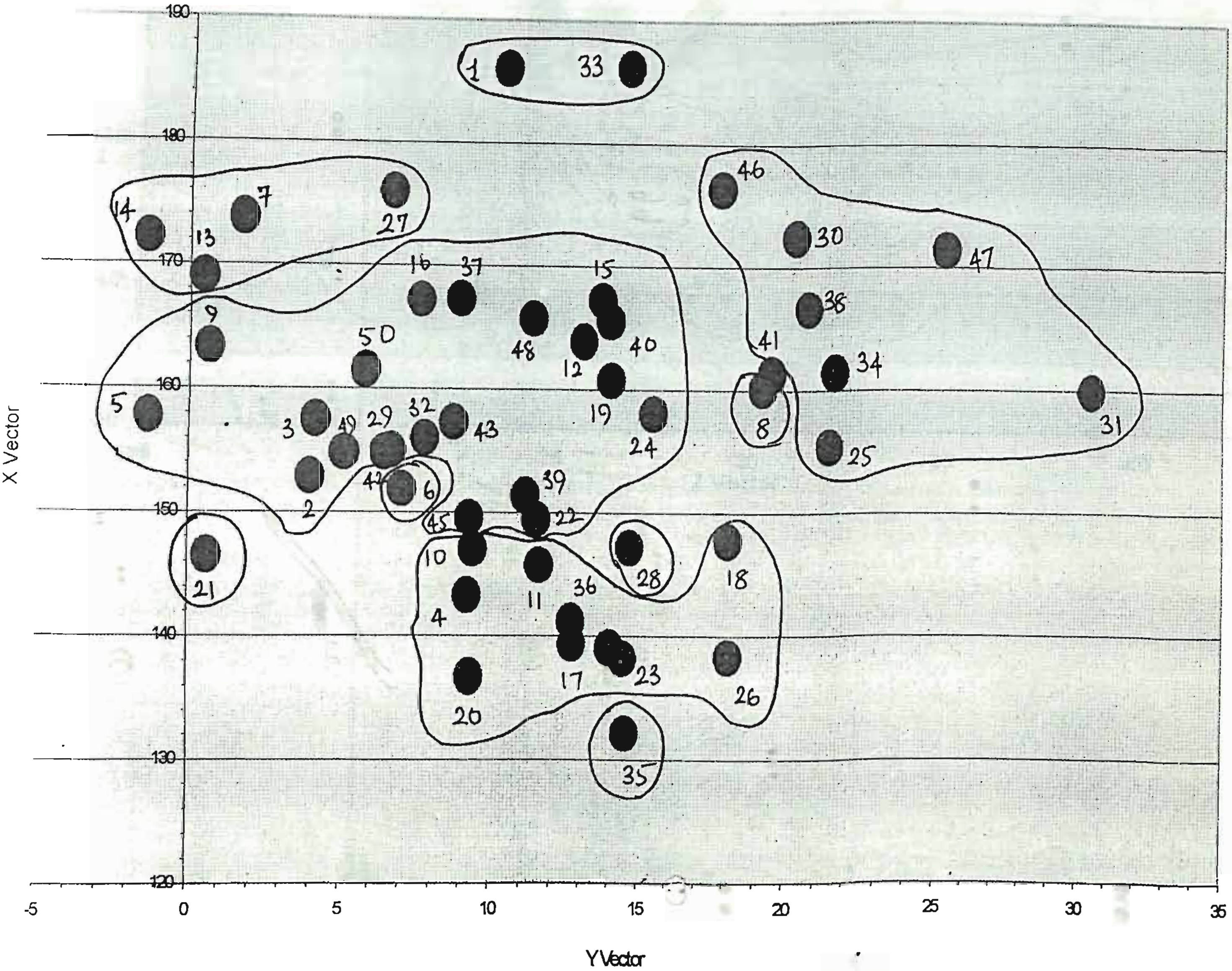

Fig. 6: Group constallations of the first (X) and third (Z) canonical variates showing the relative position of 50 genotypes of Mungbean as determined by D^2 cluster composition

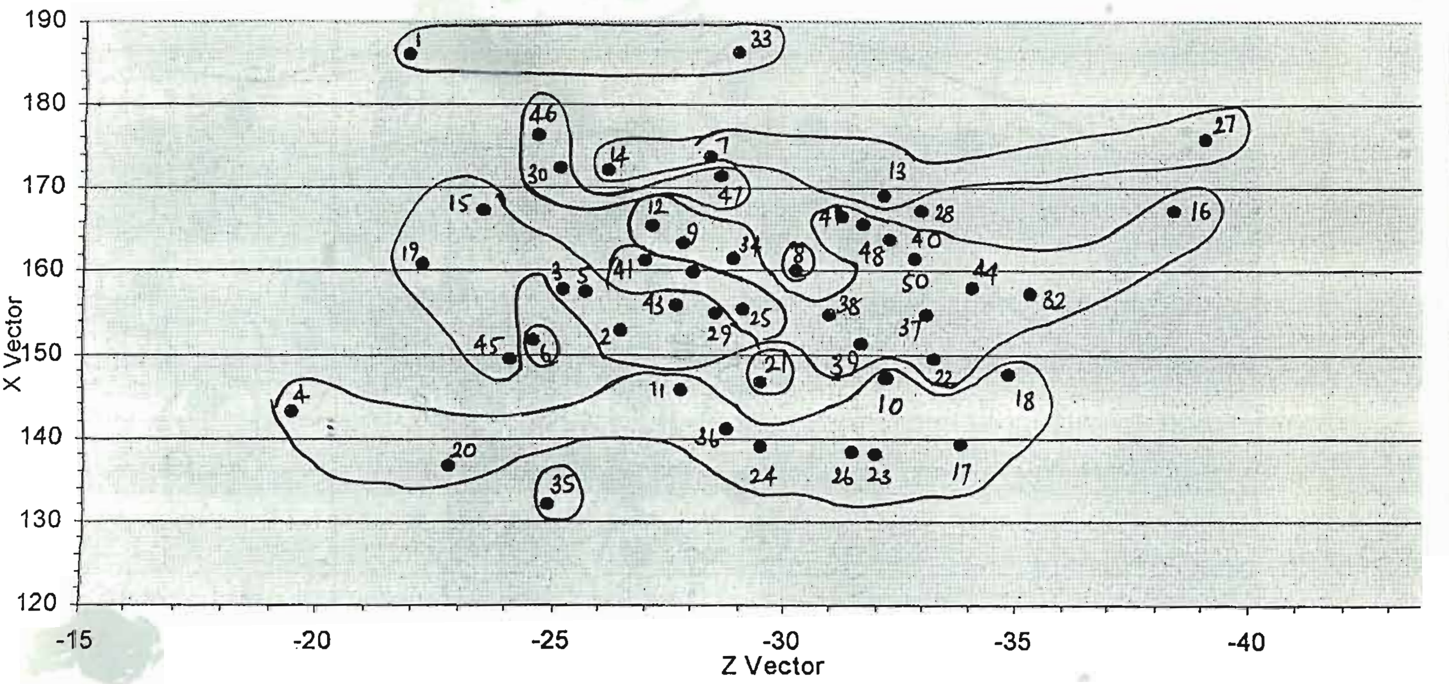

Fig. 7: Superimposition of clusters formed by Tocher's Method and complete Linkage Dendrogram on canonical 2-Dimensional Graph

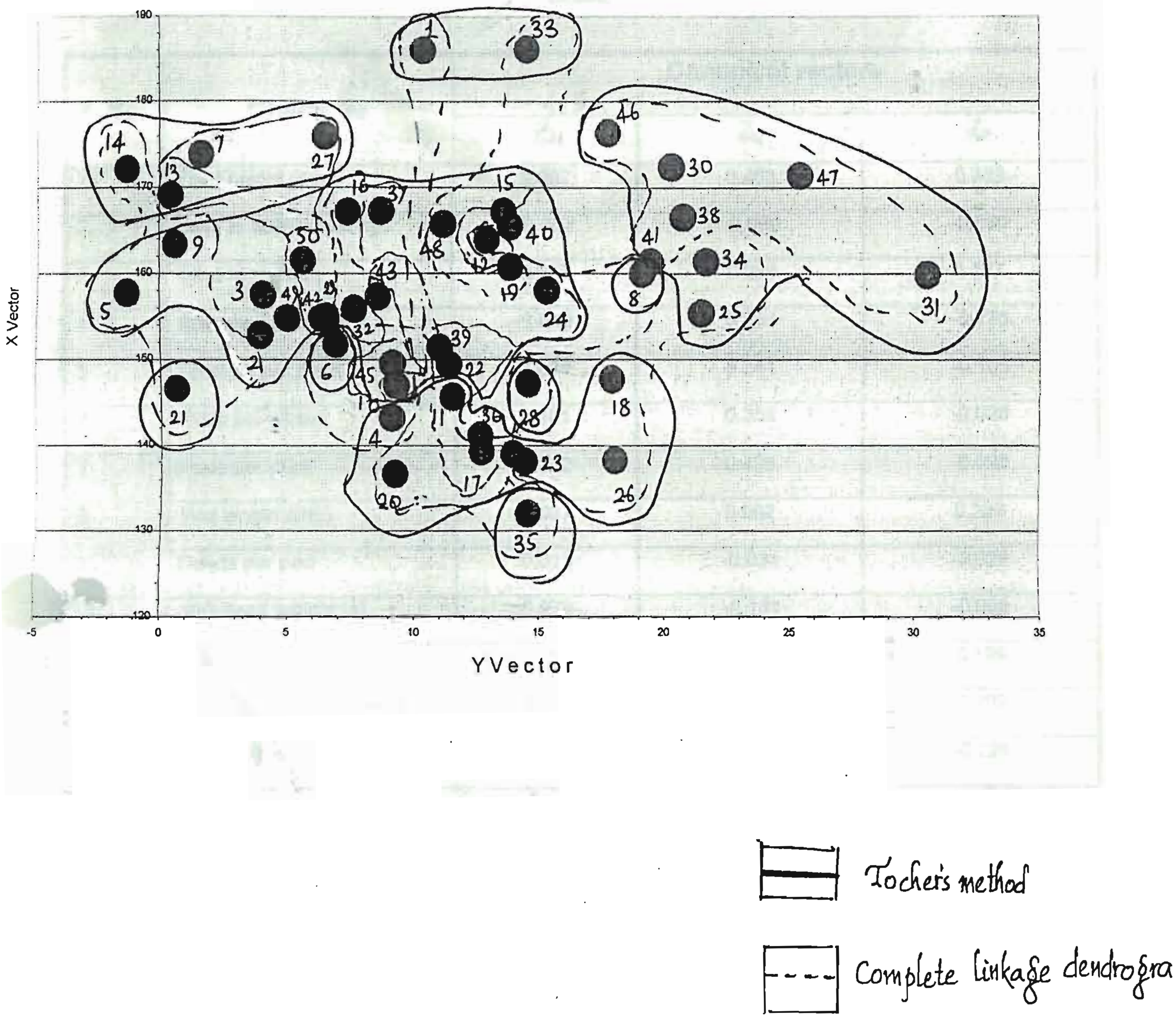

Table 13: Canonical vectors for the thirteen characters in fifty genotypes of Mung bean.

S. No.	Character	Canonical vectors		
		Z_1	Z_2	Z_3
1	Plant height (cm.)	0.097	0.453	0.363
2	Days to 50% flowering	-0.002	-0.058	-0.080
3	Days to maturity	0.077	0.086	0.177
4	Branches per plant	-0.040	0.261	-0.776
5	Clusters per plant	0.081	0.541	-0.105
6	Pods per cluster	0.101	0.354	-0.028
7	Pods per plant	0.052	0.436	-0.095
8	Pod length (cm.)	0.027	0.062	0.253
9	Seeds per pod	0.013	-0.031	-0.029
10	100-Seed weight (g)	0.979	-0.161	-0.092
11	Grain yield per plant (g)	-0.005	0.131	0.199
12	Biological yield per plant (g)	0.034	0.211	0.202
13	Harvest Index (%)	-.055	-0.119	-0.229

and pod length (0.062). The remaining four characters contributed negatively to the diversity.

In the third vector Z_3, plant height contributed maximum (0.363) to the diversity followed by pod length (0.253), biological yield per plant (0.202), grain yield per plant (0.199), days to maturity (0.177) and seeds per pod (0.029). The remaining seven characters contributed negatively towards the diversity.

