GENETIC DIVERGENCE IN COTTON
(*Gossypium hirsutum* L.)

By

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B.Sc. (Ag.)

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AGRICULTURAL COLLEGE, BAPATLA- 522 101

2009

DECLARATION

I, **Mr. VENKATESWARLU KUMBHA,** hereby declare that the thesis entitled **"GENETIC DIVERGENCE IN COTTON (***Gossypium hirsutum* L.**)"** submitted to **Acharya N. G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** in the major field of **Genetics and Plant Breeding** is the result of original research work done by me. I also declare that any material in the thesis has not been published earlier.

Date : **(VENKATESWARLU KUMBHA)**

Place :

CERTIFICATE

Mr. VENKATESWARLU KUMBHA has satisfactorily prosecuted the course of research and that the thesis entitled **“GENETIC DIVERGENCE IN COTTON** (*Gossypium hirsutum* L.)**”** submitted is the result of original research work and is of sufficiently high standard to warrant it’s presentation to the examination. I also certify that the thesis or part thereof has not been previously submitted by him for a degree of any university.

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CERTIFICATE

This is to certify that the thesis entitled **"GENETIC DIVERGENCE IN COTTON** (*Gossypium hirsutum* L.)**"** submitted in partial fulfilment of the requirements for the degree of Master of Science in Agriculture in the major field of **Genetics and Plant Breeding** of the Acharya N. G. Ranga Agricultural University, Hyderabad, is a record of the bonafied research work carried out by **Mr. VENKATESWARLU KUMBHA** under my 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 have been duly acknowledged by the author of the thesis.

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LIST OF SYMBOLS AND ABBREVIATIONS

AICCIP	All India Coordinated Cotton Improvement Project
ANOVA	Analysis of variance
ARS	Agricultural Research Station
CICR	Central Institute for Cotton Research
CICR (RS)	Central Institute for Cotton Research (Regional Station)
CV	Coefficient of variation
GA	Genetic advance
GAM	Genetic advance as per cent of mean
GAU	Gujarat Agricultural University
GCV	Genotypic coefficient of variation
HAU	Haryana Agricultural University
IARI	Indian Agricultural Research Institute
JNKV	Jawaharlal Nehru Krishi Viswa Vidyalaya
MAU	Marathwada Agricultural University
PAU	Punjab Agricultural University
NAU	Navasari Agricultural University
PCV	Phenotypic coefficient of variation
RARS	Regional Agricultural Research Station
RAU	Rajasthan Agricultural University
TNAU	Tamil Nadu Agricultural University
UAS	University of Agricultural Sciences
%	Per cent
^{0}C	Degree celcius
Df	Degrees of freedom
et al.,	and others
F_1	First generation hybrid of a cross
g	Grams
g/in	Grams per inch
g/tex	Grams per tex
h^2b	Heritability in broad sense
Kg/ha	Kilogram per hectare
No.	Number
viz.,	Namely
2D	Two dimensional
3D	Three dimensional

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ABSTRACT

The present investigation was carried out during *kharif* 2008-09 at Regional Agricultural Research Station, Lam Farm, Guntur with 50 genotypes of cotton (*Gossypium hirsutum* L.) to know the extent of genetic variability, heritability, genetic advance as per cent of mean, character association, the magnitude of direct and indirect effects of yield component on seed cotton yield traits and genetic divergence based on 16 characters viz., plant height (cm), days to 50% flowering, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), ginning out-turn (%), seed index (g), lint index (g), 2.5% span length (mm), micronaire (10^{-6}g/in), bundle strength (g/tex), uniformity ratio, oil content (%), lint yield per plant (g) and seed cotton yield per plant (g).

The genotypic coefficient of variation for all the characters studied was lesser than the phenotypic coefficients of variation indicating influence of environment on genotypes. High variability was recorded for number of monopodia per plant, lint yield per plant and seed cotton yield per plant. High heritability coupled with high genetic advance as per cent of mean was observed for the characters viz., number of monopodia per plant, number of sympodia per plant, number of bolls per plant, seed index, lint index, lint yield per plant and seed cotton yield per plant. This indicates the predominance of additive gene action and hence, direct selection may be fruitful to some extent. Where as, the other traits viz., days to 50% flowering, ginning out-turn, bundle strength, uniformity ratio and oil

percentage showed moderate to high heritability with low genetic advance indicating the role of non-additive gene action.

Correlation studies indicated that plant height, number of sympodia per plant, number of bolls per plant, boll weight, micronaire, oil content (%) and lint yield per plant had significant positive association with seed cotton yield per plant. There is scope for improvement of oil content through cyclic hybridization.

The path analysis indicated considerable positive direct effects of number of bolls per plant and lint yield per plant on seed cotton yield together with significant positive correlation revealing their true relationship. So improvement of seed cotton yield may be aimed *via* number of bolls per plant, oil content and lint yield per plant by preferring these characters during selection.

The results of multivariate analysis indicated that the presence of considerable divergence among fifty genotypes. These genotypes were grouped into eight clusters each in D^2 analysis and Ward's minimum variance method. Clustering pattern suggested that geographical distance may not be the only factor causing genetic divergence among genotypes studied.

It could be inferred from that the Mahalanobis' D^2 statistic, ginning out-turn, 2.5% span length, oil percentage, number of monopodia per plant, seed index and number of sympodia per plant contributed maximum towards the divergence. Based on intra- and inter-cluster distance among the groups, it can be suggested to attempt crosses between cluster VII (GJHV-448) and cluster VIII (LK-861) followed by cluster VI (H-1360) and cluster VIII (LK-861) for higher heterotic effects.

Principal component analysis identified six principal components (PCS), which contributed (77.41) per cent of cumulative variance. The population with high (PC_1) values were characterized by lint index and number of sympodia per plant. Where as, population with high (PC_2) values were characterized by micronaire and uniformity ratio, in (PC_3) characters like ginning out-turn and seed cotton yield per plant showed maximum weightage.2D and 3D PCA graphs showed wide divergence between GSHV-155 and HS-283 and MCU-5and CPD-1050 signifying their usefulness in the cotton breeding to develop high heterotic combinations.

Agglomerative cluster analysis revealed that wide genetic distance exists between cluster II (CCH-2623, RAH-336 and GJHV-448) and VII (LK-861) followed by cluster V (CNH-1104, CANDTS-55, HS-283, P-1752, RS-2527 and GSHV-155) and VII (LK-861). Therefore, selection of parents from these clusters will produce superior segregants through the process of hybridization for improvement of seed cotton yield, lint yield and oil content.

The above study indicated maximum divergence among GSHV-155, GJHV-448 and LK-861 genotypes which may be better exploited through heterosis breeding or selection of superior segregants with high seed cotton yield and desirable fibre quality.

CHAPTER - I

INTRODUCTION

Cotton (*Gossypium hirsutum* L), the king of apparel fibres, since times immemorial popularly called as “White gold” has played a pivotal role in the history and civilization of mankind. It provides the means of livelihood to millions of people in farming, processing, marketing and production of yarns, fabric, apparel and other value added products. Cotton and other textiles together account for one thirds of the country’s export earnings.

The genus, *Gossypium* belongs to the family Malvaceae and includes 44 species out of which viz., *Gosypium arboreum* L., *Gossypium herbaceum* L., *Gossypium hirsutum* L. and *Gossypium barbadense* L., are being cultivated. The former two are diploid, known as old world or desi and Asiatic cottons and the latter two are tetraploids, known as new world cottons. Of the four cultivated species of cotton *Gossypium hirsutum* has lion’s share in total cotton growing area in India due to its high productivity and superior quality.

In India, cotton is being grown over an area of 93.73 lakh ha with a production of 290 lakh bales (170 kg each) and a productivity of 526 kg lint / ha (AICCIP Annual Report, 2008-09). In Andhra Pradesh, cotton is a crop of great economic value, contributing its lion’s share to the national economy of the country and playing a significant role in the socio-economic status of the farmers. It occupies an area of about 13.45 lakh ha with an annual production of 53 lakh bales and productivity of 670 kg /ha (AICCIP Annual Report, 2008-09).

Before actual breeding programme is taken up under crop improvement, it is desirable to elicit information on the extent of genetic variability present in the material (Swarup and Chaugle, 1962). The extent of heritability of the selected traits and the magnitude of genetic advance are equally important. Genetic divergence is of considerable practical interest in crop improvement, since plant breeding is the utilization of the crop variability towards economic ends. The crosses involving genotypes with wider genetic base are likely to generate desirable recombinants in the progeny. The quantification of the degree of divergence present in the population is of immense value in identifying diverse genotypes for recombination breeding programmes. Mahalanobis' D^2 statistic is a powerful tool for quantifying genetic divergence in germplasm collections with respect to the characters considered together.

In cotton, as both quantity and quality of the fibre are equally important, selection based on correlation without regard to the direct and indirect effects *via* other characters may not be fruitful. Path coefficient analysis helps to determine the direct and indirect effects of each independent variable on dependent variable, in order to make selection more effective (Dewey and Lu, 1959).

Keeping in view of the above background information, the present investigation was taken up with the following objectives.

1. To assess the magnitude of the genetic variability for yield, its components and fibre quality traits.

2. To study the association of yield with yield attributing characters and among the components.
3. To estimate direct and indirect effects of component characters on yield.
4. To estimate genetic divergence in available germplasm through D^2 analysis, cluster analysis and principal component analysis and to find out the important characters contributing to the genetic divergence.

CHAPTER - II

REVIEW OF LITERATURE

The available literature in respect of genetic variability, heritability, genetic advance as per cent of mean, character association, path analysis and genetic divergence pertinenting to cotton is reviewed and presented here under.

2.1 Genetic variability

2.2 Heritability and genetic advance (GA) as per cent of mean

2.3 Character association

2.4 Path analysis

2.5 Genetic divergence

2.1 GENETIC VARIABILITY

The information on the nature and magnitude of variability for both different quantitative and qualitative traits in any crop species plays a vital role in formulating an efficient breeding programme and it's success. Superior genotypes can be isolated by selection if considerable genetic variation exists within the population. It is essential to partition the overall variability into heritable and non-heritable component with the help of genetic parameters like genotypic coefficients of variation. The literature on genetic variability on cotton is reviewed and presented in Table -1.

2.2 Heritability ($h^2_{(b)}$) and genetic advance (GA) as per cent of mean

Heritability is the measure of transmission of characters from generation to generation. Hanson *et al.* (1956) defined heritability in broad sense ($h^2_{(b)}$) as the ratio of genotypic variance to the total variance in the non-segregating populations and heritability in narrow sense ($h^2_{(n)}$) is defined as the ratio of additive and/or additive x additive genetic variance to the total phenotypic variance. Heritability in reality is the measure of the efficiency of a selection system in separating genotypes. Heritability estimates may be of some help to breeder in selecting superior individuals and utilizing them in breeding programmes.

Heritability measures the relative amount of the heritable portion of variability, while the genetic advance (GA) helps to measure the amount of progress that could be expected with selection in a character.

Estimates of heritability along with the estimates of genetic advance (GA) are more useful in choice of selection methods rather than heritability or genetic advance alone (Johnson *et al.*, 1955). High heritability coupled with high genetic advance indicates that the improvement could be made for a character by simple selection on phenotypic performance.

The literature on heritability ($h^2_{(b)}$) and genetic advance (GA) are presented in Table-2.

2.3 CHARACTER ASSOCIATION

Correlation refers to the degree and direction of association between two or more variables. Correlation studies are useful in developing an effective basis of phenotypic selection in plant populations. Yield is a complex and polygenically controlled character and highly influenced by the environment. Selection based on the component characters has been considered to be more effective as compared to the selection of yield alone. Knowledge on the association of the fibre characters with yield and other yield components is of paramount importance while aiming for improvement in yield and quality simultaneously. Unfavourable associations between the desired attributes under selection may limit genetic advance. Hence, information on the association of the yield with yield compenents is a prerequisite for taking up any breeding programme.

2.3.1 Association of component characters with seed cotton yield

The available literature on the association of component characters with seed cotton yield is presented in Table-3.

2.3.2 Association among the seed cotton yield component characters

The available literature on the associations among the seed cotton yield component characters is presented in Table- 4.

2.4 PATH COEFFICIENT ANALYSIS

Path coefficient analysis devised by Wright (1921) is a standardized partial regression coefficient, which helps in partitioning of the correlation coefficient into direct and indirect effects of independent variables on dependent variables. Dewey and Lu (1959) demonstrated the utility of path coefficient analysis in plant selection. Path analysis helps to elucidate the intrinsic nature of the observed associations and imparts a degree of confidence in the selection schemes adopted for a given situation (Dewey and Lu, 1959).

The literature on the direct and indirect effects of fibre quality parameters and other yield components on seed cotton yield are reviewed here under character wise and presented in Table -5.

2.5 GENETIC DIVERGENCE

2.5.1 Mahalanobis' D^2 analysis

Knowledge on the nature and magnitude of genetic variability present in the crop species will play an important role in formulating a successful breeding programme. It has been well known that genetically diverse parents are likely to yield desirable gene recombinants.

Mahalanobis' D^2 statistic is an effective tool in quantifying the degree of genetic divergence at genotypic level and provides quantitative measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis, 1928).

Genetic divergence as measured by Singh and Gill (1984) used the Mahalanobis' D^2 statistic to assess genetic divergence in 62 varieties of upland cotton under four agronomical environments. All the varieties were grouped into 12 clusters in each environment, except the environment II having 10 clusters. The clustering pattern on the basis of D^2 statistic was not related to geographic origin of strains. The grouping patterns under varying environments were also different. The results indicated that the clustering pattern in one environment may not be applicable in another environment.

Rajarathinam and Nadarajan (1993) used D^2 statistic to estimate genetic divergence in 40 genotypes of cotton studying ten economic characters. The genotypes were grouped into eight different clusters. The pattern of distribution of genotypes occurring in clusters cutting across geographical boundaries demonstrated that geographical isolation was not the only causing genetic diversity. Seed cotton yield, 2.5% span length and boll weight contributed more towards divergence.

Rajarathinam *et al.* (1994) used D^2 statistic to assess genetic divergence in 40 genotypes of cotton studying five characters. The genotypes were grouped into six clusters. The clustering of genotypes from different eco-geographic locations into one cluster was attributed to free exchange of breeding material from one place to other. Boll weight, number of bolls per plant and 2.5% span length contributed maximum towards genetic divergence.

Sumathi and Nadarajan (1995) used D^2 statistic to assess the genetic divergence in 51 genotypes of upland cotton studying ten characters. The genotypes were grouped into twelve clusters. The varieties represented wide genetic and geographic diversities. The analysis revealed the absence of any parallelism between genetic divergence and geographical diversity of genotypes.

Kalsy and Garg (1995) studied seven traits by using D^2 to assess genetic divergence in 15 parents along with their 105 F_1 s of American cotton genotypes. The genotypes were grouped into 10 clusters. The existence of ample genetic diversity among the genotypes as seen from the inter cluster distances was adequate for improvement by hybridization and selection for different combination of characters. The origin of different parents and pattern of group constellations indicated that the genetic diversity need not be necessarily related to geographical diversity.

Murthy *et al.* (1995a) used D^2 statistic to assess divergence in 43 genotypes of cotton studying six characters. The genotypes were grouped into six clusters. The results suggested that geographic distance was not the only factor causing genetic diversity. Mean fibre length, seed cotton yield per plant and micronaire value contributed more to total divergence.

Murthy *et al.* (1995b) used D^2 statistic to assess genetic divergence in 50 cultivars of upland cotton studying eight characters. The genotypes were grouped into nine clusters. Cultivars of similar geographic origin were found to be distributed among different clusters indicating that the geographical origin was not related to genetic diversity. Number of bolls per plant followed by ginning out turn contributed most of the total divergence indicating their importance in any cotton improvement programme.

Kumar *et al.* (2000) used D^2 statistic to assess the genetic divergence among 43 cotton genotypes. Nine fibre quality characters were studied to group them into five clusters. Cluster I was the largest with 39 genotypes. The characters yellowness followed by fibre length, fibre fineness and elongation contributed maximum towards divergence.

Jain and Yadav (2001) reported variation in grouping of populations into clusters varied from environment to environment in their study conducted with 44 genotypes of American cotton in two different locations.

Gururajan and Manickam (2002) reported maximum contribution of characters yellowness followed by fibre length, fibre fineness and elongation towards genetic divergence in their study conducted with 85 genotypes of Egyptian cotton.

Altaher and Singh (2003a) assessed genetic divergence among 50 different upland cotton varieties from all the three cotton growing zones of India for different agronomical and fibre quality traits using D^2 statistic and principal component analysis. On the basis of this 6 clusters were obtained and genotypes from different agro-climatic zones were grouped together in the same cluster indicating that their geographical diversity is not always necessarily associated with genetic diversity.

Kiran (2003) reported that the characters maximum contributed characters towards genetic divergence were bundle strength followed by seed cotton yield, numbers of sympodia per plant, 2.5% span length and uniformity ratio.

Pushpam *et al.* (2004) reported the absence of parallelism between genetic divergence and geographic diversity in their study with 150 genotypes of American cotton using D^2 statistic and grouped them into 9 clusters.

Ravikumar (2004) indicated that the character viz., seed cotton yield per plant contributed maximum towards genetic divergence.

Karunakar Raju *et al.* (2005) assessed 80 genotypes of upland cotton for 15 traits and these were grouped into ten clusters on the basis of D^2 estimates. The results indicated that the geographical diversity is not always necessarily associated with the genetic diversity. The characters 2.5% span length (mm) followed by lint index (g) and boll weight (g) contributed maximum towards divergence.