4.2.3.3 Canonical graph

The three-dimensional groups obtained from canonical analysis were split into two-dimensional canonical graphs. The X-axis refers to Z_2 variate and Y-axis to Z_1 variate. Wider distribution of the genotypes was observed in almost all the clusters except cluster I indicating the presence of considerable diversity in the germplasm.

4.2.3.4 Super imposition on canonical graph

The clusters formed by Tocher's method of grouping and complete linkage dendrogram were super-imposed on the canonical two-dimensional graph so as to compare the performance of the two clustering methods. Overlapping of clusters of the two methods of grouping was observed (fig.7).

4.2.4 Complete linkage dendrogram (Hierarchical method of grouping of genotypes)

The similarity correlation coefficients (r_{CS}) were calculated using Mahalanobis's D^2 values for each genotype. Dendrogram constructed was represented in fig.8.

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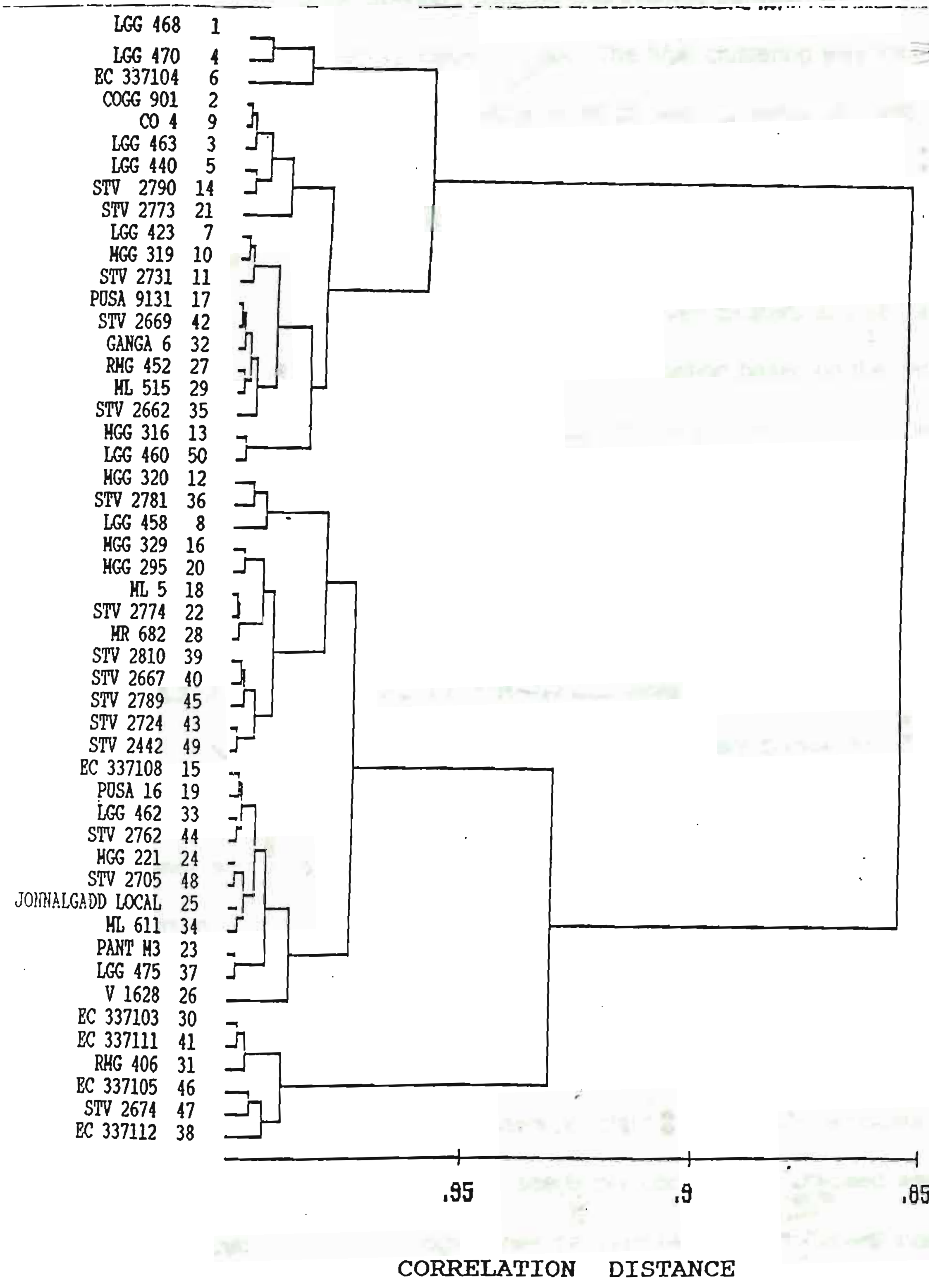
Fig. 8: Clusters formed by using complete linkage Dendrogramin Mungbean



Clustering pattern

Clustering was initiated between LGG 468 and LGG 470 at D^2 value of 1980.18 with r_{cs} value of 0.899. Second clustering was initiated between COGG 901 and CO 4 at D^2 value of 148.37 with r_{cs} value of 1.000. The final clustering was initiated between EC 337103 and EC 337105 at D^2 value of 80.28 with r_{cs} value of 0.998 to complete the dendrogram.

4.2.4.1 Cluster composition

The fifty genotypes were grouped into seven clusters at 0.983 arbitrary similarity correlation coefficient level (r_{cs}). Clustering composition based on the dendrogram pattern was presented in Table 14. The dendrogram pattern revealed that clusters III and VI included maximum number of 11 genotypes whereas cluster V comprised of 10 genotypes. Clusters VII and II included six genotypes while clusters IV and I comprised of minimum number of 3 genotypes each.

4.2.4.2 Average intra and inter cluster distances

The average intra and inter cluster distances are presented in Table 15. The intra cluster distances ranged from 154.60 (cluster III) to 253.06 (cluster VI). The inter cluster distance was maximum between clusters VII and I and was of 1964.67 whereas the minimum cluster distance of 283.08 was observed between clusters III and IV.

4.2.4.3 Cluster means of the characters

Cluster means for thirteen characters were presented in Table 16. Cluster VII recorded high mean values for clusters per plant (12.58), pods per cluster (4.42), pods per plant (53.38), pod length (6.99), seeds per pod (9.88), 100-seed weight (3.60), grain yield per plant (18.79), biological yield per plant (41.20) and harvest index (45.52) while

Table 14: Cluster composition of fifty genotypes of Mung bean (Complete linkage dendrogram)

Cluster	No. of genotypes	Genotypes	Geographic area to which adapted
I	3	LGG-468, LGG-470	Lam (A.P.)
		EC-337104	New Delhi
II	6	COGG-9O1, CO-4	Coimbatore (T.N.)
		LGG-463, LGG-440	Lam (A.P.)
		STV-2790, STV-2773	Lam (A.P.)
III	11	LGG-423, LGG-460	Lam (A.P.)
		MGG-319, MGG-316	Madhira (A.P.)
		STV-2731, STV-2669, STV-2662	Lam (A.P.)
		Pusa-9131	New Delhi
		Ganga 6	Sri Ganga nagar
		RMG-452	M. P.
		ML-515	Ludhiana (Punjab)
IV	3	MGG-320	Madhira (A.P.)
		STV-2781	Lam (A.P.)
		LGG-458	Lam (A.P.)
V	10	MGG-329, MGG-295	Madhira (A.P.)
		ML-5 ML-682	Ludhiana (Punjab)
		STV-2774, STV-2810, STV-2667 STV-2442, STV-2789, STV-2724	Lam (A.P.)
VI	11	EC-337108	New Delhi
		Pusa 16	New Delhi
		LGG-462, LGG-475	Lam (A.P.)
		STV-2762, STV-2705	Lam (A.P.)
		MGG-221	Madhira (A.P.)
		Jonnalagadd local	Lam (A.P.)
		ML-611	Ludhiana (Punjab)
		Pant M3	Pant nagar (U.P.)
		V 1628	Taiwan (Thailand)
VII	6	EC-337103, EC-33711, EC-337105, EC-337112	New Delhi
		RMG-406	M. P.
		STV-2674	Lam (A.P.)

Clustering pattern

Clustering was initiated between LGG 468 and LGG 470 at D^2 value of1980.18 with r_{cs} value of 0.899. Second clustering was initiated between COGG 901 and CO 4 at D^2 value of 148.37 with r_{cs} value of 1.000. The final clustering was initiated between EC 337103 and EC 337105 at D^2 value of 80.28 with r_{cs} value of 0.998 to complete the dendrogram.

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		EC-337104	New Delhi
II	6	COGG-9O1, CO-4	Coimbatore (T.N.)
		LGG-463, LGG-440	Lam (A.P.)
		STV-2790, STV-2773	Lam (A.P.)
III	11	LGG-423, LGG-460	Lam (A.P.)
		MGG-319, MGG-316	Madhira (A.P.)
		STV-2731, STV-2669, STV-2662	Lam (A.P.)
		Pusa-9131	New Delhi
		Ganga 6	Sri Ganga nagar
		RMG-452	M. P.
		ML-515	Ludhiana (Punjab)
IV	3	MGG-320	Madhira (A.P.)
		STV-2781	Lam (A.P.)
		LGG-458	Lam (A.P.)
V	10	MGG-329, MGG-295	Madhira (A.P.)
		ML-5 ML-682	Ludhiana (Punjab)
		STV-2774, STV-2810, STV-2667 STV-2442, STV-2789, STV-2724	Lam (A.P.)
VI	11	EC-337108	New Delhi
		Pusa 16	New Delhi
		LGG-462, LGG-475	Lam (A.P.)
		STV-2762, STV-2705	Lam (A.P.)
		MGG-221	Madhira (A.P.)
		Jonnalagadd local	Lam (A.P.)
		ML-611	Ludhiana (Punjab)
		Pant M3	Pant nagar (U.P.)
		V 1628	Taiwan (Thailand)
VII	6	EC-337103, EC-33711, EC-337105, EC-337112	New Delhi
		RMG-406	M. P.
		STV-2674	Lam (A.P.)

Table 15 : Inter cluster and Intra cluster (diagonal) average of D^2 and D values (parentheses) of fifty genotypes of Mung bean (complete linkage dendrogram)

Cluster	I	II	III	IV	V	VI	VII
I	199.83 (14.14)	537.36 (23.18)	1133.80 (33.67)	1635.88 (40.45)	780.03 (27.93)	684.92 (26.17)	1964.97 (44.33)
II		194.24 (13.94)	396.89 (19.92)	746.82 (27.33)	420.37 (20.50)	642.32 (25.34)	1026.88 (32.04)
III			154.60 (12.43)	283.08 (16.83)	300.71 (17.34)	645.97 (25.42)	370.87 (19.26)
IV				185.91 (13.64)	580.04 (24.08)	945.87 (30.75)	348.16 (18.65)
V					187.28 (13.69)	314.42 (17.73)	528.03 (22.98)
VI						253.06 (15.91)	906.13 (30.10)
VII							193.46 (13.91)

Table 16 : Cluster means for thirteen characters in fifty genotypes of Mung bean (Complete linkage dendrogram)

Cluster	Plant height (cm.)	Days to 50% flowering	Days to maturity	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm.)	Seeds per pod	100-Seed weight (g)	Grain yield per plant (g)	Biological yield per plant (g)	Harvest Index (%)
I	42.96	43.22	71.44	1.13	7.22	3.73	27.11	6.24	9.20	3.46	8.61	34.39	24.63
II	31.74	42.61	69.17	1.31	7.41	3.33	23.87	6.52	9.86	3.50	8.37	31.07	26.83
III	33.17	44.18	72.27	2.08	8.93	3.75	32.08	6.13	9.19	3.38	9.63	31.92	30.05
IV	44.55	42.33	65.67	2.11	9.42	3.80	34.84	6.05	9.64	3.35	11.04	35.11	31.39
V	35.43	42.30	66.53	2.12	9.39	3.85	34.22	6.35	9.64	3.31	10.88	33.73	32.18
VI	38.27	42.61	67.97	1.91	11.28	3.81	42.92	6.52	9.68	3.46	13.93	37.07	37.44
VII	41.18	42.44	70.28	2.08	12.58	4.42	53.38	6.99	9.88	3.60	18.80	41.20	45.51

cluster IV exhibited early 50% flowering in 42.33days and early maturity in 65.67 days. Among all clusters, cluster V exhibited maximum number of branches per plant (2.12).

4.3 GENETIC PARAMETERS

The variability estimates as phenotypic and genotypic coefficients of variation, heritability in broad sense, genetic advance and genetic advance as per cent of mean for thirteen characters in fifty genotypes of mung bean were furnished in Table 17.

The maximum genotypic and phenotypic variance was recorded for pods per plant (82.99 and 87.33) followed by harvest index (42.18 and 45.71), plant height (23.51 and 24.74), biological yield per plant (14.65 and 15.45), days to maturity (14.25 and 16.05) and grain yield per plant (12.59 and 13.33). Clusters per plant (3.05 and 3.30), days to 50% flowering (1.97 and 2.48), seeds per pod (0.21and 0.24), pods per cluster (0.15 and 0.17) and 100-seed weight (0.09 and 0.09) recorded lower phenotypic and genotypic variance.

As the phenotypic and genotypic variances are associated with units, the coefficients of variation were worked out for valid comparison between the characters. In general the phenotypic coefficients of variation were higher than genotypic coefficients of variation indicating that the variation is due to the influence of environment. The genotypic and phenotypic coefficients of variation were highest for branches per plant (34.56 and 35.70) followed by grain yield per plant (30.07 and 30.95), pods per plant (25.07 and 25.72) and harvest index (19.49 and 20.29). Clusters per plant (17.96 and 18.69), plant height (13.18 and 13.51), biological yield per plant (11.01 and 11.31) and pods per cluster (10.01 and 10.90) recorded moderate genotypic and phenotypic coefficients of variation. The characters 100-seed weight (8.69 and 8.72), seeds per pod (8.08 and 9.02), pod length (7.16 and 7.58), days to maturity (5.46 and 5.80), days to 50% flowering (3.27 and

Table 17 : Mean, Variance, Coefficients of variation, Heritability (broad sense), Genetic advance andGenetic advance as per cent of mean for 13 characters in 50 genotypes of Mung bean.

S. No.	Character	Mean	Variance		Coefficients of variation		Heritability (broad sense) (%)	Genetic Advance	Genetic advance as per cent of mean (%)
			Genotypic	Phenotypic	Genotypic (%)	Phenotypic (%)			
1	Plant height (cm.)	36.80	23.51	24.74	13.17	13.51	95.06	9.74	26.46
2	Days to 50% flowering	42.89	1.97	2.48	3.27	3.67	79.45	2.58	6.01
3	Days to maturity	69.12	14.25	16.05	5.46	5.80	88.82	7.33	10.61
4	Branches per plant	1.90	0.43	0.46	34.56	35.70	95.72	1.31	68.92
5	Clusters per plant	9.72	3.05	3.30	17.96	18.69	92.40	3.46	35.57
6	Pods per cluster	3.82	0.15	0.17	10.01	10.90	84.32	0.72	18.94
7	Pods per plant	36.33	82.99	87.33	25.07	25.72	95.03	18.30	50.35
8	Pod length (cm.)	6.41	0.21	0.24	7.16	7.58	89.28	0.89	13.94
9	Seeds per pod	9.58	0.59	0.75	8.07	9.02	80.20	1.43	14.90
10	100-Seed weight (g)	3.43	0.09	0.09	8.69	8.72	99.26	0.61	17.83
11	Grain yield per plant (g)	11.80	12.59	13.33	30.07	30.95	94.40	7.10	60.19
12	Biological yield per plant (g)	34.77	14.65	15.45	11.01	11.31	94.83	7.68	22.09
13	Harvest Index (%)	33.33	42.18	45.71	19.49	20.29	92.27	12.85	38.56

3.67) recorded lower genotypic and phenotypic coefficients of variation.

High heritability in broad sense was recorded for most of the characters. Highest heritability estimate in broad sense was recorded for 100-seed weight (99.26%) followed by branches per plant (95.72%), plant height (95.06%), pods per plant (9 5.03%), biological yield per plant (94.83%), grain yield per plant (94.40%), clusters per plant (92.40%), harvest index (92.27%), pod length (89.28%), days to maturity (88.82%) whereas pods per cluster (84.32%) and seeds per pod (80.20%) recorded moderate heritability. On the contrary, days to 50% flowering recorded the lowest heritability estimate (79.45%).

Highest genetic advance was expressed for pods per plant (18.30) followed by harvest index (12.85) and plant height (9.74). Contrarily, low genetic advance was recorded for pod length (0.89), pods per cluster (0.72) and 100-seed weight (0.61).

The character branches per plant displayed highest genetic advance as per cent of mean (68.92) followed by grain yield per plant (60.19) and pods per plant (50.35). Moderate values of genetic advance as per cent of mean were observed for harvest index (38.56), plant height (26.46) and biological yield per plant (22.09). However, low genetic advance as per cent of mean was recorded for days to 50% flowering (6.01).

4.4 CHARACTER ASSOCIATION

Phenotypic and genotypic correlation coefficients were computed in order to assess the direction and magnitude of association existing between grain yield and other component characters were furnished in Table 18, respectively. In general, the genotypic correlations were higher than the corresponding phenotypic correlations.

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Table 18 : Phenotypic (r_p) and Genotypic (r_g) Correlation coefficients among thirteen characters in fifty genotypes of Mung bean

S. No	Character		Days to 50% flowering	Days to Maturity	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	100 seed weight	Grain yield per plant	Biological yield per plant	Harvest Index
1	Plant height (cm.)	r_p	0.033	0.119	0.037	0.418**	0.459**	0.522**	0.132	-0.050	0.136	0.457**	0.554**	0.376*
		r_g	0.021	0.131	0.043	0.455	0.508	0.550	0.149	-0.067	0.142	0.485	0.583	0.405
2	Days to 50% flowering	r_p		0.808**	0.065	-0.001	0.169	0.028	-0.219	-0.315*	0.004	-0.084	-0.058	-0.096
		r_g		0.853	0.067	-0.015	0.265*	0.024	-0.271	-0.395	0.010	-0.092	-0.072	-0.101
3	Days to maturity	r_p			-0.046	0.013	0.252	0.091	-0.124	-0.328*	0.157	0.019	0.026	-0.001
		r_g			-0.059	0.016	0.336*	0.094	-0.145	-0.387	0.172	0.031	0.034	0.011
4	Branches per plant	r_p				0.295*	0.209	0.299*	-0.074	-0.086	-0.156	0.143	0.042	0.199
		r_g				0.326	0.235	0.323	-0.083	-0.103	-0.161	0.152	0.046	0.214
5	Clusters per plant	r_p					0.494**	0.917**	0.376**	0.058	0.103	0.813**	0.709**	0.822**
		r_g					0.591	0.966	0.399	0.079	0.108	0.857	0.751	0.871
6	Pods per cluster	r_p						0.701**	0.257**	0.013	0.195	0.656**	0.625**	0.642**
		r_g						0.769	0.295	-0.008	0.216	0.705	0.678	0.690
7	Pods per plant	r_p							0.387**	0.057	0.124	0.879**	0.806**	0.861**
		r_g							0.415	0.070	0.128	0.902	0.829	0.892
8	Pod length (cm.)	r_p								0.443**	0.115	0.466**	0.414**	0.469**
		r_g								0.515	0.123	0.507	0.452	0.513
9	Seeds per pod	r_p									0.164	0.359**	0.339**	0.352*
		r_g									0.181	0.368	0.364	0.358
10	100-Seed weight (g)	r_p										0.405**	0.398**	0.381**
		r_g										0.416	0.408	0.395
11	Grain yield per plant (g)	r_p											0.915**	0.971**
		r_g											0.925	0.975
12	Biological yield per plant (g)	r_p												0.805**
		r_g												0.829

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

Grain yield per plant

The character grain yield per plant had significant and positive association with harvest index ($r_p = 0.971^{**}$ $r_g = 0.975$), biological yield per plant ($r_p = 0.915^{**}$ $r_g = 0.925$), pods per plant ($r_p = 0.879^{**}$ $r_g = 0.902$), clusters per plant ($r_p = 0.813^{**}$ $r_g = 0.857$), pods per cluster ($r_p = 0.656^{**}$ $r_g = 0.705$), plant height ($r_p = 0.457^{**}$ $r_g = 0.485$), pod length ($r_p = 0.466^{**}$ $r_g = 0.507$), 100-seed weight ($r_p = 0.405^{**}$ $r_g = 0.416$) and seeds per pod ($r_p = 0.359^{**}$ $r_g = 0.368$). Similarly, positive and non-significant association of grain yield per plant with branches per plant ($r_p = 0.143$ $r_g = 0.152$) and days to maturity ($r_p = 0.198$ $r_g = 0.031$) was observed. However, the association of grain yield with days to 50% flowering was found to be non-significant and negative ($r_p = -0.084$ $r_g = -0.092$).

Harvest Index:

The association of harvest index was positive and significant with pods per plant ($r_p = 0.861^{**}$ $r_g = 0.892$), clusters per plant ($r_p = 0.822^{**}$ $r_g = 0.871$), biological yield per plant ($r_p = 0.806^{**}$ $r_g = 0.829$), pods per cluster ($r_p = 0.642^{**}$ $r_g = 0.690$), pod length ($r_p = 0.469^{**}$ $r_g = 0.513$),100-seed weight ($r_p = 0.381^{**}$ $r_g = 0.395$), plant height ($r_p = 0.376^{**}$ $r_g = 0.405$) and seeds per pod ($r_p = 0.352^{**}$ $r_g = 0.358$). However, the association of harvest index with days to 50% flowering was negative and non-significant ($r_p = -0.096$ $r_g = -0.101$).

Biological yield per plant:

Significant and positive association of biological yield per plant was observed with pods per plant ($r_p = 0.806^{**}$ $r_g = 0.829$), clusters per plant ($r_p = 0.709^{**}$ $r_g = 0.751$), pods per cluster ($r_p = 0.625^{*}$ $r_g = 0.678$), pod length ($r_p = 0.414^{**}$ $r_g = 0.452$), 100-seed weight ($r_p = 0.398^{**}$ $r_g = 0.408$) and seeds per pod ($r_p = 0.339^{**}$ $r_g = 0.364$). Non-significant and positive association of biological yield per plant was found with branches per plant ($r_p = 0.042$ $r_g = 0.046$) and days to maturity ($r_p = 0.026$ $r_g = 0.034$). However, biological yield per plant showed negative and non-significant association with days to 50% flowering ($r_p = -0.058$ $r_g = -0.072$).

Grain yield per plant

The character grain yield per plant had significant and positive association with harvest index (r_p = 0.971** r_g = 0.975), biological yield per plant (r_p = 0.915** r_g = 0.925), pods per plant (r_p = 0.879** r_g = 0.902), clusters per plant (r_p =0.813** r_g = 0.857), pods per cluster (r_p = 0.656** r_g = 0.705), plant height (r_p = 0.457** r_g = 0.485), pod length (r_p = 0.466** r_g = 0.507), 100-seed weight (r_p =0. 405** r_g = 0.416) and seeds per pod (r_p = 0.359** r_g = 0.368). Similarly, positive and non-significant association of grain yield per plant with branches per plant (r_p = 0.143 r_g = 0.152) and days to maturity (r_p = 0.198 r_g = 0.031) was observed. However, the association of grain yield with days to 50% flowering was found to be non-significant and negative (r_p = -0.084 r_g = -0.092).

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The association of harvest index was positive and significant with pods per plant (r_p = 0.861** r_g = 0.892), clusters per plant (r_p = 0.822** r_g = 0.871), biological yield per plant (r_p = 0.806** r_g = 0.829), pods per cluster (r_p = 0.642** r_g = 0.690), pod length (r_p = 0.469** r_g = 0.513),100-seed weight (r_p = 0.381** r_g = 0.395), plant height (r_p = 0.376** r_g = 0.405) and seeds per pod (r_p = 0.352** r_g = 0.358). However, the association of harvest index with days to 50% flowering was negative and non-significant (r_p = -0.096 r_g = -0.101).

Biological yield per plant:

Significant and positive association of biological yield per plant was observed with pods per plant (r_p = 0.806** r_g = 0.829), clusters per plant (r_p = 0.709** r_g = 0.751), pods per cluster (r_p = 0.625* r_g = 0.678), pod length (r_p = 0.414** r_g = 0.452), 100-seed weight (r_p = 0.398** r_g = 0.408) and seeds per pod (r_p = 0.339** r_g = 0.364). Non- significant and positive association of biological yield per plant was found with branches per plant (r_p = 0.042 r_g = 0.046) and days to maturity (r_p = 0.026 r_g = 0.034). However, biological yield per plant showed negative and non-significant association with days to 50% flowering (r_p = -0.058 r_g = -0.072).