Muraleedhar *et al*. (2005) reported the absence of parallelism between genetic divergence and geographic diversity in their study with 50 genotypes of American cotton using D^2 statistic and grouped them into 7 clusters.

Padmavathi (2008) reported that the characters viz., number of monopodia per plant, seed index, number of sympodia per plant, plant height, ginning out-turn and micronaire contributed maximum towards genetic divergence in the study of sixty genotypes.

Vijayalaxmi (2008) reported that the characters viz., number of bolls per plant, plant height, number of monopodia per plant, number of sympodia per plant and boll weight contributed maximum towards genetic divergence.

Gopinath *et al.* (2009) reported that the characters viz., boll weight, boll number and 2.5% span length contributed maximum towards total divergence in their study with sixty genotypes.

2.5.2 Principal component analysis and cluster analysis

Principal component analysis was carried out to transform the inter dependent traits into a set of independent traits as well as to reduce thedimensionality of the data structure (Banfield, 1978). It is defined as a method of data reduction to clarify the relationship between two or more characters into limited number of uncorrelated new variables. The reduction is achieved by linear transformation of the original characters into a new set of uncorrelated variables known as principal components (PCs).

Brown (1991) used principal component, hierarchical cluster analysis for the data from seven of the nine regions of the Regional Cotton Variety Tests across the U.S. cotton belt. 3D plots displayed results of the principal component analysis, while results from Ward's minimum variance clustering were presented as dendrograms.

Altaher and Singh (2003a) estimated genetic divergence in 40 genotypes of upland cotton by using principal component analysis. Clustering based on PCA scores separated the genotypes into six clusters. Cluster II was the largest cluster with 28 genotypes from different agro-climatic zones, indicating that geographical diversity is not always associated with the genetic diversity.

Karunakar Raju *et al.* (2005) used cluster analysis and PCA to estimate genetic divergence in 80 genotypes of upland cotton. Five principal components, which had a cumulative variation 74.48%, formed the basis for divergence of genotypes into nine clusters.

Muraleedhar *et al.* (2005) assessed the genetic divergence among 50 genotypes of tetraploid cotton using PCA and cluster analysis. The five principal components, which had a cumulative variation of 89.22%, formed the basis for divergence of genotypes into eight clusters.

Vijayalaxmi (2008) used cluster analysis and PCA to estimate genetic divergence in 72 genotypes of upland cotton. PCA identified seven principle components which contributed 87.47% of cumulative variance. The population with high PC_1 values were characterized by high number of bolls per plant, where as population with high PC_2 values were characterized by boll weight.

Table-1: Genetic variability in cotton (*Gossypium hirsutum* L.)

S.No.	**Character**	**Wider genetic variability**	**Narrowgenetic variability**
1.	Plant height (cm)	Neelam and Potdukhe (2002) Laxman and Ganesh (2003) Patnaik *et al.* (2004) Kale *et al.* (2006) Tuteja *et al.* (2006) Kalpande *et al.* (2008)	Sangeetha (1998) Deshpande and Baig (2003) Leela Pratap (2006) Eswararao (2008) Neelima *et al*. (2008) Vijayalaxmi (2008)
2.	Days to 50% flowering	Ahuja and Tuteja (2000) Laxman and Ganesh (2003)	Reddy (2001) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Narisireddy and Ratnakumari (2004) Karunakar Raju (2005) Prasad *et al*. (2005) Leela Pratap (2006) Eswararao (2008) Neelima *et al*. (2008) Padmavathi (2008) Vijayalaxmi (2008)
3.	Number.of monopodia per plant	Neelam and Potdukhe (2002) Altaher and Singh (2003b) Kaushik *et al.* (2003) Ravikumar (2004) Sivaprasad *et al.* (2004 b) Karunakar Raju (2005) Prasad *et al.* (2005) Kumari and Chamundeswari (2005) Tuteja *et al.* (2006) Verma *et al.* (2006) Gitte *et al.* (2007) Eswararao (2008) Kalpande *et al.* (2008) Neelima *et al*. (2008) Padmavathi (2008) Vijayalaxmi (2008)	Ahuja and Tuteja (2000) Gururajan (2000) Girase and Mehetre (2002)

Cont……..

4.	Number of sympodia per plant	Gururajan (2000) Neelam and Potdukhe (2002) Deshpande and Baig (2003) Tuteja *et al.* (2003) Tuteja *et al.* (2006) Gitte *et al.* (2007) Kalpande *et al.* (2008) Neelima *et al*. (2008)	Girase and Mehetre (2002) Laxman and Ganesh (2003) Prasad *et al.* (2005) Eswararao (2008) Vijayalaxmi (2008)
5.	Number of bolls per plant	Laxman and Ganesh (2003) Gururajan and Sundar (2004) Narisireddy and Ratnakumari (2004) Sivaprasad *et al.* (2004 b) Kale *et al.* (2006) Leela Pratap (2006) Tuteja *et al.* (2006) Gitte *et al.* (2007) Reddy and Reddy (2007) Padmavathi (2008)	Girase and Mehetre (2002) Vijayalaxmi (2008)
6.	Boll weight (g)	Kaushik *et al.* (2003) Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Sivaprasad *et al.* (2004 b) Kale *et al.* (2006) Tuteja *et al.* (2006) Gitte *et al.* (2007) Reddy and Reddy (2007) Kalpande *et al.* (2008)	Reddy (2001) Altaher and Singh (2003b) Eswararao (2008) Neelima *et al*. (2008) Vijayalaxmi (2008)
7.	Ginning out- turn (%)	Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Tuteja *et al.* (2003) Patnaik *et al.* (2004) Tuteja *et al.* (2006)	Rao and Reddy (2001) Reddy (2001) Muraleedhar (2005) Prasad *et al.,* (2005) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
8.	Seed index (g)	Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Patnaik *et al.* (2004)	Rao and Reddy (2001) Reddy (2001)

Cont……..

		Ravikumar (2004) Sivaprasad *et al.* (2004 b)	Neelam and Potdukhe (2002) Altaher and Singh (2003b) Laxman and Ganesh (2003) Neelima *et al.* (2008) Vijayalaxmi (2008)
9.	Lint index (g)	Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Patnaik *et al.* (2004) Gururajan and Sundar (2004) Sivaprasad *et al.* (2004 b)	Rao and Reddy (2001) Altaher and Singh (2003b) Vijayalaxmi (2008)
10.	2.5% span length (mm)	Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Naphade *et al.* (2004) Patnaik *et al.* (2004)	Reddy (2001) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Prasad *et al.* (2005) Leela Pratap (2006) Tuteja *et al.* (2006) Verma *et al.* (2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
11.	Micronaire value (10^{-6} g/in)	Rao and Reddy (2001) Neelam and Potdukhe (2002) Muthuswamy *et al.* (2003) Naphade *et al.* (2004) Patnaik *et al.* (2004)	Reddy (2001) Altaher and Singh (2003b) Prasad *et al.* (2005) Eswararao (2008) Vijayalaxmi(2008)
12.	Bundle strength (g/tex)	Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Naphade *et al.* (2004) Patnaik *et al.* (2004) Neelima *et al.* (2005)	Reddy (2001) Rao and Reddy (2001) Neelam and Potdukhe (2002) Girase and Mehetre (2002) Altaher and Singh (2003b) Karunakar Raju (2005) Prasad *et al.* (2005) Leela Pratap (2006) Eswararao (2008)

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			Neelima *et al.* (2008) Padmavathi (2008) Vijayalaxmi (2008)
13.	Uniformity ratio	Patnaik *et al.* (2004)	Altaher and Singh (2003b) Karunakar Raju (2005) Muraleedhar (2005) Prasad *et al*. (2005) Leela Pratap (2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
14.	Oil content (%)	Nagaraj *et al.* (1987) Patel *et al.* (2005)	Agarwal *et al.* (2003) Nagarajan (1997)
15.	Lint yield per plant (g)	Dedaniya and Pethani (1994) Deshpande and Baig (2003) Patnaik *et al.* (2004) Leela Pratap (2006) Padmavathi (2008) Vijayalaxmi (2008)	
16.	Seed cotton yield per plant (g)	Rao and Reddy (2001) Reddy (2001) Neelam and Potdukhe (2002) Kaushik *et al.* (2003) Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Tuteja *et al.* (2003) Sivaprasad *et al.* (2004 b) Gururajan and Sundar (2004) Narisireddy and Ratnakumari (2004) Karunakar Raju (2005) Kumari and Chamundeswari (2005) Leela Pratap (2006) Verma *et al.* (2006) Gitte *et al.* (2007) Reddy and Reddy (2007) Padmavathi (2008) Vijayalaxmi (2008)	

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Table- 2: Heritability ($h^2_{(b)}$) and genetic advance (GA) in cotton (*Gossypium hirsutum* L.)

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
1.	Plant height (cm)	Sangeetha (1998) Neelam and Potdukhe (2002) Roy (2006) Preetha and Raveendran (2007) Sakthi *etal.(*2007) Padmavathi (2008)	Verma *et al. (*2006) Vijayalaxmi (2008)	-	Eswararao (2008) Kumari and Chamundeswari (2005)
2.	Days to 50% flowering	Neelam and Potdukhe (2002)	Sangeetha (1998) Reddy (2001) Muraleedhar (2005) Roy (2006) Padmavathi (2008)	Vijayalaxmi (2008)	Neelima (2002) Sivaprasad *et al* (2004a) Karunakar Raju (2005)
3.	Number of monopodia Per plant	Girase and Mehetre (2002) Kaushik *et al.* (2003) Karunakar Raju (2005) Leela Pratap (2006) Verma *et al.* (2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)	Reddy (2001) Kumari and Chamundeswari (2005)	Neelima (2002) Sivaprasad *et al* (2004a)	Rao and Reddy (2001)

Cont……..

4.	Number of sympodia per plant	Neelam and Potdukhe (2002) Girase and Mehetre (2002) Kaushik *et al.* (2003) Ravikumar (2004) Verma *et al.* (2006) Preetha and Raveendran (2007) Padmavathi (2008)	Gururajan (2000) Reddy (2001) Kiran (2003) Vijayalaxmi (2008)	-	Rao and Reddy (2001) Sivaprasad *et al* (2004a) Kumari and Chamundeswari (2005)
5.	Number of bolls per plant	Rao and Reddy (2001) Reddy (2001) Girase and Mehetre (2002) Neelam and Potdukhe (2002) Kaushik *et al.* (2003) Ravikumar (2004) Sivaprasad *et al.* (2004a) Leela Pratap (2006) Roy (2006) Padmavathi (2008) Vijayalaxmi (2008)	Murthy *et al.* (1994) Gururajan and Sundar (2004)	-	-
6.	Boll weight (g)	Neelam and Potdukhe (2002) Neelima (2002) Kaushik *et al.* (2003)	Gururajan (2000) Gururajan and Sundar (2004)	Sivaprasad *et al. (*2004a)	Kiran (2003) Kumari and Chamundeswari (2005)
7.	Ginning out-turn(%)	Gururajan and Sundar (2004)	Gururajan (2000) Rao and Reddy (2001) Neelam and Potdukhe (2002)	-	Sivaprasad *et al.* (2004a)

Cont……..

			Karunakar Raju (2005) Leela Pratap (2006) Verma *et al.* (2006) Vijayalaxmi (2008) Do Thi Ha An *et al.* (2008)		
8.	Seed index (g)	Rao and Reddy (2001) Ravikumar (2004) Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008)	Gururajan (2000) Neelam and Potdukhe (2002) Sivaprasad *et al.* (2004a)	-	Reddy (2001) Gururajan and Sundar (2004)
9	Lint index (g)	Reddy (2001) Neelima (2002) KarunakarRaju (2005) Murthy *et al.* (2006) Padmavathi (2008) Vijayalaxmi (2008)	Rao and Reddy(2001) Neelam and Potdukhe (2002) Sivaprasad *et al.*(2004a)	-	Prasad (2003)
10.	2.5% span length (mm)	Rao and Reddy (2001) Reddy (2001) Gururajan and Sundar (2004) Vijayalaxmi (2008)	Kiran (2003) Tuteja *et al.* (2005a) Verma *et al.* (2006)	-	-
11.	Micronaire value (10^{-6}g/in)	Rao and Reddy (2001)	Reddy (2001) Vijayalaxmi (2008)	-	Prasad (2003) Sivaprasad *et al.* (2004a)

Cont……..

12.	Bundle strength (g/tex)	Reddy (2001) Murthy *et al.* (2006)	Rao and Reddy (2001) Kiran (2003)	-	Gururajan and Sundar (2004) Sivaprasad *et al.*(2004a) Muraleedhar (2005) Eswararao (2008) Vijayalaxmi (2008)
13.	Uniformity ratio	-	Sangeetha (1998) Neelima (2002) Kiran (2003) Karunakar Raju (2005)	-	Sivaprasad *et al.* (2004a) Muraleedhar (2005) Vijayalaxmi (2008)
14.	Oil content (%)	Nagaraj *et al* . (1987)	Nagarajan (1997)	-	Reddy and Satyanarayana *et al.* (2005)
15.	Lint yield/plant (g)	Leela Pratap (2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)	-	-	-
16.	Seed cotton yield/plant (g)	Ahuja and Tuteja (2000) Rao and Reddy (2001) Neelam and Potdukhe (2002) Girase and Mehetre (2002) Pandey *et al.*(2002) Kaushik *et al.* (2003) Sivaprasad *et al.* (2004a) Karunakar Raju (2005)	Gururajan and Sundar (2004)	-	Jain *et al.* (1984) Jain (1986)

Cont……..

		Kumari and Chamundeswari(2005) Kale *et al*.(2006) Leela Pratap (2006) Tuteja *et al*. (2006) Verma *et al*. (2006) Preetha and Raveendran (2007) Reddy and Reddy (2007) Murthy *et al*. (2006) Roy (2006) Padmavathi (2008) Vijayalaxmi (2008)			

Cont……..

Table -3: Association of component characters with seed cotton yield in cotton (*Gossypium hirsutum* L.).

S. No.	Character	Association	S/NS	Reference
1.	Plant height(cm)	Positive	S	Muraleedhar (2005) Tuteja *et al.* (2006) Padmavathi (2008)
			NS	Sumathi and Nadarajan (1995) Murthy (1997)
		Negative	S	Neelima *et al.* (2005) Leela pratap *et al.* (2007)
			NS	Pradeep and Sumalini (2005) Vijayalaxmi (2008)
2.	Days to 50% flowering	Positive	S	Ganapathy (2001) Sivaprasad (2003) Muraleedhar (2005)
			NS	Murthy (1997) Ravikumar (2004)
		Negative	S	Reddy (2001) Leela Pratap *et al.* (2007)
			NS	Kaushik *et al.* (2003) Karunakar Raju (2005) Vijayalaxmi (2008)
3.	Number of monopodia per plant	Positive	S	Ladole and Meshram (2000)
				Altaher and Singh (2003b) Kaushik *et al.* (2003) Padmavathi (2008)
			NS	Neelam and Potdukhe (2002) Altaher and Singh (2003b) Pradeep and

Cont……..

				Sumalini (2005) Vijayalaxmi (2008)
		Negative	S	Kiran (2003)
			NS	Reddy (2001) Ravikumar (2004) Karunakar Raju (2005)
4.	Number of sympodia per plant	Positive	S	Altaher and Singh (2003b) Muthu *et al.* (2004) Ravikumar (2004) Neelima *et al.* (2005) Tuteja *et al.* (2006) Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Neelam and Potdukhe (2002)
				Karunakar Raju (2005) Pradeep and Sumalini (2005)
5.	Number of bolls/plant	Positive	S	Kaushik *et al.* (2003) Sivaprasad (2003) Muthu *et al.* (2004) Gururajan and Sundar (2004) Neelima *et al.* (2005) Karunakar Raju (2005) Tuteja *et al.* (2006) Verma *et al.* (2006) Leela Pratap *et al.* (2007) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Pradeep and Sumalini (2005)

Cont……..

		Negative	S	Patil *et al.* (1991)
6.	Boll weight (g)	Positive	S	Altaher and Singh (2003b) Sivaprasad (2003) Gururajan and Sundar (2004) Muthu *et al.* (2004) Neelima *et al.* (2005) Karunakar Raju (2005) Murthy *et al.* (2006) Eswararao (2008) Padmavathi (2008)
			NS	Ladole and Meshram (2000) Reddy (2001) Kaushik *et al.* (2003) Vijayalaxmi (2008)
		Negative	S	Gururajan (2000) Rao *et al.* (2001)
			NS	Pradeep and Sumalini (2005) Ravikumar (2004)
7.	Ginning out - turn (%)	Positive	S	Gururajan (2000) Ganapathy (2001) Reddy (2001) Sivaprasad (2003) Tuteja *et al.* (2005a)
			NS	Rao *et al.* (2001) Neelam and Potdukhe (2002)
		Negative	S	Mandloi *et al.* (2003) Muthuswamy and Vivekanandan (2004)
			NS	Karunakar Raju (2005) Vijayalaxmi (2008)
8.	Seed index (g)	Positive	S	Sivaprasad (2003) Gururajan and Sundar (2004) Muthu *et al.* (2004)

Cont……..