100-seed weight

The character 100-seed weight recorded positive and non-significant association with pods per cluster (r_p = 0.195 r_g = 0.216), seeds per pod (r_p = 0.164 r_g = 0.181), days to maturity (r_p = 0.157 r_g = 0.172), plant height (r_p = 0.136 r_g = 0.142), pods per plant (r_p = 0.124 r_g = 0.128), pod length (r_p = 0.115 r_g = 0.123), clusters per plant (r_p = 0.103 r_g = 0.108) and days to 50% flowering (r_p = 0.004 r_g = 0.010). On the contrary, it displayed negative and non-significant association with branches per plant (r_p = -0.156 r_g = -0.161).

Seeds per pod

Positive and significant association of seeds per pod was recorded with pod length (r_p = 0.443** r_g = 0.515) whereas it`s positive and non-significant association was observed with pods per plant (r_p = 0.057 r_g = 0.070) and clusters per plant (r_p = 0.058 r_g = 0. 079). Negative and significant relationship of seeds per pod was recorded with days to maturity (r_p = -0.328* r_g = -0.387) and days to 50% flowering (r_p = - 0.315* r_g = -0.395). The association of seeds per pod was negative and non-significant with branches per plant (r_p = -0.086 r_g = -0.103) and plant height (r_p = -0.050 r_g = -0.067).

Pod length

The character pod length displayed significant positive association with pods per plant (r_p = 0.387** r_g = 0.415), clusters per plant (r_p = 0.376** r_g = 0.399) and pods per cluster (r_p = 0.257** r_g = =0.295). However, pod length showed positive and non-significant association with plant height (r_p = 0.132 r_g = 0.149). Negative and non-significant association of pod length was recorded with days to 50% flowering (r_p = -0.219 r_g = -0.271), days to maturity (r_p = -0.124 r_g = -0.145) and branches per plant (r_p = -0.074 r_g = -0083).

Pods per plant

Pods per plant displayed positive and significant association with clusters per plant (r_p = 0.917* r_g = 0.966), pods per cluster (r_p = 0.701** r_g = 0.769), plant height (rp =

0.522** r_g = 0.550) and branches per plant (r_p = 0.299** r_g = 0.323). Similarly, positive and and non-significant association of pods per plant was observed with days to maturity maturity (r_p = 0.091 r_g = 0.094) and days to 50% flowering (r_p = 0.028 r_g = 0.024).

Pods per cluster

The character pods per cluster displayed positive and significant association with clusters per plant (r_p = 0.494** r_g = 0.591), plant height (r_p = 0.459** r_g = 0.508) and days to maturity (r_p = 0.252* r_g = 0.336) while non-significant positive association of pods per cluster was observed with days to 50% flowering (r_p = 0.169 r_g = 0.265) and branches per plant (r_p = 0.209 r_g = 0. 235).

Clusters per plant

Clusters per plant showed significant positive relationship with plant height (r_p = 0.418** r_g = 0.455) and branches per plant (r_p =0.295** r_g = 0.326) whereas it exhibited non-significant positive association with days to maturity (r_p = 0.013 r_g = 0.016). Contrarily, it displayed negative and non-significant association with days to 50% flowering(r_p = -0.001 r_g = -0.059).

Branches per plant

Branches per plant recorded positive and non-significant association with days to 50% flowering (r_p = 0.065 r_g = 0.067) and plant height (r_p = 0.037 r_g = 0.043). However, it's association with days to maturity was negative and non-significant (r_p = -0.046 r_g = -0.059).

Days to maturity

The character days to maturity displayed positive and highly significant association with days to 50% flowering (r_p = 0.809** r_g = 0.854), while it's positive and non-significant association was observed with plant height (r_p = 0.119 r_g = 0.131).

Days to 50% flowering

Days to 50% flowering exhibited positive and non-significant association with plant height ($r_p = 0.033$ $r_g = 0.021$).

4.5 *PATH COEFFICIENT ANALYSIS*

Path coefficient analysis facilitates the partitioning of correlation coefficients into direct and indirect effects of various characters on seed yield. It provides an effective means of finding out direct and indirect causes of association and presents a critical examination of the specific forces acting to produce a given correlation and measures the relative importance of each causal factor. The path coefficient analysis of different characters on yield based on phenotypic and genotypic correlations in fifty genotypes of mung bean were presented in Table 19.

4.5.1 Phenotypic path coefficient analysis

Path coefficient analysis revealed that the character pods per plant exhibited high positive direct effect on grain yield per plant (0.442) followed by harvest index (0.317), biological yield per plant (0.290), seeds per pod (0.193), 100-seed weight (0.171), clusters per plant (0.167). However, negative direct effects of days to 50% flowering (-0.072), plant height (-0.054), pod length (-0.107) and branches per plant (-0.016) were observed on grain yield in the present study.

The character plant height had positive indirect influence through pods per plant (0.233), biological yield per plant (0.161), clusters per plant (0.070), pods per cluster (0.036), 100-seed weight (0.023) and days to maturity (0.005). On the contrary, low and negative indirect influence of plant height through seeds per pod (-0.009), days to 50% flowering (-0.002), harvest index (-0.002) and branches per plant (-0.001) was observed on grain yield.

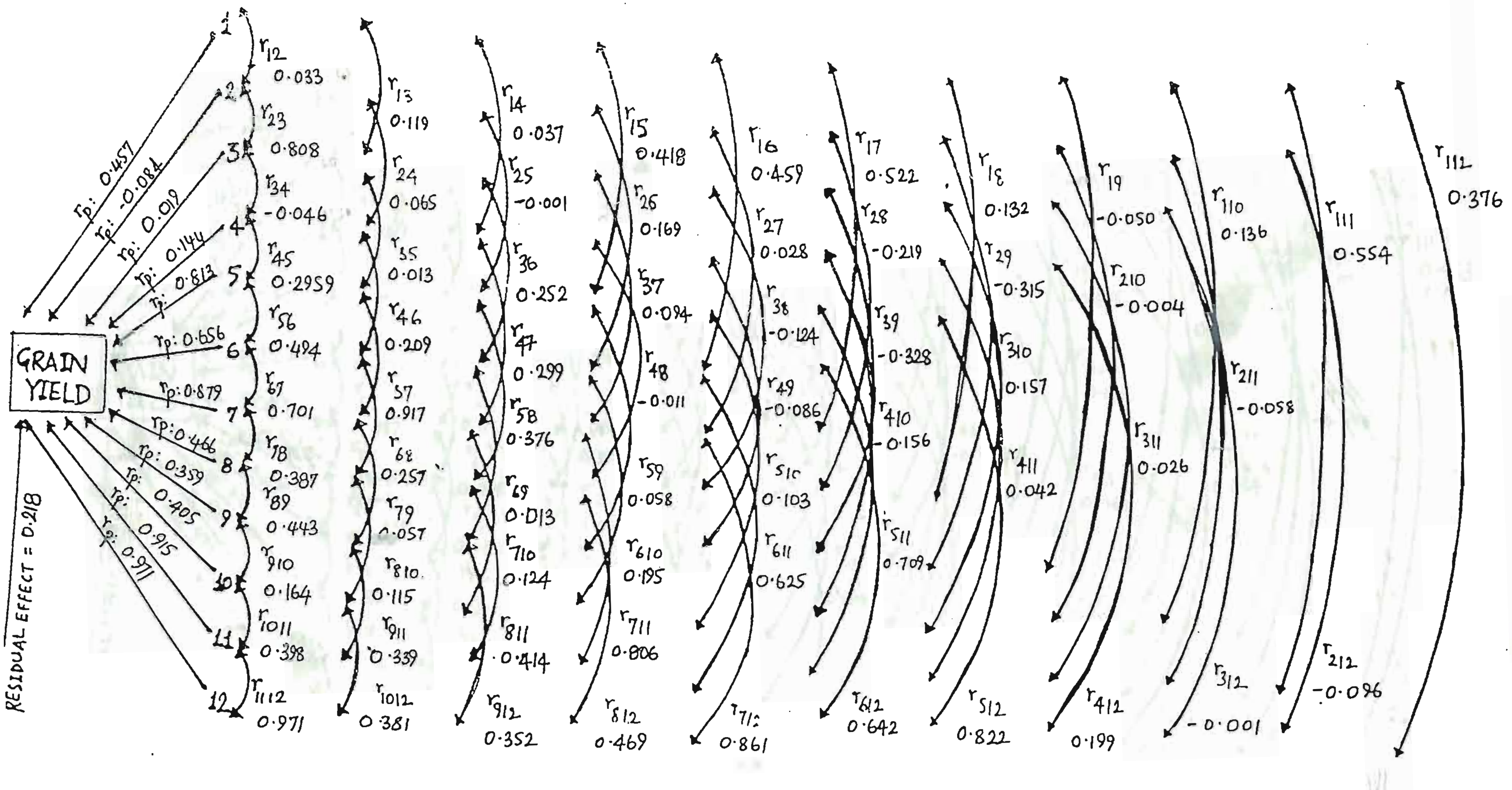
Table 19: Phenotypic (r_p) and Genotypic (r_g) Path coefficients among grain yield per plant and yield components in 50 genotypes of Mung bean

S. No	Character		Plant Height	Days to 50% flowering	Days to Maturity	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	100 seed weight	Biological yield per plant	Harvest Index	Grain yield per plant
1	Plant height	p	**-0.054**	-0.002	0.005	-0.001	0.070	0.036	0.233	-0.002	-0.009	0.023	0.161	-0.002	0.458^{**}
		g	**-0.025**	-0.088	0.031	0.001	0.689	0.292	-0.823	-0.002	-0.009	0.006	0.311	0.063	0.485
2	Days to 50% flowering	p	-0.002	**-0.072**	0.038	-0.001	-0.001	0.019	0.012	0.003	-0.061	0.001	-0.017	-0.006	-0.085
		g	-0.001	**-0.303**	0.204	0.002	-0.023	0.152	-0.036	0.005	-0.060	-0.001	-0.039	0.006	-0.092
3	Days to maturity	p	-0.006	-0.061	**0.047**	0.001	0.002	0.020	0.040	0.002	-0.063	0.026	0.007	0.003	0.019
		g	-0.003	-0.026	**0.240**	-0.001	0.025	0.193	-0.138	0.003	-0.066	0.008	0.018	0.013	0.031
4	Branches per plant	p	-0.002	-0.012	-0.009	**-0.016**	0.049	0.016	0.132	0.001	-0.016	-0.026	0.012	0.014	0.144
		g	-0.001	-0.020	-0.014	**0.024**	0.493	0.135	-0.469	0.002	-0.019	-0.007	0.025	0.012	0.152
5	Clusters per plant	p	-0.119	0.001	0.001	-0.005	**0.167**	0.039	0.405	-0.103	0.011	0.018	0.205	0.192	0.813^{**}
		g	-0.119	0.005	0.004	0.008	**1.512**	0.339	-1.408	-0.115	0.011	0.005	0.401	0.215	0.857
6	Pods per cluster	p	-0.131	-0.012	0.012	-0.003	0.082	**0.079**	0.309	-0.110	0.003	0.033	0.181	0.212	0.656^{**}
		g	-0.119	-0.081	0.081	0.006	0.893	**0.574**	-1.119	-0.112	-0.001	0.009	0.362	0.242	0.705
7	Pods per plant	p	-0.107	-0.081	0.004	-0.084	0.153	0.055	**0.442**	-0.085	0.011	0.021	0.234	0.316	0.879^{**}
		g	-0.112	-0.105	0.023	0.008	1.460	0.440	**-1.458**	-0.106	0.009	0.005	0.345	0.392	0.902
8	Pod length	p	-0.007	0.015	-0.029	0.001	0.063	0.020	0.147	**-0.107**	0.085	0.019	0.120	0.046	0.466^{**}
		g	-0.017	0.082	-0.035	-0.025	0.603	0.169	-0.606	**-0.019**	0.071	0.005	0.241	0.025	0.507
9	Seeds per pod	p	0.003	0.023	-0.016	0.001	0.079	0.001	0.025	-0.007	**0.193**	0.028	0.099	-0.070	0.359^{**}
		g	0.002	0.119	-0.093	-0.002	0.119	-0.005	-0.102	-0.010	**0.137**	0.053	0.144	-0.044	0.368
10	100-Seed weight	p	-0.011	-0.004	0.007	0.002	0.017	0.015	0.055	-0.006	0.032	**0.171**	0.115	0.011	0.405^{**}
		g	-0.028	-0.007	0.041	-0.004	0.163	0.124	-0.187	-0.006	-0.025	**0.046**	0.217	0.074	0.416
11	Biological yield per plant	p	-0.129	0.004	0.001	-0.007	0.119	0.049	0.355	-0.106	0.066	0.068	**0.290**	0.199	0.915^{**}
		g	-0.113	0.022	0.008	0.001	1.136	0.388	-1.209	-0.107	0.049	0.019	**0.534**	0.197	0.925
12	Harvest Index	p	-0.021	-0.058	-0.009	0.197	0.250	0.232	0.107	0.128	0.178	0.048	0.188	**0.317**	0.971^{**}
		g	-0.003	-0.089	0.014	0.311	0.385	0.383	0.007	0.207	-0.078	-0.078	0.311	**-0.475**	0.975

Figures in bold are direct effects

Phenotypic residual effect : 0.218
Genotypic residual effect : 0.184

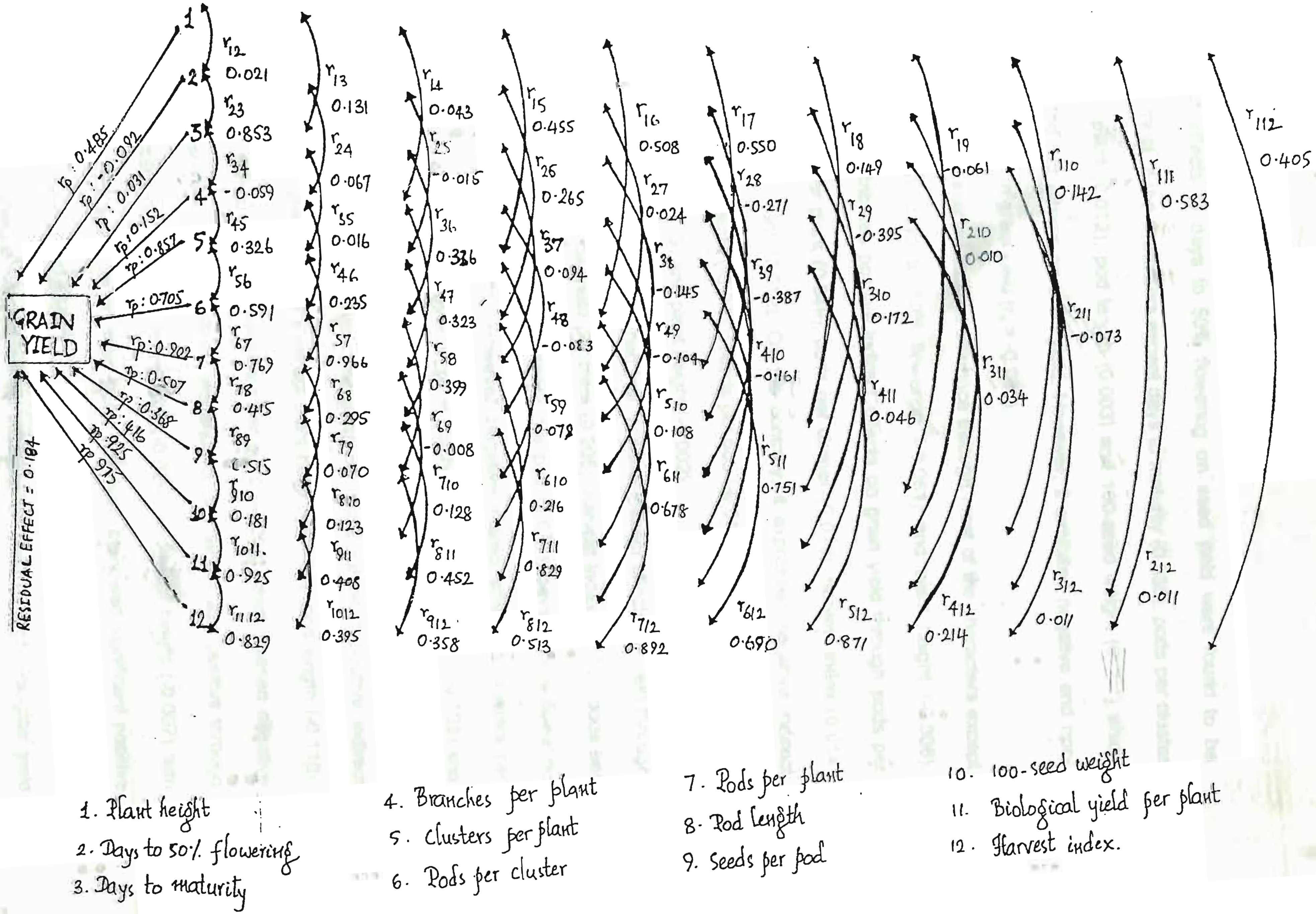
Fig 9: Phenotypic path diagram among grain yield per plant and yield components in 50 genotypes of Mungbean



1. Plant height
2. Days to 50% flowering
3. Days to maturity
4. Branches per plant
5. Clusters per plant
6. Pods per cluster
7. Pods per plant
8. Pod length
9. Seeds per pod
10. 100-Seedweight
11. Biological yield per plant
12. Harvest Index.

Fig 10: Genotypic path diagram among grain yield per plant and yield components in

50 genotypes of Mungbean



The direct effects of days to 50% flowering on seed yield were found to be negative through most of the characters except days to maturity (0.038), pods per cluster (0.019), pods per plant (0.012), pod length (0.003) and 100-seed weight (0.001) which showed positive indirect effects on seed yield. However, it exhibited negative and non-significant association with grain yield (r_p = -0.085).

Days to maturity exerted indirect influence through most of the characters except seeds per pod (-0.063), days to 50% flowering (-0.061) and plant height (-0.006). Branches per plant contributed positive indirect effects on grain yield through pods per plant (0.135), clusters per plant (0.049), pods per cluster (0.016), harvest index (0.014) and biological yield per plant (0.012). On the contrary, it expressed negative indirect effects through 100-seed weight (-0.026), seeds per pod (-0.016) days to 50% flowering (-0.012), days to maturity (-0.009) and plant height (-0.002).

The character clusters per plant had high positive indirect effects on yield through pods per plant (0.405), biological yield per plant (0.205), harvest index (0.192), pods per cluster (0.039), 100-seed weight (0.018), seeds per pod (0.011), days to 50% flowering (0.001) and days to maturity (0.001). However, negative indirect effects of clusters per plant on grain yield were observed through plant height (-0.119), pod length (-0.103) and branches per plant (-0.005).

The characters pods per cluster and pods per plant exhibited positive indirect effects through most of the characters except plant height (-0.131), pod length (-0.110), days to 50% flowering (-0.012) and branches per plant (-0.003) which exerted negative indirect effects on seed yield. The indirect influence of pod length was positive through most of the characters except days to maturity (-0.029) and plant height (-0.007) with which it recorded negative effects on seed yield. However, it showed significant positive association with grain yield (r_p =0.466**).

Seeds per pod positive exerted indirect influence on yield through biological yield per plant (0.099) followed by clusters per plant (0.079). The indirect effects of 100-seed weight was positive through most of the characters but it exerted negative indirect effects through plant height (-0.011), pod length (-0.010) and days to 50% flowering (-0.004).

Biological yield per plant contributed high positive indirect effects through pods per plant (0.355) followed by harvest index (0.199), clusters per plant (0.119) which reflected in a highly significant positive association with grain yield (r_p = 0.915**). Harvest index exhibited positive indirect effects through branches per plant (0.197), clusters per plant (0.250), pods per cluster (0.232), pods per plant (0.107), pod length (0.128), seeds per pod (0.178), 100-seed weight (0.048) and biological yield per plant (0.188) while it exhibited negative indirect effects through days to 50% flowering (-0.058), plant height (-0.021) and days to maturity (-0.009).

4.5.2 Genotypic path coefficient analysis

Genotypic path analysis coefficient analysis indicated that high positive direct effects were observed for clusters per plant (1.512) followed by pods per cluster (0.574), biological yield per plant (0.534), days to maturity (0.240), seeds per pod (0.137), 100-seed weight (0.046) and branches per plant (0.024). Direct effects in negative direction were observed for pods per plant (-1.458), harvest index (-0.475), days to 50% flowering (-0.303), plant height (-0.025) and pod length (-0.019).

The character plant height exerted high positive indirect effects through clusters per plant (0.689), biological yield per plant (0.311), pods per cluster (0.292), harvest index (0.063) days to maturity (0.031), 100-seed weight (0.006) and branches per plant (0.001) while negative indirect effects were exerted through pods per plant (-0.823), days to 50% flowering (-0.088), seeds per pod (-0.009) and pod length (-0.002).

The indirect effects of days to 50% flowering were positive through days to maturity (0.204), pods per cluster (0.152), harvest index (0.006), pod length (0.005), and branches per plant (0.002). On the contrary, high negative indirect effects of days to 50% flowering was observed through seeds per pod (-0.060), biological yield per plant (-0.039), pods per plant (-0.036), clusters per plant (-0.023) and plant height (-0.001).

The character days to maturity had positive indirect effects through pods per cluster (0.193) followed by clusters per plant (0.025) and negative indirect effects through days to 50% flowering (-0.026) followed by seeds per pod (-0.066). Branches per plant had positive indirect effects through clusters per plant (0.493) followed by pods per cluster (0.135) and negative indirect effects through pods per plant (-0.469) and seeds per pod (-0.019).

Clusters per plant exerted positive indirect effects through most of the characters and negative indirect effects through pods per plant (-1.408), plant height (-0.119) and pod length (-0.115). The indirect effects of pods per cluster were positive through clusters per plant (0.893) followed by biological yield per plant (0.362) while indirect effects were negative through pods per plant (-1.119) and plant height (-0.119).

Pods per plant displayed high positive indirect effects on seed yield through most of the characters except plant height (-0.112) pod length (-0.106) and days to 50% flowering (-0.105) through which it expressed negative indirect effects on seed yield. Pod length had positive indirect effects through clusters per plant (0.603), biological yield per plant (0.241) and negative indirect effects through pods per plant (-0.606) days to maturity (-0.035) and branches per plant (-0.025).

Seeds per pod had positive indirect effects through all the characters except harvest index (-0.044), days to maturity (-0.093) and pod length (-0.010) through which it exhibitednegative indirect effects on seed yield. Similarly, 100-seed weight exerted positive indirect effects through biological yield per plant (0.217), clusters per plant (0.163), pods per cluster (0.124), harvest index (0.074) and days to maturity (0.041) while negative indirect effects through pods per plant(-0.187), plant height (-0.028), seeds per pod (-0.025), days to 50% flowering (-0.007), pod length (-0.006) and branches per plant (-0.004).

The indirect influence of biological yield per plant was positive through all the characters except pods per plant (-1.209), plant height (-0.113) and pod length (-0.107). Similarly, harvest index expressed positive indirect effect through clusters per plant (0.385), pods per cluster (0.383), biological yield per plant (0.311), branches per plant (0.311), pod length (0.207), days to maturity (0.014) and pods per plant (0.007) while negative indirect effects through days to 50% flowering (-0.089), seeds per pod (-0.078) 100-seed weight (-0.078) and plant height (-0.003).

DISCUSSION

CHAPTER V

5 DISCUSSION

In India mung bean is one of the most important pulse crops in terms of both area and production. It is adaptable to a wide range of agroclimatic conditions, shorter in duration and suitable for inter cropping and multiple cropping systems. The low yield level of mung bean has restricted its cultivation to fields, which are relatively poor in fertility and moisture. However, owing to the beneficial effects of this crop on the yield of succeeding crop, farmers have been cultivating considerable areas with this crop in rotation. The yield can be increased by enhancing the genetic potential for higher yield of new varieties. Development of commercial hybrid varieties in a self pollinated crop like mung bean did not seem to be economically feasible due to the absence of many prerequisites such as natural out crossing and male sterile lines.

Selection of suitable parents is a difficult task for the plant breeders in planning a successful hybridization programme. The plant breeder primarily aims at improving yield and quality by evolving superior varieties. This may be achieved either by selecting promising types from the naturally existing variation or by hybridization followed by isolation of best recombinants. The nature and magnitude of genetic divergence will help to identify suitable donors having wider genetic distance. Greater the diversity in a crop species, better is the chance of evolving promising and desired types. Proper evaluation of the extent of genetic variation available for yield attributes their heritability values and genetic advance that could be effected will be of immense help to the breeders. Information on the correlation and association of different component characters among themselves and with grain yield is quite important for devising an efficient selection criterion for grain yield.