				Neelima *et al.* (2005) Murthy *et al.* (2006) Padmavathi (2008)
			NS	Reddy (2001) Ravikumar (2004) Karunakar Raju (2005) Vijayalaxmi (2008)
		Negative	S	Rao *et al.* (2001)
			NS	Ladole and Meshram (2000) Rao *et al.* (2001) Mandloi *et al.* (2003)
9.	Lint index (g)	Positive	S	Reddy (2001) Neelam and Potdukhe (2002) Sivaprasad (2003) Muthu *et al.* (2004) Karunakar Raju (2005) Neelima *et al.* (2005) Murthy *et al.* (2006) Padmavathi (2008)
			NS	Rao *et al.* (2001) Vijayalaxmi (2008)
		Negative	NS	Ladole and Meshram (2000) Mandloi *et al.* (2003)
10.	2.5% span length (mm)	Positive	S	Rajarathinam *et al.* (1993) Kiran (2003)
			NS	Rao *et al.* (2001) Reddy (2001) Mandloi *et al.* (2003)
		Negative	S	Tyagi (1994b) Gururajan and Sundar (2004)

Cont……..

			NS	Neelam and Potdukhe (2002) Pankaj Rathore *et al.* (2004) Ravikumar (2004) Karunakar Raju (2005) Tuteja *et al.* (2005a) Vijayalaxmi (2008)
11.	Micronaire value (10^{-6} g/in)	Positive	S	Reddy (2001) Altaher and Singh (2003b) Karunakar Raju (2005) Neelima *et al.* (2005) Murthy *et al.* (2006)
			NS	Rao *et al.* (2001) Neelam and Potdukhe (2002) Mandloi *et al.* (2003) Pankaj Rathore *et al.* (2004) Ravikumar (2004) Tuteja *et al.* (2005a) Vijayalaxmi (2008)
12.	Bundle strength (g/tex)	Positive	S	Rao *et al.* (2001)
				Altaher and Singh (2003b) Sivaprasad (2003) Muthu *et al.* (2004)
			NS	Neelima (2002) Neelam and Potdukhe (2002) Mandloi *et al.* (2003)
		Negative	S	Sangeetha (1998) Rao *et al.* (2001) Sivaprasad (2003)
			NS	Pankaj Rathore *et al.* (2004) Ravikumar (2004)

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				Karunakar Raju (2005) Vijayalaxmi (2008)
13.	Uniformity ratio	Positive	S	Sivaprasad (2003) Neelima *et al.* (2005)
			NS	Karunakar Raju (2005)
		Negative	S	Rajarathinam *et al.* (1993) Vijayalaxmi (2008)
			NS	Dedaniya and Pethani (1994) Ravikumar (2004) Tuteja *et al.* (2005 a,b)
14	Oil content (%)	Positive	S	Patel *et al.* (2003) Hassan *et al.* (2005)
			NS	Meena and Deshmukh (1990)
		Negative	NS	Ramalingam *et al.* (1994)
15.	Lint yield per plant (g)	Positive	S	Mandloi *et al.* (2003) Leela Pratap *et al.* (2007) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)

S: Significant **NS: Non-significant**

Cont……..

Table- 4: Association among the yield component characters in cotton (Gossypium *hirsutum* L.).

S. No.	Character	Association	S/NS	Reference
I. Days to 50% flowering with				
1.	Plant height(cm)	Positive	S	Murthy (1999) Padmavathi(2008)
			NS	Sangeetha (1998)
		Negative	S	Dedaniya and Pethani (1994)
			NS	Vijayalaxmi (2008)
2.	Number of monopodia per plant	Positive	S	Altaher and Singh (2003b) Karunakar Raju (2005) Muraleedhar (2005) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Reddy (2001)
		Negative	NS	Neelam and Potdukhe (2002)
3.	Number of sympodia per plant	Positive	S	Ladole and Meshram (2000) Muraleedhar (2005) Padmavathi (2008)
			NS	Basha (1997)
		Negative	S	Altaher and Singh (2003b) Karunakar Raju (2005) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Neelima (2002)
4.	Number of bolls/ plant	Positive	S	Muraleedhar (2005) Vijayalaxmi (2008)
			NS	Sangeetha (1998)
		Negative	S	Reddy (2001)
			NS	Ladole and Meshram (2000) Neelam and Potdukhe (2002)
				Neelima (2002) Karunakar Raju (2005)
5.	Boll weight (g)	Positive	S	Altaher and

Cont……..

				Singh (2003b) Sivaprasad (2003)
		Negative	S	Karunakar Raju (2005) Muraleedhar (2005) Leela Pratap *et al.* (2007) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Neelima (2002)
6.	Ginning out – turn (%)	Positive	S	Neelam and Potdukhe (2002) Karunakar Raju (2005)
			NS	Murthy (1997) Vijayalaxmi (2008)
		Negative	S	Leela Pratap *et al.*(2007)
			NS	Ladole and Meshram (2000) Reddy (2001) Neelima (2002)
7.	Seed index (g)	Positive	S	Basha (1997) Karunakar Raju (2005) Leela Pratap *et al.* (2007)
		Negative	S	Ladole and Meshram (2000) Neelima (2002) Muraleedhar (2005) Vijayalaxmi (2008)
			NS	Reddy (2001) Neelam and Potdukhe (2002)
8.	Lint index (g)	Positive	S	Karunakar Raju (2005)
			NS	Basha (1997) Neelam and Potdukhe (2002)
		Negative	S	Ladole and Meshram (2000) Reddy (2001) Neelima (2002) Leela Pratap *et al.* (2007)

Cont……..

			NS	Vijayalaxmi (2008)
9.	2.5% span length (mm)	Positive	S	Muraleedhar (2005)
			NS	Ladole and Meshram (2000) Neelima (2002) Karunakar Raju (2005) Vijayalaxmi (2008)
		Negative	NS	Reddy (2001) Neelam and Potdukhe (2002)
10.	Micronaire value (10^{-6} g/in)	Positive	S	Leela Pratap *et al.* (2007)
			NS	Sangeetha (1998)
		Negative	S	Altaher and Singh (2003b) Muraleedhar (2005) Vijayalaxmi (2008)
			NS	Reddy (2001) Neelima (2002) Neelam and Potdukhe (2002)
11.	Bundle strength (g/tex)	Positive	S	Sivaprasad (2003) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002)
		Negative	S	Altaher and Singh (2003b) Karunakar Raju (2005)
			NS	Reddy (2001) Neelima (2002)
12.	Uniformity ratio	Positive	S	Neelima (2002) Neelima *et al.* (2005)
			NS	Sangeetha (1998)
		Negative	NS	Karunakar Raju (2005) Vijayalaxmi (2008)
13.	Lint yield per plant (g)	Negative	S	Leela Pratap *et al.* (2007)
			NS	Vijayalaxmi (2008)
II. Plant height with				
1.	Number of	Positive	S	Neelam and

Cont……..

	monopodia per plant			Potdukhe (2002) Padmavathi (2008)
		Negative	NS	Sangeetha (1998) Pradeep and Sumalini (2005) Vijayalaxmi (2008)
2.	Number of sympodia per plant	Positive	S	Samanc and Ozkaynak (2000) Muthu *et al.* (2004) Tuteja *et al.* (2006) Verma *et al.*(2006) Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Pradeep and Sumalini (2005)
3.	Number of bolls/plant	Positive	S	Samanc and Ozkaynak (2000) Muthu *et al.* (2004) Tuteja *et al.* (2006) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Sangeetha (1998)
		Negative	NS	Pradeep and Sumalini (2005)
4.	Boll weight (g)	Positive	NS	Pradeep and Sumalini (2005) Vijayalaxmi (2008)
			S	Gnana Arul Samuel Rajan (1997)
		Negative	NS	Tyagi (1994a) Sangeetha (1998)
5.	Ginning out-turn (%)	Positive	NS	Vijayalaxmi (2008)
		Negative	S	Tyagi (1994a)
			NS	Kowsalya and Raveendran (1996) Sangeetha (1998)
6.	Seed index (g)	Positive	S	Muthu *et al.* (2004) Padmavathi (2008)
			NS	Sumathi and Nadarajan (1995)

Cont……..

				Sangeetha (1998) Padmavathi (2008) Vijayalaxmi (2008)
		Negative	NS	Tyagi (1994a)
			S	Leela Pratap *et al.* (2007)
7.	Lint index (g)	Positive	NS	Sumathi and Nadarajan (1995) Padmavathi (2008) Vijayalaxmi (2008)
		Negative	NS	Sangeetha (1998)
8.	2.5% span length (mm)	Positive	S	Muthu *et al.* (2004) Verma *et al.* (2006)
			NS	Sumathi and Nadarajan (1995) Vijayalaxmi (2008)
		Negative	NS	Sangeetha (1998)
9.	Micronaire value (10^{-6} g/in)	Positive	NS	Sangeetha (1998) Vijayalaxmi (2008)
		Negative	NS	Dedaniya and Pethani (1994)
			S	Tyagi (1994a)
10.	Bundle strength (g/tex)	Positive	S	Vijayalaxmi (2008)
			NS	Kowsalya and Raveendran (1996)
		Negative	NS	Sangeetha (1998)
11.	Uniformity ratio	Positive	NS	Dedaniya and Pethani (1994) Sangeetha (1998)
		Negative	S	Padmavathi (2008) Vijayalaxmi (2008)
12.	Lint yield/plant (g)	Positive	S	Dedaniya and Pethani (1994) Padmavathi (2008)
		Negative	NS	Samanc and Ozkaynak (2000) Vijayalaxmi (2008)
III. Number of monopodia per plant with				

Cont……..

1.	Number of sympodia per plant	Positive	S	Leela Pratap *et al.* (2007) Padmavathi (2008)
			NS	Ladole and Meshram (2000) Reddy (2001) Neelima (2002) Kaushik *et al.* (2003)
		Negative	S	Verma *et al.* (2006) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Pradeep and Sumalini (2005)
2.	Number of bolls/plant	Positive	S	Ladole and Meshram (2000) Kaushik *et al.* (2003) Verma *et al.* (2006) Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelima (2002) Neelam and Potdukhe (2002)
		Negative	NS	Reddy (2001)
3.	Boll weight (g)	Positive	S	Basha (1997)
			NS	Ladole and Meshram (2000) Reddy (2001) Neelima (2002)
		Negative	NS	Murthy (1997) Sangeetha (1998) Kaushik *et al.* (2003) Pradeep and Sumalini (2005) Vijayalaxmi (2008)
			S	Leela Pratap *et al.* (2007)
4.	Ginning out-turn (%)	Positive	S	Gururajan (2000) Muthu *et al.* (2004) Leela Pratap *et al.* (2007) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000)

Cont……..

				Reddy (2001) Neelima (2002)
		Negative	NS	Neelam and Potdukhe (2002)
5.	Seed index (g)	Positive	NS	Ladole and Meshram (2000) Reddy (2001) Neelima (2002)
		Negative	S	Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Karunakar Raju (2005)
6.	Lint index (g)	Positive	NS	Ladole and Meshram (2000) Reddy (2001) Neelima (2002)
		Negative	NS	Neelam and Potdukhe (2002) Karunakar Raju (2005) Vijayalaxmi (2008)
7.	2.5% span length (mm)	Positive	S	Reddy (2001) Sivaprasad (2003)
			NS	Ladole and Meshram (2000) Neelam and Potdukhe (2002)
		Negative	NS	Neelima (2002) Vijayalaxmi (2008)
			S	Verma *et al.* (2006)
8.	Micronaire value (10^{-6} g/in)	Positive	NS	Neelima (2002)
		Negative	NS	Reddy (2001) Neelam and Potdukhe (2002)
			S	Muraleedhar (2005) Vijayalaxmi (2008)
9.	Bundle strength (g/tex)	Positive	NS	Neelam and Potdukhe (2002) Neelima (2002) Vijayalaxmi (2008)
			S	Muraleedhar (2005)
		Negative	NS	Sangeetha (1998)

Cont……..

				Reddy (2001)
10.	Uniformity ratio	Negative	NS	Sangeetha (1998) Neelima (2002)
			S	Vijayalaxmi (2008)
		Positive	S	Altaher and Singh (2003b)
			NS	Karunakar Raju (2005)
11.	Lint yield /plant (g)	Positive	S	Padmavathi (2008) Vijayalaxmi (2008)
IV. Number of sympodia per plant with				
1.	Number of bolls/plant	Positive	S	Altaher and Singh (2003b) Sivaprasad (2003) Muthu *et al.* (2004) Muthuswamy and Vivekanandan(2004) Neelima *et al.* (2005) Tuteja *et al.* (2006) Eswararao (2008) Padmavathi (2008)
		Positive	NS	Ladole and Meshram (2000) Ganapathy (2001) Kaushik *et al.* (2003) Pradeep and Sumalini (2005)
		Negative	NS	Karunakar Raju (2005) Vijayalaxmi (2008)
2.	Boll weight (g)	Positive	S	Neelima (2002) Altaher and Singh (2003b)
			NS	Neelima *et al.* (2005) Vijayalaxmi (2008)
		Negative	S	Rao *et al.* (2001) Leela Pratap *et al.* (2007)
			NS	Pradeep and Sumalini (2005)

Cont……..

3.	Ginning out-turn (%)	Positive	S	Muthu *et al.* (2004) Muthuswamy and Vivekanandan (2004) Neelima *et al.* (2005) Padmavathi (2008)
			NS	Ladole and Meshram (2000) Rao *et al.* (2001) Reddy (2001) Neelima (2002)
		Negative	S	Altaher and Singh (2003b)
			NS	Basha (1997) Murthy (1997) Vijayalaxmi (2008)
4.	Seed index (g)	Positive	S	Ladole and Meshram (2000) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Muthu *et al.* (2004) Neelima *et al.* (2005)
			NS	Reddy (2001) Neelima (2002) Vijayalaxmi (2008)
		Negative	S	Rao *et al.* (2001)
				Muthuswamy and Vivekanandan (2004) Muraleedhar (2005)
5.	Lint index (g)	Positive	S	Ladole and Meshram (2000) Neelam and Potdukhe (2002) Neelima (2002) Muthu *et al.* (2004) Neelima *et al.* (2005) Karunakar Raju (2005) Padmavathi (2008)
			NS	Reddy (2001) Vijayalaxmi (2008)

Cont……..

		Negative	NS	Rao *et al.* (2001)
			S	Muraleedhar (2005)
6.	2.5% span length (mm)	Positive	NS	Reddy (2001) Neelam and Potdukhe (2002)
			S	Verma *et al.* (2006)
		Negative	NS	Ladole and Meshram (2000) Rao *et al.* (2001) Neelima (2002) Karunakar Raju (2005) Vijayalaxmi (2008)
			S	Muraleedhar (2005)
7.	Micronaire value (10^{-6} g/in)	Positive	S	Altaher and Singh (2003b) Karunakar Raju (2005) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Sangeetha (1998) Rao *et al.* (2001)
				Reddy (2001) Neelima (2002) Neelam and Potdukhe (2002)
8.	Bundle strength (g/tex)	Positive	S	Rao *et al.* (2001) Altaher and Singh (2003b) Muthu *et al.* (2004)
			NS	Neelam and Potdukhe (2002) Neelima (2002)
		Negative	NS	Reddy (2001) Karunakar Raju (2005) Vijayalaxmi (2008)
9.	Uniformity ratio	Negative	NS	Neelima (2002)
		Positive	S	Karunakar Raju (2005) Eswararao (2008) Padmavathi (2008)

Cont……..

				Vijayalaxmi (2008)
10.	Lint yield per plant (g)	Positive	S	Leela Pratap *et al.* (2007) Eswararao (2008) Padmavathi (2008)
			NS	Vijayalaxmi (2008)
V. Number of bolls per plant with				
1.	Boll weight (g)	Positive	S	Neelima (2002) Altaher and Singh (2003b) Neelima *et al.* (2005)
		Negative	S	Rao *etal.* (2001) Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Reddy (2001) Kaushik *et al.* (2003) Pradeep and Sumalini (2005)
2.	Ginning out-turn (%)	Positive	S	Ganapathy (2001) Muthu *et al.* (2004) Leela Pratap *et al.* (2007)
			NS	Vijayalaxmi (2008)
		Negative	S	Karunakar Raju (2005)
			NS	Sangeetha (1998)
3.	Seed index (g)	Positive	S	Neelam and Potdukhe (2002) Neelima (2002) Muthu *et al.* (2004) Neelima *et al.* (2005)
			NS	Reddy (2001)
		Negative	S	Rao *et al.* (2001) Muraleedhar (2005) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000)

Cont……..

4.	Lint index (g)	Positive	S	Neelima (2002) Neelam and Potdukhe (2002) Muthu *et al.* (2004) Neelima *et al.* (2005)
			NS	Reddy (2001)
		Negative	S	Murthy (1997) KarunakarRaju *et al.* (2005) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Rao *et al.* (2001) Neelam and Potdukhe (2002) Neelima (2002)
5.	2.5% span length (mm)	Positive	NS	Ladole and Meshram(2000) Rao *et al.* (2001) Reddy (2001) Neelam and Potdukhe (2002) Sakthi *et al.* (2007)
		Negative	NS	Neelima (2002) Vijayalaxmi (2008)
			S	Tyagi (1994a) Muraleedhar (2005)
6.	Micronaire value (10^{-6} g/in)	Positive	S	Reddy (2001) Neelima (2002) Altaher and Singh (2003b) Muthu *et al.* (2004) Karunakar Raju (2005) Sakthi *et al.* (2007) Eswararao (2008)
			NS	Rao *et al.* (2001) Neelam and Potdukhe (2002)
		Negative	S	Leela Pratap *et al.* (2007) Vijayalaxmi (2008)
7.	Bundle strength	Positive	S	Rao *et al.* (2001)

Cont……..