The present investigation was undertaken keeping the above facts in mind in order to elucidate information on genetic divergence, genetic parameters, character association and path coefficient analysis in fifty genotypes of mung bean. Observations were recorded on thirteen important morphological attributes. The results of the studies conducted on divergence, variability, correlation between yield and yield components, direct and indirect effects of these traits on yield are discussed hereunder.

5.1 MEAN PERFORMANCE

The genotype STV 2674 recorded high *per se* performance for grain yield per plant followed by EC 337105, EC 337112, EC 337103 and RMG 406 among the fifty genotypes of mung bean (Table 3). The increased grain yield in genotype STV 2674 was due to more number of clusters per plant, pods per plant and seeds per pod. Similarly EC 337105 registered fairly higher mean values for pods per plant, seeds per pod and pod length. EC 337112 recorded relatively high grain yield through more number of pods per plant, branches per plant and clusters per plant. EC 337103 registered fairly high mean values for pods per plant, clusters per plant and pod length. RMG 406 recorded high grain yield through maximum number of pods per plant and clusters per plant. Thus these genotypes viz., STV 2674, EC 337105, EC 337112, EC 337103 and RMG 406 appeared to be promising donors for grain yield and other economic traits.

Clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod are the important components of seed yield as they bear the sink in mung bean. Improvement in the above characters will result in an increase in grain yield. The genotype LGG 462 exhibited maximum 100-seed weight (g) and fairly high mean performance for number of pods per plant, pods per cluster and clusters per plant. ML 611 had fairly high mean values for pods per plant, clusters per plant and pods per cluster. Further the grain yield performance of these genotypes was fairly good. Hence these genotypes can be used for increasing productivity of mung bean.

The genotype STV 2781 was earliest to mature among the fifty genotypes followed by MGG 295, V 1628, and STV 2810. These can be used as donors for evolving early types of mung bean.

The genotype LGG 468 recorded maximum plant height and high mean performance for pods per cluster and seed per pod. ML 611 showed fairly high mean values for clusters per plant, pods per cluster and seeds per pod. These genotypes can be used in hybridization programmes for evolving superior segregants recombining these characters.

5.2 GENETIC DIVERGENCE

Genetic diversity has been considered as an important factor in discriminating the genotypes for selecting genetically diverse parents for obtaining high-yielding lines for efficient and successful hybridization programme. This will not only result in inducing genetic variability in self-pollinated crops like mung bean but also provide new recombinations of genes in the gene pool. Choice of parents for any crop improvement programme based on genetic divergence is the outcome of the hypothesis that divergent parents offer substantial variability that reflects in segregating generations, thus, the selection of desirable recombinants becomes easy.

Earlier workers regarded geographical isolation as a reasonable index of genetic diversity (Vavilov 1926, Ram and Panvar 1970). However this criterion may not be so effective in quantifying or differentiating between genotypes. Among the techniques identified for the purpose, multivariate analysis was found to be the best technique to classify germ plasm collections on the basis of genetic diversity. Several other methods such as metroglyph analysis and hierarchical methods have been shown to be useful in the selection of desirable parents.

Multivariate analysis using Mahalnobis's D^2 statistic has been found to be a potential biometrical tool in quantifying the degree of divergence in germ plasm collections of crop plants. This technique was used in different crops viz., by Singh and Bains (1968) in cotton, Gupta and Singh (1970), Malhotra *et al* (1974), Mishra (1987), Ramana and Singh (1987) in green gram, Ranga Rao *et al* (1980) in safflower, Das and Gupta (1984) in black gram. Suitability of Metroglyph analysis technique given by Andersen (1957) to measure the genetic diversity has not been adequately tested in different crop plants. Hence, an attempt was made to compare the findings of D^2 analysis and Metroglyph analysis in Mung bean in the present investigation.

5.2.1 Mahalanobis's D^2 Analysis

Mahalanobis D^2 statistic provides a useful statistical method for measuring the amount of genetic diversity in a given population in respect of characters considered together and to classify the genotypes on the basis of genetic diversity. In the present study, the data collected on the yield and yield component characters of the fifty genotypes of mung bean were subjected to D^2 analysis and the genetic diversity was estimated. Tocher's method of grouping is most widely used procedure of clustering using Mahalanobis's D^2 statistic. All the genotypes were grouped into ten clusters (Table 5). The magnitude of D^2 value ranged from 31.85 to 3164.56 suggesting that there was substantial variability in the material. Prasanna Rajesh(1995) also reported such substantial variability.

In the present study, the clustering pattern revealed that the genotypes originating from different geographical regions got them grouped together into different clusters. The genotypes originating from Andhra Pradesh, Punjab, Tamil Nadu and New Delhi states had been grouped together in cluster I. On the contrary, the genotypes originating from Lam (A.P.) had been distributed in different clusters indicating that geographic diversity though important may not necessarily be the only factor in determining genetic diversity. These results were in conformity with the findings of Tawar *et al* (1988), Appalaswamy (1997) and Manivannan *et al* (1998). The clustering pattern obtained in the present investigation showed that there is no relationship between geographic distribution and genotypic diversity as the genotypes from different geographic origin were grouped into one cluster. Murthy and Arunachalam (1966) stated that genetic drift and selection in different environments could cause greater diversity than geographic distance.

Factors other than the geographic diversity may be attributed for grouping of different genotypes in the same cluster. The variation may be due to the fact that ecotypes in a particular inhabitant could have been evolved with different objectives and varied local situations and needs thus, giving importance to different characters. Hence, genotypes originating at the same place might have different architecture and could have undergone change for different characters under selection during the process of evolution. The clustering pattern failed to establish the fact that the genetic divergence is due to geographic distribution (Veerabadhiran *et al,* 1996). However, in some cases the influence of geographic origin on clustering was observed. The majority of the genotypes from Andhra Pradesh and exotic collections clustered together. This indicated that although geographic distribution was not the sole criterion of genetic diversity, the importance of free exchange of genetic material among the genotypes in a particular region could still be traced. Appalaswamy (1994) made similar reports on mung bean.

Among the clusters, cluster I contained 22 genotypes, while clusters II, VI, VII, VIII and X had single genotype each (Table 5). The cluster IX consisted types from the same geographical region, showing similar genetic architecture among the types of the cluster. Shanmugam and Sreerangaswamy (1982), Natarajan *et al* (1988) and Veerabadhiran *et al* (1996) also reported such a parallelism in clustering of genotypes into different characters.

The inter-cluster distances were minimum between clusters II and III indicating a close relationship and similar magnitude for most of the characters of the genotypes in these clusters (Table 6). The inter-cluster distances were maximum between clusters III and IX followed by clusters IV and X. The genotypes in these clusters may serve as potential parents and crossing between the genotypes may result in heterotic expression for yield components. Selection of parents from such clusters for hybridization programmes would result in novel recombinants. Shanmugam and Sreerangaswamy (1982) and Manivannan *et al* (1998) made similar study for identifying genotypes resulting in heterotic expression for yield components.

The cluster means for different characters indicated considerable differences between the clusters for all the characters. (Table. 7) The cluster V (STV 2674) recorded maximum values for number of pods per plant, longest pods, number of seeds per pod, grain yield per plant, biological yield per plant, and harvest index. Cluster VI showed maximum values for number of clusters per plant and number of pods per cluster. Cluster II had increased mean values for days to 50 per cent flowering, days to maturity and number of branches per plant. Cluster IX recorded increased mean values for plant height and 100-seed weight. Inter-crossing the genotypes from these clusters might result in wide array of variability for exercising effective selection for these traits.

The relative contribution of different plant characters to the total genetic divergence estimated by D^2 analysis indicated that 100-seed weight contributed maximum to genetic divergence followed by plant height (Fig. 2). Apart from the high divergence, the performance of genotypes and the characters with maximum contribution towards divergence should also be given due consideration which appear desirable for inclusion for improvement of mung bean.

5.2.2 METROGLYPH ANALYSIS

In the present study, Metroglyph analysis classified the genotypes into 8 sub groups (Fig. 3). Seed yield and 100-seed weight are the most important characters which showed a wide range of variability. Other characters have been represented by rays at different positions on the glyph and the range by the length of the ray. An examination of the scatter diagram revealed that the 8 sub-groups could be distinguished on the basis of morphological variation. Out of 8 sub-groups, the first subgroup consisted of seven genotypes in which the genotypes LGG 470 and STV 2731 superimposed over each other. The sub-group V contained a maximum number of 8 genotypes and the genotypes STV 2667 and MGG 221 occupied the same glyph and similar index score. Satyan *et al*

(1991) also observed nine distinct complexes of the same pattern in mung bean based on yielding ability and pods per plant. It was observed that the pattern of variability as represented by ray pattern was also more or less similar among the varieties of a group.

The frequency diagram shows the index score values of all the characters under study. The range of index scores was from 10 to 28. The genotypes RMG 406 and ML 611 scored the highest index score while MGG 295 scored the lowest index score. (fig. 4) Maximum frequency of genotypes occurred around an index score of 12.

Out of the 50 genotypes, five genotypes viz., RMG 406, EC 337112, EC 337105, EC 337103 and LGG 462 were included in high yielding groups (clusters VII and VIII). While 14 genotypes constituted the medium yielding and the remaining 33 genotypes come under low yielding group. Singh and Chowdhury (1974), Borah and Hazarika (1991) and Satyan *et al* (1991) carried out similar studies to study genetic divergence. The present study on metroglyph analysis revealed that most of the plant characters exhibiting large variability offer valuable criteria for a systematic cataloguing of the germ plasm. The results of genetic divergence analysis can be utilized in hybridization programmes in order to combine the characters of different germ plasm complexes.

5.2.3 COMPARATIVE STUDY OF CLUSTER FORMATION BY MAHALANOBIS'S D^2 METHOD (TOCHER'S METHOD) AND METROGLYPH ANALYSIS

The clustering pattern of the Mahalanobis's D^2 method (Tocher's method) was compared with that of metroglyph analysis and the implications are discussed hereunder.

The fifty diverse genotypes formed 10 clusters on the basis of D^2 analysis, while they formed into 8 clusters in metroglyph analysis. The possible reason for cluster difference in D^2 and metroglyph analysis could be that only two most variable characters namely 100-seed weight and grain-yield have been considered for cluster formation by metroglyph analysis. No consideration has been given to other major characters. Clusters IX and X of D^2 analysis disappeared due to their merging with clusters VIII, VI and I respectively of metroglyph analysis. Some of the genotypes were superimposed over each other in the ultimate configuration as compared to the clustering on the basis of D^2 values. A distance of 153.87 in D^2 analysis separated the genotypes LGG 463 and LGG 440, but they were superimposed over each other in metroglyph analysis. Similar observations were found between genotypes LGG 470 and STV 2731, Pusa 16 and STV 2762. Similar results confirming the present study were reported by Mishra *et al* (1987) in soybean, Chhabra *et al* (1988) in faba bean, Mishra and Rao (1990) in chickpea, Ramesh babu (1998) in blackgram.

When large number of germ plasm lines are considered at a time, metroglyph analysis would be suitable for preliminary grouping whereas D^2 method would be valuable for final grouping of large number of germ plasm collections. So, metroglyph analysis is a semi-quantitative technique useful for grouping large number of genotypes.

Mahalanobis's D^2 statistic would be a powerful tool in the hands of the breeder for estimation of genetic divergence among populations. It measures the forces of differentiation at intra and inter-cluster levels and determines the relative contribution of each component trait to the total divergence. Though the results are obtained by the interpolation of values in the scatter diagram of the metroglyph analysis, D^2 values prove more apt as these values are based on pooled means of all the characters considered together. While in the metroglyph analysis, the values are based on only two most variable characters. Some of the minor deviations observed between the two methods regarding the characters considered for grouping and super-imposition of genotypes within the clusters point out the refinement of D^2 technique in classifying germ plasm collection.

5.2.4 COMPLETE LINKAGE DENDROGRAM

One of the basic problems faced by breeders is to classify a large number of genotypes into fewer numbers of homogenous clusters. D^2 statistic of Mahalanobis (1936) has been widely used by the breeders as the measure of genetic distance between two populations for the past thirty years. The Tocher's technique given by Rao (1952) is the most widely used procedure of clustering using D^2 technique. The stopping rule for formation of any cluster is the drawback in this technique. The genotypes are wrongly clustered which increases the average intra-cluster distance.

The method of grouping suggested by Tocher (Rao, 1952) uses norm to decide whether a genetic stock can be included in cluster. Singh and Chowdhury (1977) defined this norm without logic. Grouping based on their norm results in one or two groups containing a large proportion of genetic stocks and the rest ending up in single stock clusters. The problem needs to be looked in proper perspective (Arunachalam and Bandyopadhyay, 1989).

The hierarchical method of clustering is one among the six different methods reported by Everitt (1974) which is promising for effective grouping of genotypes under multivariate analysis. Complete linkage dendrogram is one of the agglomerative methods of hierarchical clustering approach. It is a novel device for clustering the genotypes with a set of norm (similarity or dissimilarity correlation coefficient) by utilizing D^2 statistic (Sneath and Sokal 1973).

In the present study, an attempt was made to compare the Tocher's method of clustering with complete linkage dendrogram technique. The fifty genotypes of diverse origin were clustered at a desirable similarity correlation coefficient level depending upon the dendrogram pattern. The genotypes were grouped into 7 clusters (Fig.7). Mahapatra *et al* (1995) and Sitaramaiah *et al* (1996) in rice, Shoeeb (1997) in coffee, Appalaswamy

(1997) in mung bean and Rameshbabu (1998) in blackgram reported this type of grouping based on the dendrogram pattern.

The genotypes STV 2674, EC 337105 and RMG 406 of cluster VII recorded high means values for all the characters except plant height, days to 50% flowering, days to maturity and number of branches per plant. The genotypes of cluster III were earliest to mature. Cluster I recorded high mean values for plant height.

Comparison of the two methods of clusteringclearly indicated that clusters with single genotype were observed more in number in Tocher's method of clustering where as there is no cluster with single genotype in complete linkage dendrogram. More number of genotypes were grouped into a single cluster in Tocher's method of clustering as compared to complete linkage dendrogram which indicated lack of methodology for clustering the genotypes in Tocher's method of clustering. The clustering procedure would be based on the choice of plant breeder in case of complete linkage dendrogram, which is lacking in case of Tocher's method due to lack of a formulated norm.

The present investigation on complete linkage dendrogram revealed that the genotypes were grouped proportionately which in Tocher's method, most of the genotypes were grouped into one or two clusters confirmed by zero intra- cluster D^2 values. Theoretically, the best method of clustering will be the one which gives the more homogenous clusters (minimum intra-cluster distance) along with maximum possible inter-cluster distance (Wahi and Kher, 1991). As none of these two procedures satisfy both the conditions uniformly, taking the ratio of intra-cluster to inter-cluster distance to compare the efficiency of the two procedures formed a homogeneity index of clusters. Lower the values of this index, the more homogenous will be the clusters.

Table 20: Ratio of average intra and inter cluster D^2 values (homogeneity index) of the clusters formed by two procedures in Mung bean.

CLUSTER NO.	TOCHER'S METHOD	COMPLETE LINKAGE DENDROGRAM
I	0.652	0.433
II	-	0.563
III	0.572	0.564
IV	0.469	0.517
V	0.571	0.629
VI	-	0.614
VII	-	0.498
VIII	-	
IX	0.380	
X	-	

Uniformity of the homogeneity index was observed in case of Complete linkage dendrogram whereas in Tocher's method, the uniformity was lacking due to grouping of maximum number of genotypes into one or two clusters and the remaining clusters with only single genotype (Table 20).

The present investigation also revealed that optimum number of clusters and uniform grouping of genotypes with uniform index of homogeneity can be obtained by Complete linkage dendrogram.

5.2.5 CANONICAL ROOT ANALYSIS

Canonical analysis was used to confirm the clustering pattern obtained by D^2 statistic and to plot the fifty-mung bean genotypes in two-dimensional graph. The three vectors were responsible for 81.02 per cent of the total variance of uncorrelated Y variable, which indicated that the differentiation of these traits was nearly complete in these genotypes in three phases (Table 11). The relative distribution of genotypes reflected existence of broad parallelism between grouping obtained by D^2 analysis and vector analysis.

The first two vectors should be more than 95 per. cent for getting a clear two dimensional representation. Contrary to the above, the three vectors as a whole contributed 81.02 per cent towards genetic diversity because of which discernible overlapping was observed in group constellations. The differentiation in the clustering pattern of Tocher's method and complete linkage dendrogram was clearly shown by the superimposition of clusters formed by the two methods on the canonical graph (Fig. 8).

The characters 100-seed weight in the first vector, clusters per plant in the second vector, plant height in the third vector contributed maximum towards divergence. This was in accordance with the relative contribution of characters as observed through D2 analysis. Hence, these characters were the important traits contributing towards divergence. The maximum contribution of 100-seed weight and plant height to genetic divergence in mung bean were reported earlier by Satyan *et al* (1991) and Tawar *et al* (1988).

5.3 GENETIC PARAMETERS

5.3.1 VARIABILITY

The success of any crop improvement programme essentially depends upon the nature and magnitude of the genetic variability present in the crop. Knowledge of nature and magnitude of genetic variability in the population is of immense value for planning efficient breeding programme to improve the yield potential of the genotypes. The extent of variability available for various quantitative characters determines the success that can be achieved in the genetic improvement of that species. The present day breeding activities do involve hybridization, mutation and other such techniques to create variability. It must be said that a proper and thorough examination of the naturally occurring variability in the collections with an objective of identifying high yielding genotypes and which can be considered for release for commercial cultivation should be examined. This will also help in identifying donors excelling in one or few yield contributing traits and such genotypes can be profitably used in combination breeding for yield improvement.

The extent of variability as measured by GCV and PCV provides an information regarding the relative amount of variation in different characters. In the present study, the estimates of phenotypic coefficients of variation for all the characters were higher than the estimates of genotypic coefficient of variation. The results are discussed hereunder.

The characters pods per plant, harvest index and plant height showed higher GCV and PCV. This was in conformity with the findings of Renganayaki and Sree

Rangaswasmy (1993) and Byregowda (1997) for pods per plant, Rathnaswamy *et al* (1986) and Madhavi latha (1998) for harvest index, Veerabadhiran *et al* (1996) and Ganesh Ram (1997) for plant height.

The estimates of variability for the characters biological yield per plant, days to maturity, grain-yield per plant were relatively higher and selection for these traits will be much effective.

The characters clusters per plant, days to 50% flowering, seeds per pod, pods per cluster and 100-seed weight recorded low variability estimates indicating little scope for selection. Similar findings were reported by Paramasivam and Rajasekharan (1980), Ramana and Singh (1987), Patil and Deshmukh (1988), Borah and Hazarika (1995) for days to 50% flowering, clusters per plant and seeds per pod and Ramana and Singh (1987), Veerabadhiran and Jehangir (1995) for 100-seed weight.

5.3.2 HERITABILITY AND GENETIC ADVANCE

Improvement in any crop species depends on the quantum of genetic variability, which reflects the heritable portion of variability. The estimates of the heritable variation alone could not provide the necessary variation for selection. Hence, information on heritability and genetic advance will be of immense value to the breeders. Knowledge on the nature of the component characters towards yield is the prime requisite for an efficient plant breeding programme. Burton (1952) suggested that genetic variation along with heritability estimates would give a better idea about the efficiency of selection.

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al* 1955). If high heritability is accompanied by high genetic advance, it indicates that the heritability is due to additive gene effects and selection is effective for the character under study. If high heritability is accompanied by low genetic advance, it indicates non additive gene effects and selection for such traits may not be rewarding.

Rangaswasmy (1993) and Byregowda (1997) for pods per plant, Rathnaswamy *et al* (1986) and Madhavi latha (1998) for harvest index, Veerabadhiran *et al* (1996) and Ganesh Ram (1997) for plant height.

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In the present investigation, high heritability was recorded for all the characters with 100-seed weight exhibiting the highest heritability (Table 17). Paramasivam and Rajasekharan (1980) reported similar high estimates of heritability for all the characters. High heritability coupled with high genetic advance was recorded for pods per plant, plant height and harvest Index indicating that additive genes govern these characters and selection will be rewarding for improvement of such trait. This was in consonance with the findings of Rosaiah *et al* (1987), Lakshmaiah *et al* (1989), Vijayabharathi (1993), Patil and Shinde (1995) for pods per plant, Patil and Shinde (1985), Manivannan *et al* (1996), Veerabadhiran *et al* (1996) and Ganesh Ram (1997) for plant height.

The characters pod length, pods per cluster and 100-seed weight recorded high heritability accompanied by low genetic advance which may be due to non additive gene effects such as epistasis and dominance type of interaction. Selection will be ineffective for such characters. Similar reports were made by Patil and Shinde (1995), Borah and Hazarika (1995), Appalaswamy (1997) for pod length and 100-seed weight; Lakshmaiah *et al* (1988), Prasanna Rajesh(1995); and Appalaswamy *et al* (1997) for pods per cluster.

The characters seeds per pod, days to 50% flowering, days to maturity exhibited moderate heritability and moderate genetic advance indicating little scope for selection.

5.3.3 HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN

High heritability coupled with high genetic advance; as per cent of mean was recorded for branches per plant, grain yield per plant and pods per plant. High heritability accompanied with low genetic advance as per cent of mean was observed for the characters days to 50% flowering, which indicated that selection for such character may not be rewarding. These findings were in conformity with the reports made by Giriraj (1973), Ramana and Singh (1987), Patil and Shinde (1995) for Grain yield per plant, Mishra and Sahu (1985), Ramana and Singh (1987), Borah and Hazarika (1995) and Sreedevi (1998) for pods per plant. Ramana and Singh (1987) and Manivannan *et al* (1996) made similar reports for days to 50% flowering.

From the foregoing discussion, it can be concluded that high GCV, heritability and genetic advance were observed for characters pods per plant, harvest index and plant height indicating that the variation in the above characters was most likely due to additive gene effects, hence, simple directional selection may be effective to improve these characters.

5.4 CHARACTER ASSOCIATION

A thorough understanding of the association of plant characters with yield and among themselves is essential for successful crop improvement programme. It enables the breeders to manipulate the expression of these traits in crop improvement. The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its components and among themselves. Correlation analysis provides information on the nature and magnitude of the association of different component characters with seed yield, which is regarded as highly complex trait in which the breeder is ultimately interested in. It also helps us to understand the nature of inter relationship among the component traits themselves. Ultimately this kind of analysis could help the breeder to design his selection strategies to improve seed yield.

In the present investigation, a number of yield components were investigated and their relationship with yield as well as among themselves was examined using correlation analysis.

A perusal of correlation analysis indicated that seed yield was significantly correlated with most of the traits except branches per plant, days to maturity and days to 50% flowering (Table18). However based on the magnitude of correlation values harvest Index, biological yield per plant, pods per plant, cluster per plant and pods per cluster may be regarded as very closely related characters with seed yield per plant. Similar kind of association was revealed by Malik *et al* (1987), Appalaswamy (1997) and Madhavi latha (1998) for harvest index; Malik *et al* (1987), Lampang *et al* (1987) and Natarajan *et al* (1988) for biological yield per plant; Reddy sekhar (1992), Renganayaki and

Sreerangaswamy (1993), Borah and Hazarika (1995), Byregowda *et al* (1997) and Sreedevi (1998) for pods per plant; Prasanna Rajesh(1995), Manivannan and Nadarajan (1996), Appalaswamy (1997) and Sreedevi (1998) for cluster per plant and pods per cluster.

The character harvest index and biological yield per plant highly correlated traits with seed yield showed positive significant relationship with pods per plant, clusters per plant and pods per cluster. These results indicated that simultaneous selection of these characters would help for improvement of yield. On the contrary, harvest index and biological yield per plant showed negative correlation with days to 50% flowering, which indicated negative impact on partitioning efficiency in early flowering genotypes. The characters 100-seed weight and number of pods per plant represent the sink size and sink number, which together determine the seed yield per plant. The association between these two traits was found to be positive and non-significant. Such situation provides scope to the breeder for improving both the traits simultaneously. Parameshwarappa (1989) in black gram and Renganayaki and Sreerangaswamy (1992) in mung bean indicated positive relationship between these two traits.

The relationship between number of seeds per pod and pod length was positive and significant and is on the expected line, since more the pod length more number of seeds it would accommodate. Similarly, Lakshmaiah *et al* (1988), Renganayaki and Sreerangaswamy (1992), Poornachandra Rao (1995) also reported a positive correlation between seeds per pod and pod length.