	(g/tex)			Altaher and Singh (2003b) Muthu *et al.* (2004)
			NS	Reddy (2001) Neelam and Potdukhe (2002) Neelima (2002) Vijayalaxmi (2008)
		Negative	S	Sangeetha (1998)
			NS	Karunakar Raju (2005)
8.	Uniformity ratio	Positive	S	Muthu *et al.* (2004)
		Negative	S	Vijayalaxmi (2008)
			NS	Sangeetha (1998) Neelima (2002)
9	Lint yield/plant (g)	Positive	S	Dedaniya and Pethani (1994) Leela Pratap *et al.* (2007) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
VI. Boll weight (g) with				
1.	Ginning out-turn (%)	Positive	S	Reddy (2001) Muthuswamy and Vivekanandan (2004) Karunakar Raju (2005)
			NS	Neelima (2002)
		Negative	NS	Murthy (1997) Ladole and Meshram (2000) Vijayalaxmi (2008)
2.	Seed index (g)	Positive	S	Ladole and Meshram (2000) Altaher and Singh (2003b) Sivaprasad (2003) Muthu *et al.* (2004) Karunakar Raju (2005) Neelima *et al.* (2005)

Cont……..

				Padmavathi (2008) Vijayalaxmi (2008)
3.	Lint index (g)	Positive	S	Neelima (2002) Altaher and Singh (2003b) Sivaprasad (2003) Muthuswamy and Vivekanandan(2004) Neelima *et al.* (2005) Karunakar Raju (2005) Padmavathi(2008) Vijayalaxmi (2008)
4.	2.5% span length (mm)	Positive	NS	Rao *et al.* (2001) Reddy (2001)
			S	Sivaprasad (2003) Verma *et al.* (2006) Vijayalaxmi (2008)
		Negative	NS	Neelima (2002)
5.	Micronaire value (10^{-6} g/in)	Positive	S	Tyagi (1994a)
			NS	Sangeetha (1998) Reddy (2001)
		Negative	S	Rao *et al.* (2001) Neelima (2002)
			NS	Sangeetha (1998) Vijayalaxmi (2008)
6.	Bundle strength (g/tex)	Positive	NS	Neelima (2002) Muthuswamy and Vivekanandan (2004) Vijayalaxmi (2008)
			S	Muraleedhar (2005)
		Negative	S	Rao *et al.* (2001)
			NS	Sangeetha (1998) Reddy (2001)
7.	Uniformity ratio	Negative	S	Neelima (2002) Muraleedhar (2005) Eswararao (2008)

Cont……..

			NS	Vijayalaxmi (2008)
8	Oil content %	Positive	NS	Ramalingam *et al.* (1994)
9.	Lint yield/plant (g)	Positive	S	Dedaniya and Pethani (1994) Eswararao (2008) Padmavathi (2008)
VII. Ginning out turn (%) with				
1	Seed index (g)	Positive	NS	Reddy (2001) Neelima (2002) Mandloi *et al.* (2003) Altaher and Singh (2003b) Leela Pratap *et al.* (2007) Padmavathi (2008)
		Negative	S	Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Rao *et al.* (2001) Neelam and Potdukhe (2002)
2.	Lint index (g)	Positive	S	Reddy (2001) Neelima (2002) Altaher and Singh (2003b) Mandloi *et al.* (2003) Muthu *et al.* (2004)
				Karunakar Raju (2005) Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Rao *et al.* (2001) Neelam and Potdukhe (2002)
3.	2.5% span length (mm)	Positive	S	Sivaprasad (2003)
			NS	Ladole and

Cont……..

				Meshram (2000) Rao *et al.* (2001) Reddy (2001) Neelima (2002)
		Negative	S	Muthu *et al.* (2004) Padmavathi (2008)
			NS	Mandloi *et al.* (2003) Neelam and Potdukhe (2002) Vijayalaxmi (2008)
4.	Micronaire value (10^{-6} g/in)	Positive	S	Rao *et al.* (2001) Muthu *et al.* (2004) Padmavathi (2008)
			NS	Reddy (2001) Neelam and Potdukhe (2002) Neelima (2002)
		Negative	S	Vijayalaxmi (2008)
			NS	Mandloi *et al.* (2003) Karunakar Raju (2005)
5.	Bundle strength (g/tex)	Positive	S	Mandloi *et al.* (2003) Murthy *et al.(*2006)
			NS	Rao *et al.* (2001) Reddy (2001) Neelima (2002) Vijayalaxmi (2008)
		Negative	S	Neelam and Potdukhe (2002) Padmavathi (2008)
			NS	Neelam and Potdukhe (2002)
6.	Uniformity ratio	Positive	S	Muthu *et al.* (2004) Karunakar Raju (2005) Padmavathi (2008)
			NS	Sangeetha (1998)
		Negative	S	Altaher and Singh (2003b)
			NS	Neelima (2002) Vijayalaxmi (2008)

Cont……..

7.	Oil content (%)	Nnegative	NS	Ramalaingam *et al.* (1994)
8.	Lint yield / plant (g)	Positive	S	Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Dedaniya and Pethani (1994) Mandloi *et al.* (2003)
VIII. Seed index (g) with				
1.	Lint index (g)	Positive	S	Mandloi *et al.* (2003) Altaher and Singh (2003b) Muthu *et al.* (2004) Karunakar Raju (2005) Neelima *et al.* (2005) Leela Pratap *et al.* (2007) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002)
2.	2.5% span length (mm)	Positive	S	Rao *et al.* (2001) Karunakar Raju (2005) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002)
		Negative	NS	Ladole and Meshram (2000) Neelima (2002) Mandloi *et al.* (2003)
3.	Micronaire value (10^{-6} g/in)	Positive	S	Sivaprasad (2003) Eswararao (2008) Vijayalaxmi (2008)
			NS	Reddy (2001) Neelam and Potdukhe (2002) Neelima (2002)
		Negative	NS	Rao *et al.* (2001) Mandloi *et al.* (2003)
4.	Bundle strength (g/tex)	Positive	S	Muthu *et al.* (2004) Padmavathi (2008)

Cont……..

			NS	Sangeetha (1998) Neelima (2002) Neelam and Potdukhe (2002) Altaher and Singh (2003b)
		Negative	S	Rao *et al.* (2001)
			NS	Reddy (2001) Vijayalaxmi (2008)
5.	Uniformity ratio	Positive	NS	Sangeetha (1998) Vijayalaxmi (2008)
		Negative	S	Neelima (2002) Muraleedhar (2005)
6.	Oil content (%)	Positive	S	Hassan *et al.* (2005)
			NS	Ramalingam *et al.* (1994)
7.	Lint yield/plant (g)	Negative	NS	Mandloi *et al.* (2003) Vijayalaxmi (2008)
IX. Lint index (g) with				
1.	2.5% span length (mm)	Positive	S	Muthu *et al.* (2004) Murthy *et al.* (2006) Vijayalaxmi (2008)
			NS	Reddy (2001)
		Negative	NS	Ladole and Meshram (2000) Neelam and Potdukhe (2002) Neelima (2002) Mandloi *et al.* (2003)
2.	Micronaire value (10^{-6} g/in)	Positive	S	Reddy (2001) Neelima (2002) Neelam and Potdukhe (2002) Eswararao(2008)
			NS	Karunakar Raju (2005) Vijayalaxmi (2008)
		Negative	NS	Rao *et al.* (2001)
			S	Mandloi *et al.* (2003)
3.	Bundle strength (g/tex)	Positive	S	Muthu *et al.* (2004) Murthy *et al.* (2006)

Cont……..

			NS	Neelima (2002) Vijayalaxmi (2008)
		Negative	NS	Reddy (2001) Neelam and Potdukhe (2002) Mandloi *et al.* (2003) Karunakar Raju (2005)
.	Uniformity ratio	Positive	NS	Karunakar Raju (2005) Vijayalaxmi (2008)
		Negative	S	Muthu *et al.* (2004)
			NS	Sangeetha (1998) Neelima (2002)
5.	Oil content (%)	Negative	NS	Ramalingam *et al.* (1994)
6.	Lint yield/plant (g)	Positive	S	Leela Pratap *et al.* (2007) Padmavathi (2008)
			NS	Vijayalaxmi (2008)
X. 2.5% Span length with				
1.	Micronaire value (10^{-6} g/in)	Positive	S	Mandloi *et al.* (2003) Muthuswamy and Vivekanandan (2004)
			NS	Reddy (2001) Tuteja (2005b)
		Negative	S	Neelam and Potdukhe (2002) Karunakar Raju (2005) Altaher and Singh(2003b) Leela Pratap *et al.* (2007) Padmavathi(2008) Vijayalaxmi (2008)
			NS	Neelima (2002)
2.	Bundle strength (g/tex)	Positive	S	Neelam and Potdukhe (2002)
			S	Mandloi *et al.* (2003) Muthuswamy and Vivekanandan(2004)

Cont……..

				Muthu *et al.* (2004) Pankaj Rathore *et al.* (2004) Karunakar Raju (2005) Tuteja *et al.* (2005 b) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Rao *et al.* (2001) Reddy (2001) Neelima (2002)
		Negative	S	Rao *et al.* (2001)
3.	Uniformity ratio	Positive	S	Sivaprasad (2003)
			NS	Neelima (2002)
		Negative	S	Altaher and Singh (2003b) Karunakar Raju (2005) Leela Pratap *et al.* (2007) Padmavathi(2008) Vijayalaxmi (2008)
			NS	Muthu *et al.* (2004) Tuteja *et al.* (2005b)
4.	Lint yield / plant (g)	Positive	NS	Dedaniya and Pethani (1994) Mandloi *et al.* (2003) Vijayalaxmi (2008)
		Negative	S	Padmavathi (2008)
XI. Micronaire value with				
1.	Bundle strength (g/tex)	Positive	S	Neelima (2002)
			NS	Rao *et al.* (2001) Reddy (2001) Mandloi *et al.* (2003)
		Negative	S	Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Tuteja *et al.* (2005 b)
2.	Uniformity ratio	Positive	S	Altaher and

Cont……..

				Singh (2003b) Pankaj Rathore *et al.* (2004) Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Muthu *et al.* (2004)
		Negative	S	Tuteja *et al.* (2005a)
			NS	Sangeetha (1998) Neelima (2002)
3.	Oil content (%)	positive	NS	Turner *et al.* (1976a &1976$_b$)
4.	Lint yield/plant (g)	Positive	S	Eswararao (2008)
			NS	Mandloi *et al.* (2003)
		Negative	NS	Dedaniya and Pethani (1994) Vijayalaxmi (2008)
XII. Bundle strength (g/tex) with				
1.	Uniformity ratio	Positive	S	Gnana Arul Samuel Rajan (1997)
			NS	Sangeetha (1998)
		Negative	S	Tuteja *et al.* (2005a) Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelima (2002)
2.	Lint yield/ plant (g)	Positive	S	Dedaniya and Pethani (1994)
			NS	Vijayalaxmi (2008)
		Negative	S	Mandloi *et al.* (2003)
XIII. Uniformity ratio (%) with				
1.	Lint yield / plant (g)	Negative	S	Padmavathi (2008) Vijayalaxmi (2008)
			NS	Dedaniya and Pethani (1994)

S: Significant **NS: Non-significant**

Cont……..

Table- 5: Direct effects of component characters on seed cotton yield in cotton (*Gossypium hirsutum* L.).

S. No.	Character	Positive Direct effect	Negative Direct effect
1.	Plant height (cm)	Reddy (2001) Altaher and Singh (2003b) Sivaprasad (2003) Ahuja *et al.*(2004) Muthu *et al.* (2004) Eswararao (2008)	Ladole and Meshram (2000) Karunakar Raju (2005) Verma *etal*. (2006) Padmavathi (2008) Vijayalaxmi (2008)
2.	Days to 50% flowering	Sangeetha (1998) Tuteja *et al.* (2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)	Gururajan (2000) Muthu *etal.* (2004)
3.	Number of monopodia per plant	Gururajan (2000) Reddy (2001) Kaushik *et al* (2003) Altaher and Singh (2003a) Muthu *et al.* (2004) Eswararao (2008)	Ladole and Meshram (2000) Sivaprasad (2003) Karunakar Raju (2005) Tuteja *etal.* (2006) Verma *etal*. (2006) Padmavathi (2008) Vijayalaxmi (2008)
4.	Number of sympodia per plant	Ladole and Meshram (2000) Rao *et al.* (2001) Kaushik *et al.* (2003) Neelima *et al.* (2005) Verma *et al.* (2006) Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008)	Sumathi and Nadarajan (1995) Gururajan (2000) Reddy(2001) Sivaprasad (2003) Muthu *et al.* (2004) Karunakar Raju (2005) Tuteja *et al.* (2006) Eswararao (2008)
5.	Number of bolls/plant	Altaher and Singh (2003b) Sivaprasad (2003) Ahuja *et al.*(2004) Muthu *et al.* (2004) Gururajan and Sundar (2004) Saeed *et al.*(2004) Karunakar Raju (2005)	Kaushik *et al.* (2003) Tuteja *et al.* (2006)

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		Neelima *et al.* (2005) Verma *et al.* (2006) Leela Pratap *et al.* (2007) Sakthi *et al.*(2007) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)	
6.	Boll weight (g)	Neelima (2002) Altaher and Singh (2003b) Kaushik *et al.* (2003) Muthu *et al.* (2004) Gururajan and Sundar (2004) Karunakar Raju (2005) Sakthi *et al.*(2007) Padmavathi (2008)	Ladole and Meshram (2000) Verma *et al.* (2006) Eswararao (2008) Vijayalaxmi (2008)
7.	Ginning out- turn (%)	Gururajan (2000) Reddy (2001) Muthu *et al.* (2004) Tuteja *et al.* (2006) Verma *et al.* (2006) Leela Pratap *et al.* (2007) Vijayalaxmi (2008)	Ladole and Meshram (2000) Altaher and Singh (2003b) Sivaprasad (2003) Gururajan and Sundar (2004) Karunakar Raju (2005) Eswararao (2008) Padmavathi (2008)
8.	Seed index (g)	Gururajan (2000) Rao *et al.* (2001) Reddy (2001) Sivaprasad (2003) Murthy *et al.*(2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)	Ladole and Meshram (2000) Neelima (2002) Altaher and Singh (2003a) Gururajan and Sundar (2004) Karunakar Raju (2005)
9.	Lint index (g)	Reddy (2001) Altaher and Singh(2003b) Gururajan and Sundar (2004) Neelima *et al.*(2005) Karunakar Raju (2005) Sakthi *et al.*(2007) Eswararao (2008)	Sivaprasad (2003) Muthu *et al.* (2004) Leela Pratap *et al.* (2007) Padmavathi (2008)

Cont………

		Vijayalaxmi (2008)	
10.	2.5% span length (mm)	Ladole and Meshram (2000) Muthu *et al.* (2004) Karunakar Raju (2005) Tuteja *et al.* (2006) Vijayalaxmi (2008)	Reddy (2001) Neelima (2002) Sivaprasad (2003) Gururajan and Sundar (2004) Verma *et al.* (2006) Eswararao (2008) Padmavathi (2008)
11.	Micronaire value (10^{-6} g/in)	Rao *et al.* (2001) Reddy (2001) Sivaprasad (2003) Muthu *et al.* (2004) Neelima *et al.* (2005) Murthy *et al. (*2006) Leela Pratap *et al.* (2007) Padmayathi (2008) Vijayalaxmi (2008)	Dedaniya and Pethani (1994) Karunakar Raju (2005) Eswararao (2008)
12.	Bundle strength (g/tex)	Sivaprasad (2003) Murthy *et al.*(2006) Padmavathi (2008)	Muthu *et al.* (2004) Gururajan and Sundar (2004) Karunakar Raju (2005) Eswararao (2008) Vijayalaxmi (2008)
13.	Uniformity ratio	Sivaprasad (2003) Karunakar Raju (2005) Murthy *et al.*(2006) Eswararao (2008) Vijayalaxmi (2008)	Muthu *et al.* (2004) Leela Pratap *et al.* (2007) Padmavathi (2008)
14.	Oil content (%)	Patel *et al.*(2003) Punitha and Raveendran (2005)	
15.	Lint yield/plant (g)	Dedaniya and Pethani (1994) Leela Pratap *et al.*(2007) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)	

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CHAPTER -III

MATERIALS AND METHODS

The present investigation entitled, “Genetic divergence in cotton (*Gossypium hirsutum* L.)” was taken up during *kharif* 2008-09 at Regional Agricultural Research Station, Lam Farm, Guntur, Andhra Pradesh. The site of the experiment is situated at $16^0$2’ North and $80^0$3’ East longitude at a height of 31.5 m above mean sea level. The soils are black cotton type with clay texture.

3.1 MATERIALS

The experimental material used in the present study consisted of 50 genotypes of cotton (*Gossypium hirsutum* L.), which were obtained from different cotton research centers across the country. The information on source of these 50 genotypes is presented in Table-6.

3.2 METHODS

3.2.1 Experimental Technique

The detailed experimental technique adopted for the present investigation are furnished.

Experimental details of the present investigation.

Location	:	Regional Agricultural Research Station, Lam Farm, Guntur, Andhra Pradesh.
Season	:	*Kharif* 2008-09
Entries	:	50 Genotypes of cotton (*Gossypium hirsutum* L.)
Design	:	Randomized complete block design
Replications	:	3
Plot size	:	1 row of 6 m length
Spacing	:	105 cm between rows and 60 cm within rows
Fertilizers	:	90 N kg : 45 P_2O_5 kg : 45 K_2O kg ha^{-1}
Plant protection	:	Need based plant protection measures were taken up against pest and diseases.