Number of pods per plant correlated positively and significantly with the components clusters per plant and pods per cluster though its association with the former is of slightly higher magnitude. Therefore, these characters can be also used as selection criteria for improving seed yield. Similar reports were made by Khorgade *et al* (1990), Borah and Hazarika (1995), and Sreedevi (1998) for clusters per plant, Reddy sekhar (1992), Shantipriya (1997), and Sreedevi (1998) for pods per cluster.

The character pods per cluster showed positive and significant association with clusters per plant and plant height as reported by Shantipriya (1997). Days to maturity displayed positive and highly significant association with Days to 50% flowering suggesting that days taken for maturity can be predicted by days to 50% flowering. This was in conformity with the results of Yohe and Poehlman (1975), Patil and Deshmukh (1988), Hirankumar (1990) and Madhavilatha (1998).

To conclude, the correlation studies revealed that harvest index, biological yield per plant, pods per plant, clusters per plant and pods per cluster showed positive and significant association with grain yield and also among themselves indicating simultaneous selection for these characters would result in improvement of high yielding genotypes.

5.5 PATH COEFFICIENT ANALYSIS

The association of different component characters among themselves and with grain yield is quite important for devising an efficient selection criterion for grain yield. The total correlation between grain yield and a component character may sometimes be misleading, as it might be an over-estimate or under-estimate because of its association with other characters which are also associated with economic yield. Hence, indirect selection by correlated response may sometimes be not fruitful. When many characters are affecting a given character, splitting the total correlation into direct and indirect effects of cause as devised by Wright (1921) would give more meaningful interpretation to the causes of association between the dependent variable like seed yield and independent variables like yield components. This kind of information will help in rationalizing the basis of selection more meaningful for breeding programme.

Path coefficient analysis was used to compute direct and indirect effects of 12 characters on seed yield in the present study (Table19). The characters clusters per plant, pods per cluster, seeds per pod, 100-seed weight, biological yield per plant exhibited positive direct effects on yield revealing that these were major yield contributing traits in mung bean. These findings were in agreement with the reports made by Pundir *et al* (1992), Reddy sekhar (1992), and Sreedevi (1998) for clusters per plant; Sarma and Talukdar (1996) and Madhavilatha (1998) for pods per cluster; Reddy *et al* (1994) and, Madhavilatha (1998) for seeds per pod; Pundir *et al* (1992), Kumar *et al* (1995), Byregowda *et al* (1997) and Sreedevi (1998) for 100-seed weight. On the contrary, negative direct effects were exerted by plant height, days to 50% to flowering and pod length on seed yield. Reddy *et al* (1994) and Appalaswamy (1997) for plant height, Kumar *et al* (1995) and Shantipriya (1997) for days to 50% flowering; Sandhu *et al* (1980) for pod length revealed the similar kind of negative effects.

The characters plant height, days to maturity, branches per plant, clusters per plant, pods per cluster, pod length and biological yield per plant showed highest positive indirect effects on grain yield through pods per plant. Similarly, the positive indirect effects of other characters viz., pods per plant through harvest index, 100-seed weight and harvest index through biological yield per plant, days to 50% flowering through pods per cluster and seeds per pod through 100-seed weight were observed on grain yield.

Though the characters plant height and pod length exerted negative direct effects on grain yield, their association with grain yield was found to be positive. This is due to the fact that indirect effects of these characters through pods per plant, clusters per plant and seeds per pod were high and positive. This was inconsonance with the results of Pokle and Patil (1975), Natarajan *et al* (1988) and Reddy sekhar (1992) for plant height; Chandel *et al* (1973) and Sandhu *et al* (1980) for pod length.

Critical analysis of the results by path analysis revealed the importance of the characters pods per cluster, clusters per plant, pods per plant, seeds per pod, 100-seed weight and harvest index in influencing the seed yield. Hence, selection should be practiced for these characters in order to isolate superior plant types for improvement of grain yield.

SUMMARY

CHAPTER VI

6 SUMMARY

The present investigation was carried-out with 50 diverse genotypes of mung bean with a view to study the nature and amount of variability, to know the degree of association between yield and its component characters, direct and indirect effects of the different quantitative characters on seed yield and to identify the genotypes which are highly efficient with respect to different traits besides their yielding ability.

The experimental material was sown in a randomized block design with three replications at S.V. Agricultural College Farm, Tirupati of Acharya N.G. Ranga Agricultural University during *rabi* 1998-'99. Observations were recorded on randomly selected ten plants for thirteen characters viz., plant height, days to 50% flowering, days to maturity, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, grain yield per plant, biological yield per plant and harvest index.

Analysis of variance indicated highly significant variation among the genotypes for all the traits. The genotypes STV 2674, EC 337105, EC 337103 and RMG 406 showed high mean performance for grain yield and its components.

The results of Mahalanobis's D^2 analysis revealed considerable variability among the fifty genotypes and were grouped into ten clusters. The mode of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that geographical distribution and genetic diversity were not related. The nature of selection forces operating under one eco-geographical region seems to be similar to that of other regions since genotypes from distant places were grouped together in the same cluster.

Differences in clustering pattern was observed between D^2 analysis and metroglyph analysis. The most variable characters 100-seed weight and grain yield were taken into consideration in Metroglyph analysis whereas all the thirteen characters were considered together in D^2 analysis. The comparative study indicated that metroglyph analysis would be suitable for preliminary grouping prior to undertaking D^2 analysis.

In Metroglyph analysis, superimposition of genotypes was observed because of the close proximity of characters taken for plotting the genotypes. The cluster distances were not representing the actual distances as only two variables were considered for clustering whereas D^2 values were based on pooled means of all the values thereby the actual divergence was represented in D^2 analysis. Hence, Mahalanobis's D^2 statistic would be a powerful tool in measuring the genetic divergence.

A study comparing Tocher's method of clustering and Complete linkage dendrogram revealed the superiority of complete linkage dendrogram over Tocher's method with a defined norm (similarity correlation coefficient) of grouping. Canonical analysis confirmed the clustering pattern obtained by D^2 analysis. It revealed that among the 13 characters studied 100-seed weight, pods per cluster, pods per plant, clusters per plant and plant height contributed maximum towards genetic divergence. Further, this analysis also supported the presence of significant differences between the two methods of clustering i.e., Tocher's method and Complete linkage dendrogram.

Based on Tocher's method of clustering, the genotypes STV 2667, EC 337105 (cluster V), LGG 462 (cluster IX), MGG 316 (cluster IV), EC 337108 (cluster I) and RMG 406 (cluster V) were suggested for inclusion in hybridization programme. Similarly, STV 2667 (cluster V), LGG 462 and ML 611 (cluster VI), STV 2674 (cluster VII), MGG 320 (cluster IV) and LGG 470 (cluster III) were suggested for inclusion in hybridization programmes for obtaining superior and desirable recombinants based on Complete linkage dendrogram.

High estimates of genotypic and phenotypic coefficients of variation were observed for branches per plant followed by grain yield per plant, pods per plant, harvest index and

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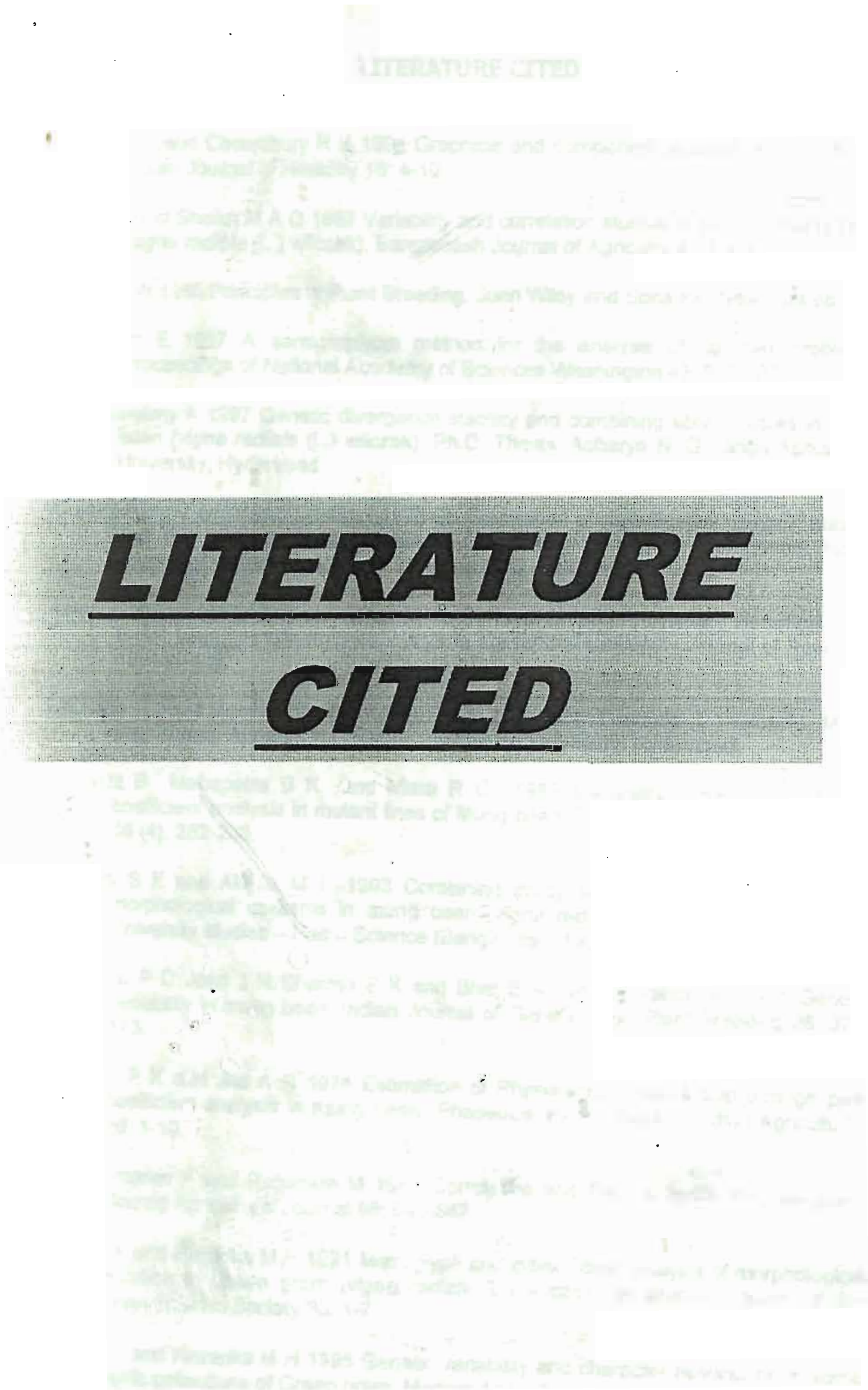
High estimates of genotypic and phenotypic coefficients of variation were observed for branches per plant followed by grain yield per plant, pods per plant, harvest index and clusters per plant. This abundant variability reflects possible chances of improving these traits by exercising selection. However, days to maturity and days to 50% flowering recorded low genotypic and phenotypic coefficients of variation.

The characters pods per plant, plant height and harvest index recorded high heritability coupled with high genetic advance indicating that selection will be fruitful for the improvement of such traits. High heritability accompanied by low genetic advance was recorded for pod length, pods per cluster and 100-seed weight. Hence, selection for such characters may not be rewarding.

In general, it was observed that the genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients. This indicated that strong inherent associations were somewhat masked at phenotypic level due to environmental effect. Among the different quantitative characters, harvest index, biological yield per plant, pods per plant, clusters per plant and pods per cluster were significantly and positively associated with grain yield. Therefore, these characters can be used as criteria for selection of genotypes with high yield potential.

The correlation of the yield components *inter se* revealed strong positive association of seeds per pod with pod length, pod length with pods per plant, clusters per plant and pods per cluster respectively. Similarly, harvest index showed strong positive association with pods per plant and clusters per plant. Hence, simultaneous selection for these characters might bring an improvement in grain yield.

Path coefficient analysis revealed that clusters per plant followed by pods per cluster, seeds per pod and 100-seed weight were the most important characters which could be used as selection criteria for effective improvement of seed yield. Though the direct effects of plant height, pod length and branches per plant were negative, their association with grain yield was found to be positive and high because of indirect influence of these characters through pods per plant, clusters per plant, pods per cluster and 100-seed weight were high and positive.



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