Table-6: Cotton (*Gossypium hirsutum* L.) **genotypes employed in the study and their source**

S. No.	**Name of the Genotype**	**Source**
1	CSH 612	CICR, Sirsa
2	TSH 9908	TANU, Srivilliputtore.
3	RS252	RAU, Sriganganagar.
4	TCH 1716	TANU, Coimbatore.
5	CPD 801	UAS, Dharwad.
6	GJHV 448	JAU, Junagadh.
7	KH 140	JNKV, Khandwa.
8	F 2168	PAU, Faridkot.
9	CNH 1104	CICR, Nagpur.
10	NDLH 1938	RARS, Nandyal.
11	LH 2123	PAU, Ludhiana.
12	L 604	RARS, Lam.
13	BS 51	AICCIP.
14	CCH 2623	CICR, Coimbatore.
15	CSH 3129	CICR, Sirsa.
16	CCH 4474	CICR, Coimbatore.
17	F 2170	PAU, Faridkot.
18	GISV 216	NAU, Surat.
19	HS 283	HAU, Hissar.
20	RAH 336	UAS, Raichur.
21	RS 2527	RAU, Sriganganagar.
22	BS 41	AICCIP.
23	RS 2013	RAU, Sriganganagar
24	LH 2132	PAU, Ludhiana.
25	P 1752	IARI, New Delhi.

26	IHANI 251	AICCIP.
27	SCS 415	UAS, Siriguppa.
28	L 801	RARS, Lam.
29	HAG 1015	UAS, Hagari.
30	F 1861	PAU, Faridkot.
31	GSHV 155	NAU, Surat.
32	H 1360	HAU, Hissar.
33	CA 7	CICR, Nagpur.
34	TCH 1715	TNAU, Coimbatore.
35	CANDTS 55	AICCIP
36	NH 630	MAU, Nanded.
37	RAH 61	UAS, Raichur.
38	BS 277	AICCIP.
39	CPD 1050	UAS, Dharwad.
40	GISV 218	NAU, Surat.
41	RHC 9854	AICCIP.
42	BS 279	AICCIP.
43	MCU 5	TNAU, Coimbatore.
44	ARBH 225	UAS, Arbhavi.
45	CPD 1019	UAS, Dharwad
46	ARBH 813	UAS, Arbhavi.
47	P 57-6	AICCIP.
48	RAH 216	UAS, Raichur.
49	SURABHI	CICR, Coimbatore.
50	LK 861	RARS, Lam.

3.2.2 Recording Observations

Five plants from each genotype in each replication were selected at random and labelled for recording observations. The mean of the five plants was used for statistical analysis. For estimating the fibre quality parameters composite sample of 250g of kapas was obtained from each replication and ginned for seed and lint. The lint sample was used for estimating the fibre properties. The data on the following yield and yield component traits and quality parameters were recorded.

3.2.2.1 Plant height (cm)

Measured from the base to the tip of the apical bud at the time of harvest.

3.2.2.2 Days to 50% flowering

The number of days taken by each genotype from sowing to the day on when 50 per cent of the plants attained flowering in the population.

3.2.2.3 Number of monopodia per plant

The branches on the main stem which are lateral and axillary in position with vertical growth in acropetal succession were regarded as monopodia and counted at maturity stage avoiding small sprouts.

3.2.2.4 Number of sympodia per plant

Branches which are extra-axillary in position and normally horizontal with zig-zag pattern of fruiting points were taken as sympodia. The number of such sympodia on main stem was counted at maturity stage.

3.2.2.5 Number of bolls per plant

The total number of fully opened bolls harvested from each plant were counted and averaged.

3.2.2.6 Boll weight (g)

The boll weight was obtained by taking the average weight of seed cotton from randomly collected 20 bolls per plot.

3.2.2.7 Ginning-out turn (%)

This is the weight of the lint expressed as percentage of weight of seed cotton calculated according to the following formula.

$$\text{Ginning-out turn (\%)} = \frac{\text{Weight of lint}}{\text{Weight of seed cotton}} \times 100$$

3.2.2.8 Seed index (g)

It is the absolute weight of 100 seeds recorded in grams.

3.2.2.9 Lint index (g)

It is the absolute weight of lint obtained from 100 seed kapas recorded in grams.

3.2.2.10 2.5% span length (mm)

Average length of the fibres expressed as span length in mm was determined by Uster Fibrograph 430 instrument in which, the amount of light transmitted through a fibre board is measured in determining the length of the fibre.

3.2.2.11 Micronaire (10^{-6} g/inch)

The fibre fineness was measured with Sheffield micronaire using spacer technique. In micronaire instrument, air is passed through a fibre plug of

3.24 m compressed in a cylinder of specific dimension. The dimension of airflow reflected by the fibre plug is measured in a calibrated scale.

3.2.2.12 Bundle strength (g/tex)

This was measured by using Pressly strength tester. A tuft of fibres was taken between two special clamps and the breaking strength was determined. The bundle strength test was carried out at 1/8th gauge length.

3.2.2.13 Uniformity ratio

The ratio between two span lengths (2.5% and 50%) expressed as a percentage of the longer length and was determined by Fibrograph model 430.

3.2.2.14 Oil content (%)

Oil content in seeds was estimated using nuclear magnetic resonance (NMR), at Directorate of Oil Seeds Research (DOR) Rajendra Nagar, Hyderabad and expressed as per cent.

$$\textbf{Oil per cent} = \frac{\textbf{Weight of oil extracted}}{\textbf{Weight of seed sample}} \times 100$$

3.2.2.15 Lint yield per plant (g)

Total weight of lint in grams obtained from each plant was recorded and averaged.

3.2.2.16 Seed cotton yield per plant (g)

Total weight of seed cotton in grams obtained from each plant was recorded and averaged.

3.3 STATISTICAL ANALYSIS

The data recorded on various characters were subjected to the following statistical analysis.

3.3.1 Analysis of variance

The data for different characters were statistically analyzed on the basis of the model given by Cochran and Cox (1950) for randomized complete block design.

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

Y_{ij} = Observation of the i^{th} block in the j^{th} genotype

μ = General mean

b_i = Effect of i^{th} block

t_j = Effect of j^{th} genotype

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

The analysis of variance for each character was carried out as indicated below:

Source of variation	**d.f**	**SS**	**MSS**	**F ratio**
Replications	r-1	RSS	$Mr = \sigma^2_e + \sigma^2_r$	M_r/M_e
Treatments (genotypes)	t-1	TrSS	$Mt = \sigma^2_e + \sigma^2_g$	M_t/M_e
Error	(r-1)(t-1)	ESS	$Me = \sigma^2_e$	
Total	**(rt-1)**	**TSS**		

Where, r = Number of replications
t = Number of genotypes
df = Degrees of freedom
SS = Sum of squares
MSS = Mean sum of squares
σ^2_e = Error variance
σ^2_g = Variance due to genotypes
σ^2_r = Variance due to replications
M_r = Mean squares due to replications
M_t = Mean squares due to treatments
M_e = Mean squares due to error

3.3.2 Estimation of genetic parameters

1. Coefficient of Variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952).

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{General mean } (\overline{X})} \times 100$$

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean } (\overline{X})} \times 100$$

Categorization of range of variation was given by Sivasubramanian and Menon (1973)

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

2. Heritability in broad sense [$h^2_{(b)}$]

Heritability in broad sense was estimated as per Lush (1940) and Allard (1960).

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

Heritability categorization was given as per Johnson *et al.* (1955).

0 – 30%	=	Low
31-60%	=	Moderate
61% and above	=	High

3. Genetic advance (GA)

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

GA = $k \times \sigma_p \times h^2$ (b)

GA = Genetic advance

k = Selection differential at 5 per cent selection intensity which accounts to a constant value 2.06

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

σ_p = Phenotypic standard deviation

4. Genetic advance as per cent of mean (GAM)

$$\text{GAM} = \frac{\text{Genetic advance (GA)}}{\text{Grand mean } (\overline{X})} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.* (1955).

Low = Less than 10%

Moderate = 10-20%

High = More than 20%

3.3.3 Correlation studies

Analysis of covariance

Analysis of covariance was computed by following procedure.

$$Y_{ij} = M + t_i + b_j + B\,(X_{ij} - \underline{X}\,) + e_{ij}$$

Where,

Y_{ij} = Performance of i^{th} genotype in the j^{th} replication

μ = General mean

t_i = True effect of i^{th} treatment

b_j = True effect of j^{th} block

b_{yx} = Tegression coefficient of y on x

$X_{ij} - \overline{X}$ = Covariate

e_{ij} = Random error

The structure of analysis of covariance is as follows

Source	**df**	**SS$_y$**	**SS$_x$**	**SP$_{xy}$**	**MSS$_y$**	**MSS$_x$**	**MSP$_{xy}$**
Replications	(r-1)	RY	RX	RXY	ry	rx	rxy
Genotypes	(t-1)	TY	TX	TXY	ty	tx	txy
Error	(r-1)(t-1)	EY	EX	EXY	ey	ex	exy

Where,

df	= Degrees of freedom
SP	= Sum of products
SS	= Sum of squares
MSP	= Mean sum of products
MSS	= Mean sum of squares
r	= Number of replications
t	= Number of genotypes

Genotypic covariance $(X_i.X_j)g$ = (MSPr – MSPe) / r

$(X_i.X_j)g$ = Genotypic covariance between ith and jth characters

MSPr = Mean sum of products of genotypes

MSPe = Error mean sum of products = environmental covariance

Phenotypic covariance $(X_i.X_j)$ p = $(X_i.X_j)$ g + e_ie_j

$(X_i.X_j)$ p = Phenotypic covariance between ith and jth characters

$(X_i.X_j)g$ = Genotypic covariance between ith and jth characters

e_ie_j = Environmental covariance between ith and jth characters

Phenotypic and genotypic correlations were worked out by using the formulae suggested by Falconer (1964).

Phenotypic coefficients of correlation (r_p)

$$r(x_{i}.x_{j})_{p} = \frac{Cov(x_{i}.x_{j})p}{(V(X_{i})\,p \text{ x } V(X_{j})\,p)^{1/2}}$$

Genotypic coefficient of correlation (r_g)

$$r(x_{i}.x_{j})_{g} = \frac{Cov(x_{i}.x_{j})g}{(V(X_{i})\,g \text{ x } V(X_{j})\,g)^{1/2}}$$

Where,

r ($x_i.x_j$) g = Genotypic correlation between i^{th} and j^{th} characters
COV ($x_i.x_j$) g = Genotypic covariance between i^{th} and j^{th}characters
$V(X_i)_g$ = Genotype variance of i^{th} character
$V(X_j)_g$ = Genotypic variance of j^{th} character
r ($x_i.x_j$) $_g$ = Phenotypic correlation between i^{th} and j^{th} characters
COV ($x_i.x_j$) $_p$ = Phenotypic covariance between i^{th} and j^{th}characters
$V(X_i)_p$ = Phenotype variance of i^{th} character
$V(X_j)_p$ = Phenotypic variance of j^{th} character

3.3.3.1 Test of significance

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the table values (Fisher and Yates, 1963) at (n-2) degrees of freedom at 5% and 1% level where, ‘n’ denotes the number of pairs of observations used in the calculation.

3.3.4 Path coefficient analysis

Path coefficient analysis suggested by Wright (1921) and elaborated by Dewey and Lu (1959) was used to calculate the direct and indirect contribution of various traits to yield.

For estimation of various direct and indirect effects, a set of simultaneous equations were formed:

$$\begin{aligned} r_{1y} &= P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \ldots. + r_{1k} P_{ky} \\ r_{2y} &= r_{21} P_{1y} + P_{2y} + r_{23} P_{3y} + \ldots. + r_{2k} P_{ky} \\ r_{iy} &= r_{i1} P_{1y} + r_{i2} P_{2y} + r_{i3} P_{3y} + \ldots. + r_{ik} P_{ky} \\ r_{ky} &= r_{k1} P_{1y} + r_{k2} P_{2y} + r_{k3} P_{3y} + \ldots. + r_{kk} P_{k} \end{aligned}$$

Where,

r_{1y} to r_{ky} = Coefficient of correlations between causal factors 1 to K and dependent character

r_{12} to r_{k-1},k = Coefficient of correlations among causal factors

P_{1y} to P_{ky} = Direct effects of characters 1 to k on character y

The above equations were written in a matrix form as under:

$$\begin{array}{cccc} \textbf{A} & & \textbf{C} & \textbf{B} \\ \begin{bmatrix} r_{1y} \\ r_{2y} \\ \cdot \\ \cdot \\ r_{ky} \end{bmatrix} & = & \begin{bmatrix} 1 & r_{12} & r_{13} & \cdot\;\cdot\;\cdot & r_{1k} \\ r_{21} & 1 & r_{23} & \cdot\;\cdot\;\cdot & r_{2k} \\ \cdot & \cdot & \cdot & \cdot\;\cdot\;\cdot\;\cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot\;\cdot\;\cdot\;\cdot & \cdot \\ r_{k1} & r_{k2} & r_{k3} & \cdot\;\cdot\;\cdot & 1 \end{bmatrix} & \begin{bmatrix} P_{1y} \\ P_{2y} \\ \cdot \\ \cdot \\ P_{ky} \end{bmatrix} \end{array}$$

Then $B=(C)^{-1} A$

$$\text{Where } (C)^{-1} = \begin{bmatrix} C_{11} & C_{12} & \cdots & C_{1k} \\ C_{21} & C_{22} & \cdots & C_{2k} \\ \vdots & \vdots & & \vdots \\ \vdots & \vdots & & \vdots \\ C_{k1} & C_{k2} & \cdots & C_{kk} \end{bmatrix}$$

Then direct effects were calculated as follows,

$$P_{1y} = \sum_{i=1}^{k} C_{1i} . r_{iy}$$

$$P_{2y} = \sum_{i=1}^{k} C_{2i} . r_{iy}$$

$$P_{ky} = \sum_{i=1}^{k} C_{ki} . r_{iy}$$

3.3.4.1 Residual effect

In plant breeding, it is very difficult to have complete knowledge of all component traits on yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures a role of other possible independent variables which were not included in the study on the dependent variable. The residual effect estimated with the help of direct effects and simple correlation coefficients.

$$1 = P^2 R_y + \Sigma P_{iy} \; r_{iy}$$

Where, $P^2 R_y$ is the square of the residual effect.

3.3.5 Genetic divergence

3.3.5.1 Mahalanobis' D^2 analysis

The data collected on different characters was analysed using Mahalanobis' D^2 analysis to determine the genetic divergence among the genotypes (Mahalanobis, 1928).

3.3.5.1.1 Test of significance

Variances were calculated for all the 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, 1978). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using 'V' statistic, which in turn utilizes Wilk's criterion. The sum of squares and sum of products of error, error + variety and variance – covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using the following relationship.

$$\wedge = \frac{|\mathbf{E}|}{|\mathbf{E+V}|}$$

Where,

$\wedge$ = Wilk's criterion

$|\mathbf{E}|$ = Determinant of error matrix and

$|\mathbf{E+V}|$ = Determinant of error + variety matrix

$$V\,(\text{Stat}) = -m \log_e^{\wedge} = -\left(n - \frac{P+Q+1}{2}\right) \log e^{\wedge}$$

Where,

$m = n - (P+Q+1)/2$

n = degrees of freedom for error + varieties

$\log_e \wedge = 2.3026 \log_{10}^{\wedge}$

P = Number of variables or characters (16)

Q = Number of varieties – 1(or d.f for populations49)

e = 2.7183

Accordingly, V $_{(Stat)}$ value is 4573.35

V (Stat) is distributed asχ^2 with PQ (784= 16 x49) degrees of freedom.

The tabulated value of χ^2 for 784 degrees of freedom is 556.45 at 5 per cent level which is lower than the calculated χ^2 value (4573.35).

Transformation of correlated variables

In the present model, computation of D^2 values was reduced to simple summation of the differences in the mean values of various characters of the two genotypes *i.e.* Σd^2_i. Therefore, transformation of the correlated variables into uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method.

3.3.5.1.2 Computation of D^2 values

For the given combination of i and j genotypes, the mean deviation *i.e.*, $Y_i^t - Y_j^t$ for t=1,2…p variables are computed and the D^2 values were calculated as

$$D^2_{ij} = \sum_{t=1}^{k} (Y_i^t - Y_j^t)^2$$

Where,

Y_i^t is uncorrelated mean value of ith genotype for character't'

Y_j^t is uncorrelated mean value of jth genotype for character't'

D^2_{ij} is D^2 between ith and jth genotypes.

3.3.5.1.3 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of χ^2 (Table 14) and is tested against the tabulated value of χ^2 for p (16) degrees of freedom where p (16) is the number of characters considered. The tabulated value of χ^2 at 5 per cent level of significance for 16 degrees of freedom being 26.29 which is lower than calculated values of D^2 in most cases clearly shows that most of D^2 values are significant.

3.3.5.1.4 Contribution of individual characters towards divergence

In all combinations, each character was ranked based on their contribution towards divergence between two entries ($d_i = Y_i^t - Y_j^t$). Rank 1 is given to the highest mean difference and the rank P to the lowest mean difference, where, P is the total number of characters. Percentage contribution towards genetic divergence was calculated using the following formula.

$$\text{Percentage contribution of the character} \quad x = \frac{N \times 100}{M}$$

Where,

N = Number of genotype combinations where the character was ranked first.

M = All possible combinations of number of genotypes considered.

3.3.5.1.5 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1977). To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2, that population was not considered for including in that cluster.

The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued till all the genotypes were included into one or other cluster.

3.3.5.1.6 Average intra- cluster distance

For the measurement of intra-cluster distances, the formula used was $\Sigma D^2_i/n$ where, D^2_i was the sum of distances between all possible combinations (n) of the populations included in a cluster.

3.3.5.1.7 Average inter- cluster distance

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

$$\text{Averages inter-cluster distance} = \frac{D^2}{(n_1 \text{ x } n_2)}$$

Where,

n_1 and n_2 are the number of genotypes in each of the two clusters.

3.3.5.2 Principal component analysis and cluster analysis

Principal component analysis was carried according to procedure described by Banfield (1978). PCA can be performed on two types of data matrices viz., variance – covariance matrix and correlation matrix. With characters of different scale a correlation matrix standardizing the original data set is preferred. If the characters are of same scale, a variance – covariance matrix can be used. In the present study, PCA was performed on the correlation matrix of traits, thereby removing the effects of scale (Jackson, 1991).

3.3.5.2.1 Eigen values and eigen vectors

The eigen values and eigen vectors were computed from data matrix. Eigen values define the amount of total variation that is displayed on principal components. The proportion of variation accounted for each principal component (PC) is expressed as the eigen value divided by the sum of the eigen values.

$$\text{Per cent variance explained for } PC_1 = \frac{\text{Eigen value } (PC_1)}{\text{Sum of eigen values}}$$

The eigen vector (loading) defines the correlation of each variable with the principal components.

The principal components were identified by the following procedure.

The j^{th} principal component (Y_j) of the observation X is the linear combination given as follows:

$$Y_j = A_{1j}X_1 + \ldots\ldots\ldots\ldots + A_{pj}\,X_p$$

Where,

A_{ij} are found such that Y_j is uncorrelated $Y_1, Y_{2,}\ldots\ldots\ldots Y_{j}\text{-}_1$ the j^{th} largest variance. The A_{ij} are the elements of the normalized eigen vector associated with largest j^{th} eigen value. The variance of the j^{th} principal component of the λ_j and the total system variance trace (S) = $\lambda_1+\lambda_2 +\ldots+ \lambda_{p.}$ The importance of the j^{th} principal component is given by

$$\frac{\lambda_j}{\text{Trace (S)}}$$

This is informative about the proportion of total variation that can be accounted for the i^{th} principal component. The correlation between the i^{th} original variable X_i and the j^{th} principal component Y_j is given by

$$\rho(Xi,\ Y_j) = \frac{A_{ij}}{} \frac{\sqrt{\lambda_j}}{\sqrt{S_i}}$$

Where,

S_i is the standard deviation of X_i.

Thus, a principal component is linear function of the test variables given as follows

Principal component = $ax_1 + bx_2 + \ldots\ldots\ldots + hx_8$

Where, a,b,…. are coefficients and x_1, x_2 ….. *etc.*, are the variables in such a way that the principal component has a unit variance as reported by Ehrenberg (1985).

PCA scores for each genotype under concerned PCs were computed and utilized to derive a 2D and 3D (dimensional) scatter diagram as plot of individuals.

3.3.5.2.2 Cluster analysis

Agglomerative hierarchical clustering technique was followed as given by Anderberg (1993) for cluster analysis.

1. Obtaining data matrix

PCA scores for 50 genotypes were used as input for clustering because principal component analysis provides variable independence and balanced weighting of traits, which leads to an effective contribution of different characters on the basis of respective variation.

2. Standardizing the data matrix

To compare the similarities among the genotypes, the data matrix was standardizing function *i.e.*, Q analysis. The data matrix was a standardized in cluster analysis to make the characters contribute more equally to the similarities among genotypes and to nullify the arbitrarily affect of the units chosen for measuring the attributes among the genotypes.

Column standardizing function CA-Q analysis was carried by the following formula.

$$Z_{ij} = X_{ij} - \overline{X}_j \Big/ S_{ij}$$

$$\text{Where} \quad \overline{X}_j = \sum_{i=1}^{n} X_{ij} \Big/ n$$

$$\text{Where} \quad S_{ij} = \sum_{i=1}^{n} \frac{X_{ij} - X_j / n}{n-1}$$

Where, i = no.of genotypes *i.e.*, 50 in this case

j = total number of variables *i.e.*, 16 in this case

The resulting data after standardization is unit less and have mean zero and variance one.

3. Computing the resemblance matrix

A resemblance coefficient, which measures the over all resemblance (the degree of similarity or distance) between a pair of genotypes was computed. Here 50 genotypes were taken in data matrix and therefore resemblance coefficient was computed for total 1225 combinations *i.e.*, ${}^{50}C_2$ ways.

The data matrix was transformed to distance matrix (resemblance matrix) based on the dissimilarity coefficients using squared Euclidean distance method.

$$\text{Squared Euclidean distance } [\, d_{ij}] \;=\; \sum_{K=1}^{p} (X_{ik} - X_{jk})^2$$

Where,

P = number of genotypes *i.e.*, 50

X_{ik} = value of i th genotype for k PCA scores

X_{jk} = value of j th genotype for k PCA scores

4. Execution of the clustering method

Distance matrix was converted into dendrogram by using Ward’s method where the distance between two clusters is the sum of squares between two clusters summed over all variables. At each stage in the clustering procedure within cluster sum of squares is minimized over all partitions obtained by combining 2 clusters from previous stage.

3.3.5.2.3 Complete linkage diagram

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 of complete linkage dendrogram. 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’ 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 have 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 follows:

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.

CHAPTER IV

RESULTS

The data collected on 50 genotypes studied during *kharif* 2008-09 at Regional Agricultural Research Station, Lam Farm, Guntur for 16 characters viz., plant height (cm), days to 50% flowering, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), ginning out-turn (%), seed index (g), lint index (g), 2.5% span length (mm), micronaire (10^{-6} g/in), bundle strength (g/tex), uniformity ratio, oil content (%), lint yield per plant (g) and seed cotton yield per plant (g) of cotton (*Gossypium hirsutum* L.) were subjected to statistical analysis for drawing valid conclusions. The details of results obtained from the above investigation are presented here under.

Analysis of variance

The analysis of variance revealed significant differences among the genotypes for all the 16 characters, indicating the presence of genetic variability in the genotypes studied and are presented in Table - 7.

The results of statistical analysis of the data are presented under the following heads.

4.1 Genetic variability, heritability and genetic advance as per cent of mean

4.2 Character association

4.3 Path coefficient analysis

4.4 Genetic divergence

4.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN

The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2_{(b)}$) in broad sense and genetic advance as per cent of mean (GAM) were calculated and are presented in Table 8 and Table 9 and described character- wise here under. The graphical representation of ECV, PCV, GCV, heritability in broad sense ($h^2_{(b)}$) and genetic advance as the per cent of mean (GAM) are depicted in Fig.-1.

4.1.1 Plant height (cm)

The range of variation for this character varied from 101.40 cm (L-801) to 137.86cm (RAH-216) with a mean of 123.64cm. The estimates of PCV (7.84) and GCV (6.80) are low. High heritability (75.0%) coupled with moderate genetic advance as per cent of mean (12.16) was observed for plant height.

4.1.2 Days to 50% flowering

The number of days to 50% flowering ranged from 53.66 (GISV216) to 61.00 days (LK861) with a mean of 57.48 days. The estimates of PCV (2.77) and GCV (2.29) are low. High heritability (68.0%) coupled with low genetic advance as per cent of mean (3.89) were observed for days to 50% flowering.

4.1.3 Number of monopodia per plant

The number of monopodia per plant ranged from 0.33 (H1360) to 2.56 (GSHV448) with a mean of 1.27. The estimates of PCV (40.39) and GCV (37.26) were high. High heritability (85.0%) and high genetic advance as per cent of mean (70.79) were observed for this trait.

4.1.4 Number of sympodia per plant

The number of sympodia per plant ranged from 12.60 (SCS415 and TCH1715) to 22.53 (ARBH225) with a mean of 15.62. The estimates of PCV (17.61) and GCV (15.04) were moderate. High heritability (73.0%) coupled with high genetic advance as per cent of mean (26.49) was recorded for number of sympodia per plant.

4.1.5 Number of bolls per plant

The number of bolls per plant ranged from 19.80 (LK861) to 56.86 (MCU5) with an average of 40.60. The estimates of PCV (20.29) and GCV (18.06) were high and moderate and high heritability (79.0%) coupled with high genetic advance as per cent of mean (33.12) was observed for this character.

4.1.6 Boll weight (g)

The boll weight ranged from 3.13 (TSSH-9908) to 4.69 g (SCS-415) with a mean of 3.81 g. The estimates of PCV and GCV (11.29 and 8.71) were moderate and low. Moderate heritability (60.0%) and moderate genetic advance as per cent of mean (13.85) were recorded for this trait.

4.1.7 Ginning out-turn (%)

The range of variation among the genotypes for this trait was 32.44 (P57-6) to 39.29 (CSH612) with a mean of 35.60. The estimates of both PCV and GCV (4.11 and 3.73) were low. High heritability (83.0%) coupled with low genetic advance as per- cent of mean (6.99) was recorded for this trait.

4.1.8 Seed index (g)

Seed index was in the range of 7.40 (KH-140) to 13.16 g (NDLH-1938) with a mean of 9.35 g. The estimates of PCV and GCV (14.98 and 13.23) were moderate. High heritability (78.0%) and high genetic advance as per cent of mean (24.08) were observed for this trait.

4.1.9 Lint index (g)

The range of variation observed for this character was from 4.20 (SURABHI) to 7.06 g (CCH-4474) with a mean of 5.22g. The estimates of both PCV and GCV (16.98 and 14.94) were moderate. High heritability (77.0%) coupled with high genetic advance as per cent of mean (27.08) was observed for lint index.

4.1.10 2.5% span length (mm)

The mean span length ranged from 23.70 (RS-2525) to 35.41 mm (LK-861) mm with a mean of 27.37 mm. The estimates of both PCV and GCV (8.63 and

7.92) were low. High heritability (84.0%) coupled with moderate genetic advance as per cent of mean (14.97) was observed for this trait.

4.1.11 Micronaire (10^{-6} g/in)

The range of variation for the character was 2.52 (LK-861) to 4.83 (10^{-6} g/in) (RAH-336) with a mean of 4.15. The estimates of both PCV and GCV (10.33 and 8.85) were moderate and low. High heritability (73.0%) coupled with moderate genetic advance as per cent of mean (15.63) was recorded for this trait.

4.1.12 Bundle strength (g/tex)

The range of variation for bundle strength was from 19.66 (CA-7) to 28.20 g/tex (LK-861) with a mean of 22.63. The estimates of both PCV and GCV (7.04 and 5.67) were low. High heritability (65.0%) coupled with low genetic advance as per cent of mean (9.40) was recorded for this trait.

4.1.13 Uniformity ratio

The range of variation was 42.83 (LK-861) to 52.56 per cent (H-1360) with a mean of 49.62 per cent for this character. The estimates of both PCV and GCV (4.75 and 3.14) were low. Moderate heritability (44.0%) coupled with low genetic advance as per cent of mean (4.27) was observed for uniformity ratio.

4.1.14 Oil content (%)

The range of variation was 18.35 (LK-861) to 21.83 per cent (NDLH-1938) with a mean of 20.53 per cent for this character. The estimates of both PCV and

GCV (3.42 and 3.17) were low and high heritability (86.0%) coupled with low genetic advance as per cent of mean (6.06) was observed for oil percentage.

4.1.15 Lint yield per plant (g)

The mean variation ranged from 20.83 (LK-861) to 78.50 g (GISV-218) with an average of 52.33 g. The PCV and GCV estimates (24.93 and 20.26) were high. High heritability (66.0%) coupled with high genetic advance as per cent of mean (33.93) was recorded for this trait.

4.1.16 Seed cotton yield per plant (g)

The range of variation was from 59.16 (LK-861) to 225.70 g (GISV-218) with a mean of 147.34 g. The estimates of both PCV and GCV (25.79 and 21.52) were high. High heritability (70.0%) coupled with high genetic advance as per cent of mean (37.01) was observed for seed cotton yield per plant.

4.2 CHARACTER ASSOCIATION

The phenotypic and genotypic correlation coefficients between seed cotton yield and its component characters were worked out and furnished in Table -10.

4.2.1 Plant height (cm)

Plant height recorded significant positive association with number of sympodia per plant (0.3248** and 0.3859**), number of bolls per plant (0.3764** and 0.4687**), oil percentage (0.2877** and 0.3566**), lint yield per plant (0.3889** and 0.5290**) and seed cotton yield per plant (0.3726** and 0.4943**) at both phenotypic and genotypic levels. At genotypic level this trait showed significant positive association with boll weight (0.215**) and micronaire (0.1995*).

4.2.2 Days to 50% flowering

Days to 50%flowering showed significant positive association with number of sympodia per plant (0.2163** and 0.3147**) and bundle strength (0.2915** and 0.4362**) at both phenotypic and genotypic levels. Where as, it showed significant negative association with oil percentage (-0.2189** and -0.2474**), uniformity ratio (-0.1738* and -0.3186**) and boll weight (-0.1954* and -0.2515**). At genotypic level, this trait showed significant negative association with micronaire (-0.2590**).

4.2.3 Number of monopodia per plant

At both genotypic and phenotypic levels, this trait recorded significant positive association with 2.5% span length (0.2837** and 0.2288**) and bundle strength (0.2438** and 0.1630*). While,it was negative and significant association with boll weight (-0.2792** and -0.1828*), uniformity ratio (-0.3224** and -0.2135**) and micronaire (-0.2306** and -0.2066*).

4.2.4 Number of sympodia per plant

At both genotypic and phenotypic levels, correlations revealed significant and positive association with number of bolls per plant (0.4656** and 0.5644**), bundle strength (0.2449** and 0.4168**), lint yield per plant (0.4526** and

0.5837**) and seed cotton yield per plant (0.4669** and 0.5888**). Negative and significant association was observed with uniformity ratio (-0.3389** and -0.6309**), ginning out-turn (-0.1792* and -0.2379**) and lint index (-0.1748* and -0.2979**).

At genotypic level, this trait recorded significant positive association with boll weight (0.1833*). While, negative direction significant association was observed with seed index (-0.1764*).

4.2.5 Number of bolls per plant

At both genotypic and phenotypic levels, this trait showed highly significant positive association with seed cotton yield per plant (0.9385** and 0.9015**), lint yield per plant (0.9109** and 0.8706**) Oil percentage (0.2714** and 0.2174**) and micronaire (0.3465** and 0.2259**).

This character showed significant negative association with lint index

(-0.3115** and -0.2440**) and ginning out-turn (-0.4544** and -0.3737**) at both genotypic and phenotypic levels. 2.5% span length (-0.2327**) showed significant negative association only at genotypic level.

4.2.6 Boll weight (g)

Boll weight showed significant positive association with seed cotton yield per plant (0.4484** and 0.3626**), lint yield per plant (0.4884** and 0.3911**), oil percentage (0.3728** and 0.2665**), micronaire (0.2827** and 0.1922*), lint index (0.2234** and 0.2475**) and seed index (0.2893** and 0.2487**) at both genotypic and phenotypic levels.

At genotypic level, this trait recorded significant positive association with uniformity ratio (0.2164**).

4.2.7 Ginning out-turn (%)

At both genotypic and phenotypic levels, this character showed significant negative association with seed cotton yield per plant (-0.4208** and -0.2937**) where as lint index (0.3822** and 0.3457**) positively and significant. At genotypic level, this trait recorded significant positive association with uniformity ratio (0.2460**).

4.2.8 Seed index (g)

This trait showed highly significant positive association with lint index (0.8986** and 0.8392**) and uniformity ratio (0.4028** and 0.2449**) where as oil percentage (0.2462** and 0.1855*) showed significant positive association at both genotypic and phenotypic levels. At genotypic level, this trait showed significant positive association with micronaire (0.1875*).

4.2.9 Lint index (g)

This character showed highly significant positive association with uniformity ratio (0.5219** and 0.3053**) and at significant level with oil percentage (0.2578** and 0.1740*) at both genotypic and phenotypic levels, where as micronaire (0.2172**) showed significant positive association only at genotypic level.This trait recorded significant negative association with lint yield per plant (-0.1649*) and seed cotton yield per plant (-0.2213**) at genotypic level.

4.2.10 2.5% span length (mm)

Both genotypic and phenotypic levels, this trait showed significant negative association with uniformity ratio (-0.6387** and -0.4409**) and micronaire (-0.7635** and -0.6159**). Where as bundle strength (0.8098** and 0.6584**) showed high significant positive association. It also exhibited significant negative association with lint yield per plant (-0.2597**) and seed cotton yield per plant (-0.2306**)

4.2.11 Micronaire (10^{-6} g/in)

At both genotypic and phenotypic levels, this trait showed significant positive association with seed cotton yield per plant (0.3669** and 0.2197**), lint yield per plant (0.4055** and 0.2369**) and oil percentage (0.3365** and 0.2841**). Where as bundle strength (-0.6640** and -0.4641**) showed significant negative association.

4.2.12 Uniformity ratio

This trait recorded significant positive association with micronaire (0.6465** and 0.3972**) and oil percentage (0.2031* and 0.1644*) at both genotypic and phenotypic levels. Where as bundle strength (-0.6582** and -0.4169**) showed significant negative association.

4.2.13 Oil content (%)

At both phenotypic and genotypic levels, this character showed significant positive association with lint yield per plant (0.2936** and 0.4032**) and seed cotton yield per plant (0.2726** and 0.3663**).

4.2.14 Lint yield per plant (g)

This trait showed highly significant positive association with seed cotton yield per plant (0.9854** and 0.9870**) both at genotypic and phenotypic levels.

4.3 PATH COEFFICIENT ANALYSIS

The direct and indirect effects of different yield component traits on seed cotton yield per plant were estimated through path analysis at phenotypic and genotypic levels and are presented in Tables -11 and 12, respectively. The phenotypic and genotypic path diagrams are given in Fig.-2 and 3, respectively.

4.3.1 Plant height (cm)

The direct contribution of this character on seed cotton yield per plant was negative (-0.0093). The indirect effects *via* number of monopodia per plant (0.0001), number of sympodia per plant (0.0018), number of bolls per plant (0.0103), boll weight (0.0009), ginning out-turn (0.0021), 2.5% span length (0.0005), bundle strength (0.0001), oil percentage (0.0017) and lint yield per plant

(0.3657) were positive. While, seed index (-0.0001), lint index (-0.0001), uniformity ratio (-0.0001) and micronaire (-0.0012), were negative. This trait had significant positive phenotypic correlation with seed cotton yield per plant (0.3726**).

4.3.2 Days to 50% flowering

The direct contribution of this character on seed cotton yield per plant was positive (0.0003). The indirect effects *via* number of monopodia per plant (0.0013), number of sympodia per plant (0.0012), ginning out-turn (0.0028), lint index (0.0003) and micronaire (0.0013) were positive.

While, plant height (-0.0008), number of bolls per plant (-0.0021), boll weight (-0.0014), seed index (-0.0002),2.5% span length (-0.0010), uniformity ratio(-0.0005), bundle strength (-0.0007),oil percentage (-0.0013) and lint yield per plant (-0.1089) showed negative indirect effect. This trait had negative phenotypic correlation with seed cotton yield per plant (-0.1097).

4.3.3 Number of monopodia per plant

The direct contribution of this character on seed cotton yield per plant was positive (0.0105). The indirect effects *via* lint index (0.0004) and micronaire (0.0019) were also positive.

While, plant height (-0.0001), number of bolls per plant (-0.0004), boll weight (-0.0013), ginning out-turn (-0.0021), seed index (-0.0006), 2.5% span length (-0.0021), uniformity ratio (-0.0006), bundle strength (-0.0004),oil percentage (-0.0003) and lint yield per plant (-0.1052) showed negative indirect effect. This trait had negative phenotypic correlation with seed cotton yield per plant(-0.1003).

4.3.4 Number of sympodia per plant

The direct contribution of this character on seed cotton yield per plant was positive (0.0054). The indirect effects *via* plant height (-0.0030),seed index(-0.0007), uniformity ratio (-0.0010), micronaire (-0.0006) and bundle strength (-0.0006) were negative. While, days to 50% flowering (0.0001), number of monopodia per plant (0.0001) number of bolls per plant (0.0127), boll weight (0.0009), ginning out-turn (0.0265), lint index (0.0009), 2.5% span length (0.0002), oil percentage (0.0005) and lint yield per plant (0.4256) were showed positive indirect effect, This trait had significant positive phenotypic correlation with seed cotton yield per plant (0. 4669**).

4.3.5 Number of bolls per plant

The direct contribution of this character on seed cotton yield per plant was positive (0.0274). The indirect effects through number of sympodia per plant (0.0025), boll weight (0.0002), ginning out-turn (0.0553), lint index (0.0012), 2.5% span length (0.0015), bundle strength (0.0001), oil percentage (0.0013) and lint yield per plant (0.8188) were positive. While, plant height (-0.0035), number of monopodia per plant (-0.0002), seed index (-0.0005), uniformity ratio (-0.0004) and micronaire (-0.0021) showed negative indirect effects. This trait had significant positive phenotypic correlation with seed cotton yield per plant (0.9015**).

4.3.6 Boll weight (g)

The direct contribution of this character on seed cotton yield per plant was positive (0.0071). The indirect effects *via* plant height (-0.0012), days to 50% flowering (-0.0001), number of monopodia per plant (-0.0019), ginning out-turn (-0.0119), lint index (-0.0012) and micronaire (-0.0018) were negative. While, the characters number of sympodia per plant (0.0007), number of bolls per plant (0.0008), seed index (0.0017), 2.5% span length (0.0009), uniformity ratio (0.0001), oil percentage (0.0015) and lint yield per plant (0.3678) showed positive indirect effects. This trait had significant positive phenotypic correlation with seed cotton yield per plant (0.3626**).

4.3.7 Ginning out-turn (%)

The direct contribution of this character on seed cotton yield per plant was negative (-0.1480). The indirect effects *via* plant height (0.0001), number of monopodia (0.0002), boll weight (0.0006), 2.5% span length (0.0007), uniformity ratio (0.0004), bundle strength (0.0003) and oil percentage (0.0005) were positive. While, the characters number of sympodia per plant (-0.0010), number of bolls per plant (-0.0102), seed index (-0.0003), lint index (-0.0017), micronaire (-0.0005) and lint yield per plant (-0.1348) showed negative indirect effect.

This trait had significant negative phenotypic correlation with seed cotton yield per plant (-0.2937**).

4.3.8 Seed index (g)

The direct contribution of this character on seed cotton yield per plant was positive (0.0068). The indirect effects *via* plant height (0.0001), boll weight (0.0018), ginning out-turn (0.0063), uniformity ratio (0.0007), oil percentage (0.0011) and lint yield per plant (0.0035) were positive. While, the characters number of monopodia per plant (-0.0009), number of symmpodia per plant (-0.0005), number of bolls per plant (-0.0020), lint index (-0.0041), 2.5% span length (-0.0002), micronaire (-0.0010) and bundle strength (-0.0003) showed negative indirect effect This trait had positive phenotypic correlation with seed cotton yield per plant (0.0111).

4.3.9 Lint index (g)

The direct contribution of this character on seed cotton yield per plant was negative (-0.0049). The indirect effects through boll weight (0.0018), seed index (0.0057), 2.5% span length (0.0006), uniformity ratio (0.0009) and oil percentage (0.0010) were positive.

While, plant height (-0.0002), number of monopodia per plant (-0.0008), number of sympodia per plant (-0.0009), number of bolls per plant (-0.0067), ginning out-turn (-0.0512), micronaire (-0.0010), bundle strength (-0.0001) and lint yield per plant (-0.0855) showed negative indirect effects. This trait had negative phenotypic correlation with seed cotton yield per plant (-0.1414).

4.3.10 2.5% span length (mm)

The direct contribution of this character on seed cotton yield per plant was negative (-0.0093). The indirect effects through number of sympodia per plant (-0.0001), number of bolls per plant (-0.0043), boll weight (-0.0007), uniformity ratio (-0.0012), bundle strength (-0.0016), oil percentage (-0.0007) and lint yield per plant (-0.1445) were negative. While, the characters viz., plant height (0.0005), number of monopodia per plant (0.0024), ginning out-turn (0.0114), seed index (0.0001), lint index (0.0003) and micronaire (0.0057) showed positive indirect effects. This trait had negative phenotypic correlation with seed cotton yield per plant (-0.1420).

4.3.11 Uniformity ratio

The direct contribution of this character on seed cotton yield per plant was positive (0.0028). The indirect effects *via* plant height (0.0002), boll weight (0.0002), seed index (0.0017), 2.5% span length (0.0041), bundle strength (0.0010) and oil percentage (0.0010) were positive.

While, the characters days to 50% flowering (-0.0001), number of monopodia per plant (-0.0022), number of sympodia per plant (-0.0018), number of bolls per plant (-0.0038), ginning out-turn (-0.0206), lint index (-0.0015), micronaire (-0.0037) and lint yield per plant (-0.1174) showed negative indirect effects. This trait had negative phenotypic correlation with seed cotton yield per plant (-0.1402).

4.3.12 Micronaire (10^{-6} g/in)

The direct contribution of this character on seed cotton yield per plant was negative (-0.0093). The indirect effects through plant height (-0.0012), number of monopodia per plant (-0.0022), ginning out-turn (-0.0081) and lint index (-0.0005) were negative. While, the characters viz., number of sympodia per plant (0.0004), number of bolls per plant (0.0062), boll weight (0.0014), seed index (0.0007), 2.5% span length (0.0057), uniformity ratio (0.0011), bundle strength (0.0011), oil percentage (0.0016) and lint yield per plant (0.2228) showed positive indirect effects. This trait had significant positive phenotypic correlation with seed cotton yield per plant (0.2197**).

4.3.13 Bundle strength (g/tex)

The direct contribution of this character on seed cotton yield per plant was negative (-0.0025). The indirect effects *via* number of bolls per plant (-0.0007), lint index (-0.0001), 2.5% span length (-0.0061), uniformity ratio (-0.0012), oil percentage (-0.0006) and lint yield per plant (-0.0148) were negative. While, the characters of plant height (0.0003), days to 50% flowering (0.0001), number of monopodia per plant (0.0017), number of sympodia per plant (0.0013), ginning out-turn (0.0159), seed index (0.0009) and micronaire (0.0043) showed positive indirect effects. This trait had negative phenotypic correlation with seed cotton yield per plant (-0.0014).

4.3.14 Oil percentage (%)

The direct contribution of this character on seed cotton yield per plant was positive (0.0058). The indirect effects through plant height (-0.0027), days to 50% flowering (-0.0001), number of monopodia per plant (-0.0005), ginning out-turn (-0.0140), lint index (-0.0009) and micronaire (-0.0026) were negative. While, the characters, number of sympodia per plant (0.0004), number of bolls per plant (0.0060), boll weight (0.0019), seed index (0.0013), 2.5% span length (0.0012) uniformity ratio (0.0005), bundle strength (0.0002) and lint yield per plant (0.2761) showed positive indirect effects. This trait had significant positive phenotypic correlation with seed cotton yield per plant (0.2726**).

4.3.15 Lint yield per plant (g)

The direct contribution of this trait on seed cotton yield per plant was positive (0.9405). The indirect effects *via* number of sympodia per plant (0.0025), number of bolls per plant (0.0238), boll weight (0.0028), ginning out-turn (0.0212), lint index (0.0004), 2.5% span length (0.0014) and oil percentage (0.0017) were positive.

While, the characters plant height (-0.0036), number of monopodia per plant (-0.0012), uniformity ratio (-0.0004) and micronaire (-0.0022) showed negative indirect effects. This trait had significant positive phenotypic correlation with seed cotton yield per plant (0.9870**).

4.4 GENETIC DIVERGENCE

The quantitative assessment of genetic divergence was carried out in 50 genotypes of cotton for all the 16 contributing characters studied in the present investigation by using Mahalanobis' D^2 statistic, PCA analysis and cluster analysis.

4.4.1 Mahalanobis' D^2 analysis

4.4.1.1 Test with *Wilk's* criterion ('/\\')

Significant differences among the genotypes for individual characters were first determined and later the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the *Wilk's criterion* '/\\'. The *Wilk's* criterion thus obtained was used in calculations of 'V' statistic. The statistic was highly significant indicating that genotypes differed significantly when all the characters were considered simultaneously. The tabulated value of $\chi 2$ for 784 degrees of freedom is 556.45 at 5 per cent level which is lower than the calculated $\chi 2$ value (4573.35).

4.4.1.2 Mahalanobis' D^2 values

To estimate the D^2 values, correlated mean of characters were transformed into standardized uncorrelated characters using pivotal condensation method. The statistical differences (D^2) between pairs of genotypes was obtained as the sum of squares of the differences between the pairs of corresponding uncorrelated values of any two genotypes considered at a time. Thus the possible 1225 combinations and the corresponding D^2 values were obtained.

The per cent contribution towards genetic divergence by all the 16 contributing characters is presented in Table -13. The maximum contribution towards genetic divergence is by ginning out-turn (15.92%) followed by 2.5% span length (14.86%), oil percentage (14.12%), number of monopodia per plant (13.71%), seed index (10.12%), number of sympodia per plant (6.86%), plant height (5.80%), number of bolls per plant (3.59%), lint index (3.27%), micronaire (3.10%), days to 50% flowering (2.94%), seed cotton yield per plant (2.61%), boll weight (1.96%), bundle strength (1.06%) and lint yield per plant (0.08%).

4.4.1.3 Grouping of genotypes into various clusters

The 50 genotypes were grouped into eight clusters using the Tocher's method, with the criterion that the intra-cluster average D^2 values should be less than the inter-cluster D^2 values. The mutual relationships among the clusters were also presented diagrammatically in Fig.-4.

4.4.1.4 Average intra- and inter- cluster D^2 values

The average intra- and inter- cluster D^2 values were estimated as per the procedure given by Singh and Chowdhary (1977) and are presented in Table -14. The proximity and divergence among eight clusters are presented Table -15.

Intra-cluster D^2 values ranged from zero (cluster IV,VI,VII and VIII) to 39.67 (cluster V), while the inter-cluster D^2 values ranged from 27.66 between (cluster I and cluster IV) to 180.30 between cluster (VII and VIII). The maximum inter cluster distance (180.30) was observed between cluster VII and VIII followed by cluster VI and VIII (175.43) and cluster III and VIII (153.15). The minimum inter cluster distance of (27.66) recorded between cluster I and IV.

Cluster I was comprised of 13 genotypes. It was nearest to cluster IV (27.66) and farthest from cluster VIII (133.50).

Cluster II was comprised of 12 genotypes. It was nearest to cluster I (28.13) followed by cluster V (38.91) and farthest from cluster VIII (151.93) followed by cluster VII (62.92).

Cluster III was comprised of 17 genotypes and was the largest of all clusters. It was nearest to the cluster I (29.34) followed by cluster II (42.79) and farthest from cluster VIII (153.15) followed by VII (55.99).

Cluster IV was comprised of only one genotype. It was the nearest to the cluster I (27.66) followed by cluster V (38.39) and farthest from the cluster VIII (105.36) followed by cluster VII (85.65).

Cluster V was comprised of four genotypes. It was the nearest to the cluster IV (38.39) followed by cluster II (38.91) and farthest from the cluster VIII (96.47) followed by cluster VI (66.59).

Cluster VI was also consisted of only one genotype. It was the nearest to the cluster I (33.47) followed by cluster II (55.02) and farthest from cluster VIII (175.43) followed by the cluster VII (108.44).

Cluster VII was comprised of one genotype. It was nearest to the cluster III (55.99) followed by cluster I (61.00) and farthest from cluster VIII (180.30) followed by cluster VI (108.44).

Cluster VIII was comprised of only one genotype. It was nearest to the cluster V (96.47) followed by cluster IV (105.36) and farthest from the cluster VII (180.30) followed by cluster VI (175.43).

4.4.1.5 Cluster Mean Values

The clusters mean values for all the sixteen characters are presented in Table -17. Cluster II recorded high mean values for seed cotton yield per plant (187.13), lint yield per plant (65.61), boll weight (3.94), number of bolls per plant (49.42) and number of sympodia per plant (19.11); cluster III recorded high mean values for seed index (10.22) and lint index (5.93); cluster IV recorded high mean for plant height (131.93) and oil percentage (21.23); cluster VI recorded high mean for micronaire (4.70) and uniformity ratio (52.56); cluster VII recorded high mean for number monopodia per plant (2.56) and ginning out-turn (38.14) and cluster VIII recorded high mean for days to 50% flowering (61.00), 2.5% span length (35.41) and bundle strength (28.20) .

4.4.2 Application of principal component analysis in genetic divergence

In principal component analysis on correlation matrix the standardization of columns (here characters) created 16 new variables for 50 genotypes without changing their relative positions. These 16 new variables are the principal components (PC_1, PC_2 …….PC_{16}). Each principal component is a linear combination of the 16 attributes of data matrix. The loading values are scaled or standardized in such a manner that the sum of square of loadings within a principal component is equal to one. The loadings are viewed as weights defining the contribution of characters in respective principal component. Like regression coefficients, loadings sign (+ / -) are indicative of the direction of contribution. But unlike regression, only the relative contributions are important, so all signs can be changed without affecting the analysis (Jackson, 1991).

The loadings for first principal component were chosen so as to make its variance as large as possible. Loadings of second principal component were chosen such that the variance of PC_2 is as large as possible, subject to the constraint that PC_1 and PC_2 are uncorrelated. The process was continued to create 16 principal components, but PC's having eigen value less than one is not having any practical significance (Legendre and Legendre, 1984).

Principal components (eigen value greater than one), eigen values (latent root), per cent variability, cumulative per cent variability and component loading of different characters are presented in Table -18.

In the present studyes, the first six principal components with eigen values more than one contributed 77.41 per cent towards the total variability. The principal component with eigen values less than one were considered as non-significant. It was therefore inferred that the essential features of data set had been represented in the first six principal components. The first principal component contributed maximum towards variability (22.08%). The characters viz., number of sympodia per plant (0.42), bundle strength (0.37), number of bolls per plant (0.35), plant height (0.24) and boll weight (0.11) had positive loading and negative loadings of lint index (-0.45), lint yield per plant (-0.35) and seed index (-0.30) explained the maximum variance in the first principal component (PC_1) and signifying their importance in seed cotton yield per plant.

The second principal component (PC_2) described 20.47 per cent of total variance and it reflected significant positive loading of micronaire (0.43), uniformity ratio (0.41), number of bolls per plant (0.29), boll weight (0.28) and oil percentage (0.24) and negative loading of 2.5% span length (-0.40), days to 50% flowering (-0.25) and lint yield per plant (-0.21).

The third principal component (PC_3) was characterized by 12.41 per cent contribution towards the total variability. The characters *viz*, seed cotton yield (0.45), boll weight (0.31), lint yield per plant (0.29), ginning out-turn (-0.53), number of monopodia per plant (-0.40) and micronaire (-0.26) showed the maximum variance in this principal component. Seed cotton yield, boll weight and lint yield per plant loaded positively whereas, ginning out-turn, number of monopodia per plant and micronaire were negatively loaded.

The fourth principal component (PC_4) was conspicuously characterized by high loading of oil percentage (0.52), plant height (0.35), seed index (0.32), ginning out-turn (0.31), bundle strength (0.30), days to 50% flowering (0.25), number of monopodia per plant (0.18) and number of sympodia per plant (0.17) which were positively loaded. Number of bolls per plant (-0.11) and uniformity ratio (-0.07) were negatively loaded. Contribution of this principal component towards the total variability was 9.41 per cent.

Similarly, the fifth principal component (PC_5) and sixth (PC_6) contributed 7.3 per cent and 5.73 per cent , respectively towards total variability. In $PC_{5\,,}$ seed cotton yield per plant (-0.55), number of monopodia per plant (-0.45), 2.5% span length (-0.28), oil percentage (-0.23) and uniformity ratio (-0.22) were negatively loaded and boll weight (0.33), lint yield per plant (0.23) and plant height (0.19) positively loaded.

While, PC_6 was characterized by high loading value for boll weight (0.3), oil percentage (0.27) and 2.5% span length (0.25) as positive and day to 50% flowering (-0.68), seed index (-0.25) and lint index (-0.25) in negative side.

The PCA scores for 50 cotton genotypes in the first three principal components were computed. Principal component I, II and III were considered as three axes as X, Y and Z and squared distance of each genotype from these three axes were calculated and presented in Table -19.

These three PCA scores for 50 genotypes were plotted in graph to get two dimensional and three dimensional scatter diagrams (Fig-5 and Fig -6).

4.5.3 Cluster analysis

To group the 50 genotypes into various clusters, agglomerative hierarchical cluster analysis was followed. Principal component scores for genotypes were used as a input for clustering in Ward's minimum variance method. The tree like structure called dendrogram (Fig-7) was constructed based on Euclidean^2 distance computed from PCA scores of genotypes.

The 50 genotypes were grouped into 8 clusters. The distribution of genotypes into 8 clusters is presented in Table -20. The mutual relationship between clusters is represented diagrammatically (Fig -8) by taking average intra- and inter- cluster Euclidean^2 distances.

4.5.3.1 Average intra- and inter- cluster Euclidean^2 distance values

The average intra- and inter- cluster Euclidean^2 distance were estimated based on Ward's minimum variance and are presented in the Table -21.

The 50 genotypes were grouped into 8 clusters,by ward's method. Of the 8 clusters formed, cluster V had minimum intra cluster Euclidean^2 distance value of 56.79 followed by cluster VIII (59.75) and cluster III (59.82). The inter cluster

Euclidean^2 distances varied from 86.97 (between cluster III and cluster IV) to 556.96 (cluster II and VII). All the inter-cluster euclidean^2 values were lying between these values.

Cluster I had 3 genotypes. It was nearest to cluster III (101.99) followed by cluster V (135.00) and farthest from cluster VII (248.16) followed by cluster IV (156.79).

Cluster II consisted of 3 genotypes. It was nearest to cluster III (120.09) followed by cluster V (122.18) and farthest from cluster VII (556.96) followed by cluster IV (174.46).

Cluster III was the largest and consisted of 13 genotypes. It was nearest to cluster V (86.93) followed by cluster IV (86.97) and farthest from cluster VII (405.80) followed by cluster VI (126.93).

Cluster IV was consisted of 8 genotypes. It was nearest to the cluster III (86.97) followed by cluster V (92.85) and farthest from cluster VII (428.33) followed by cluster II (174.46).

Cluster V was comprised of 6 genotypes. It was closest to cluster III (86.93) followed by cluster IV (92.85) and farthest from cluster VII (454.16) followed by cluster VIII (142.29).

Cluster VI was comprised of 4 genotypes. It was nearest to cluster V (109.11) followed by cluster IV (117.58) and farthest from cluster VII (438.34) followed by cluster II (166.90).

Cluster VII comprised of only one genotype. It was closest to cluster I (248.16) followed by cluster III (405.80) and farthest from cluster II (556.96) followed by cluster V (454.16).

Cluster VIII was consisted of 12 genotypes. It was closest to cluster III (96.74) followed by cluster IV (113.32) and farthest from cluster VII (452.66) followed by cluster II (148.22).

4.5.3.2 Cluster means

Cluster means were computed for the 16 characters on pooled basis and are presented in Table -22.

Cluster I recorded high mean value for number of monopodia per plant (2.11), where it showed low mean value for number of sympodia per plant (13.68).

Cluster II recorded high mean value for ginning out-turn (37.96), micronaire (4.64) and uniformity ratio (51.07). While it showed low mean value for 2.5% span length (25.85) and bundle strength (21.82).

Cluster III recorded low mean value for days to 50% flowering (56.43).

Cluster IV recorded low mean value for number of monopodia per plant (0.75), where it showed high mean value for boll weight (4.09).

Cluster V registered high mean value for seed index (11.00) and lint index (6.47).

Cluster VI recorded low mean value for ginning out-turn (34.69), where it showed high mean value for oil percentage (21.49).

Cluster VII registered low mean value for plant height (113.6), number of bolls per plant (19.8), boll weight (3.33), seed index (8.033), lint index (4.36), micronaire (2.52), uniformity ratio (42.83), oil percentage (18.35), lint yield per plant (20.83) and seed cotton yield per plant (59.16). While it showed high mean value for days to 50% flowering (61.00), 2.5% span length (35.41) and bundle strength (28.20).

Cluster VIII recorded high mean value for plant height (129.80), number of sympodia per plant (19.37), number of bolls per plant (49.96), lint yield per plant (65.76) and seed cotton yield per plant (188.36).

Table- 8: Mean performance of 50 genotypes of cotton (*Gossypium hirsutum* L.) for 16 characters.

S. No.	Genotype	Plant height (cm)	Days to 50% flowering	No. of monopodia Plant^{-1}	No. of sympodia plant^{-1}	No. of bolls plant^{-1}	Boll weight (g)	Ginning out turn (%)	Seed index (g)
1	CSH 612	120.53	56.33	1.20	14.73	37.30	4.14	**39.29**	7.96
2	TSH 9908	118.53	59.00	2.00	14.53	28.83	**3.13**	35.83	7.90
3	RS 2525	124.13	58.33	1.00	13.20	29.90	4.07	34.96	9.50
4	TCH 1716	135.66	58.33	2.20	13.93	40.66	3.52	35.85	8.16
5	CPD 801	120.80	58.00	0.60	15.33	33.56	3.58	36.68	8.80
6	GJHV 448	107.06	58.33	**2.56**	13.66	29.23	3.65	38.14	7.56
7	KH 140	116.73	57.33	1.33	13.33	37.56	3.24	36.73	**7.40**
8	F 2168	129.20	58.33	1.06	14.06	39.36	3.56	35.56	8.53
9	CNH 1104	120.53	60.00	1.46	13.80	36.06	3.71	36.24	11.40
10	NDLH 1938	125.00	58.33	1.33	14.26	48.30	3.57	34.44	**13.16**
11	LH 2123	127.93	58.00	0.46	15.73	43.86	3.64	36.10	8.20
12	L 604	115.20	58.00	1.43	14.40	39.06	3.92	37.31	9.40
13	BS 51	115.66	56.66	1.66	14.13	36.16	4.12	34.78	8.90
14	CCH 2623	134.73	56.66	1.26	14.60	33.53	4.54	37.90	10.70
15	CSH 3129	124.46	57.33	0.80	13.80	40.13	4.34	35.33	9.46

Cont………

Table-8..

16	CCH 4474	119.06	55.66	1.13	16.73	34.53	4.17	35.14	12.96
17	F 2170	135.13	58.00	0.60	15.00	38.86	4.02	34.54	8.93
18	GISV 216	128.06	**53.66**	2.00	14.26	42.80	3.69	35.01	8.46
19	HS 283	118.06	56.33	0.86	12.86	37.93	3.73	35.47	10.96
20	RAH 336	142.86	57.00	1.80	15.80	37.40	3.92	37.85	10.56
21	RS 2527	126.53	59.00	1.20	14.46	32.50	3.22	37.47	9.46
22	BS 41	116.80	55.33	1.13	15.33	39.30	4.06	35.84	8.76
23	RS 2013	131.93	57.00	1.40	13.93	40.83	3.33	33.35	9.06
24	LH 2132	135.20	58.00	0.73	14.66	39.93	4.22	35.73	9.16
25	P 1752	123.80	56.33	0.93	14.03	35.31	4.18	34.80	12.23
26	BIHANI 251	118.06	55.33	1.13	12.86	43.16	3.79	36.37	9.50
27	SCS 415	119.40	56.33	1.00	**12.60**	39.36	**4.69**	36.05	9.63
28	L 801	**101.40**	54.00	1.26	14.00	33.63	3.53	36.68	8.80
29	HAG 1015	123.06	56.66	1.03	14.60	38.26	3.86	35.87	9.26
30	F 1861	127.13	57.66	0.80	15.93	50.40	3.65	35.09	8.90
31	GSHV 155	117.20	57.66	0.60	14.86	34.06	3.50	37.93	11.30
32	H 1360	109.86	57.00	**0.33**	13.33	39.00	3.91	33.66	8.33
33	CA 7	129.06	54.66	0.73	15.26	42.36	3.60	35.40	7.90
34	TCH 1715	121.00	57.66	2.13	**12.60**	33.60	4.16	36.67	11.03

Cont………

Table-8..

35	CANDTS 55	110.06	58.33	1.60	13.33	36.56	3.20	34.09	10.66
36	NH 630	115.86	57.00	1.13	13.73	46.80	3.32	35.14	9.10
37	RAH 61	130.80	59.33	1.40	20.20	49.63	3.90	36.80	9.10
38	BS 277	105.26	58.66	0.93	18.33	40.60	3.90	33.17	9.53
39	CPD 1050	134.26	57.33	1.73	19.86	45.50	4.03	35.12	9.40
40	GISV 218	128.93	57.33	0.93	19.53	54.00	4.30	34.78	8.96
41	RHC 9854	129.20	58.66	1.40	18.93	50.33	3.96	35.50	9.93
42	BS 279	121.60	56.66	1.53	19.40	53.26	4.20	34.01	9.03
43	MCU 5	130.26	58.33	2.20	19.00	**56.86**	3.30	33.34	8.53
44	ARBH 225	123.33	59.00	1.13	**22.53**	36.83	4.23	35.40	9.33
45	CPD 1019	131.60	56.66	1.60	19.66	52.73	3.80	34.37	9.13
46	ARBH 813	132.86	58.66	1.33	19.13	50.66	4.10	35.63	8.80
47	P 57-6	126.00	58.00	1.66	15.46	51.86	3.96	**32.44**	9.63
48	RAH 216	**137.86**	58.33	0.73	20.33	46.13	3.93	35.65	8.40
49	SURABHI	130.93	58.33	1.60	18.40	51.76	3.30	35.59	7.60
50	LK 861	113.60	**61.00**	1.66	16.53	**19.80**	3.33	35.20	8.03
	Mean	123.64	57.48	1.27	15.62	40.60	3.81	35.60	9.35
	C.V. %	3.89	1.56	15.60	9.14	9.25	7.18	1.71	7.02
	C.D. (5%)	7.80	1.46	0.32	2.31	6.08	0.44	0.99	1.06

Cont……….

Table-8..

S.No.	Genotype	Lint index (g)	2.5% span length (mm)	Micronaire (10^{-6}g/in)	Bundle strength (g/tex)	Uniformity ratio	Oil content (%)	Lint yield plant^{-1} (g)	Seed cotton yield plant^{-1} (g)
1	CSH 612	5.20	26.70	4.03	22.76	49.16	20.82	55.99	142.50
2	TSH 9908	4.40	28.99	3.26	21.93	48.36	19.89	30.44	85.00
3	RS 2525	5.13	**23.700**	4.26	19.83	52.30	20.35	39.06	111.66
4	TCH 1716	4.56	30.88	3.86	22.23	46.93	19.87	49.80	138.75
5	CPD 801	5.10	26.79	4.04	22.53	51.40	21.60	40.05	109.16
6	GJHV 448	4.73	24.53	4.62	21.40	51.20	21.09	34.02	89.58
7	KH 140	4.30	25.95	4.61	21.83	49.63	19.69	42.21	115.00
8	F 2168	4.73	26.03	4.13	21.26	49.93	19.85	46.23	130.00
9	CNH 1104	6.50	28.26	4.44	22.73	50.10	20.65	44.08	121.66
10	NDLH 1938	6.86	28.84	4.39	23.83	51.63	**21.83**	58.53	170.00
11	LH 2123	4.63	26.53	4.47	23.53	51.10	20.36	58.03	160.00
12	L 604	5.63	27.63	4.16	22.36	50.40	20.55	56.42	151.25
13	BS 51	4.80	29.18	3.87	22.86	48.66	20.59	49.55	142.50
14	CCH 2623	6.53	26.96	4.46	22.56	50.30	21.32	54.00	142.50
15	CSH 3129	5.20	30.20	3.89	24.13	50.66	20.76	58.37	165.41
16	CCH 4474	**7.06**	29.36	4.02	24.73	49.90	21.16	48.64	138.33

Cont………

Table-8..

17	F 2170	4.76	26.69	4.31	22.56	50.83	20.92	53.28	154.16
18	GISV 216	4.66	25.71	4.37	21.30	50.93	20.31	52.98	150.00
19	HS 283	6.70	26.41	4.29	21.06	50.73	20.02	47.97	135.00
20	RAH 336	6.86	26.05	**4.83**	21.50	51.73	20.68	49.76	131.66
21	RS 2527	6.63	25.41	3.73	21.76	50.56	20.49	37.04	98.75
22	BS 41	4.90	32.39	4.09	23.03	47.46	21.73	53.77	150.00
23	RS 2013	4.53	31.37	3.69	23.53	46.66	21.23	45.60	136.66
24	LH 2132	5.10	27.37	4.21	23.23	50.56	21.08	59.70	167.08
25	P 1752	6.60	26.82	4.32	21.90	51.36	19.81	47.43	136.25
26	BIHANI 251	5.43	25.98	4.12	21.50	49.43	20.76	57.78	158.75
27	SCS 415	5.43	25.51	3.89	21.46	50.93	20.95	61.39	170.41
28	L 801	5.00	29.06	3.67	22.73	49.23	19.93	39.81	108.75
29	HAG 1015	5.16	28.62	4.03	22.63	49.73	20.74	47.68	132.91
30	F 1861	4.63	26.04	4.04	22.56	51.46	19.66	62.29	177.58
31	GSHV 155	6.86	25.23	4.22	21.80	50.76	20.32	44.61	117.50
32	H 1360	4.50	24.47	4.70	20.00	**52.56**	19.67	49.50	147.08
33	CA 7	4.33	25.10	4.72	**19.66**	50.80	20.66	47.35	133.75
34	TCH 1715	6.33	31.12	3.79	25.13	52.26	20.07	44.61	121.66
35	CANDTS 55	5.53	25.06	4.62	22.06	51.80	20.68	37.90	111.25

Cont………

Table-8..

36	NH 630	4.93	29.32	3.83	22.90	49.83	19.94	52.94	150.83
37	RAH 61	5.30	27.45	4.21	23.06	48.93	20.82	69.00	187.49
38	BS 277	4.73	26.98	4.32	23.26	47.86	19.35	47.72	144.16
39	CPD 1050	5.13	26.35	4.24	23.13	49.03	21.53	54.34	154.77
40	GISV 218	4.80	26.48	4.39	21.76	47.23	21.55	**78.50**	225.77
41	RHC 9854	5.00	25.78	4.39	23.30	46.60	20.12	68.39	192.27
42	BS 279	4.66	25.56	4.47	22.36	49.06	20.17	73.27	215.55
43	MCU 5	4.26	29.62	3.84	23.90	49.30	20.16	64.10	192.33
44	ARBH 225	5.13	27.34	4.36	24.60	47.96	20.38	52.91	149.44
45	CPD 1019	4.80	26.89	3.99	23.63	46.70	21.20	69.45	201.94
46	ARBH 813	5.03	26.56	4.37	22.80	47.86	20.25	68.86	189.44
47	P 57-6	4.66	25.97	3.89	23.00	48.86	20.93	61.83	190.55
48	RAH 216	4.66	26.93	4.25	22.93	49.50	20.89	59.38	166.66
49	SURABHI	**4.20**	27.17	4.21	22.73	47.90	20.72	69.11	194.16
50	LK 861	4.36	**35.41**	**2.52**	**28.20**	**42.83**	**18.35**	**20.83**	**59.16**
	Mean	**5.22**	**27.37**	**4.15**	**22.63**	**49.62**	**20.53**	**52.33**	**147.30**
	C.V. %	8.06	3.43	5.32	4.17	3.56	1.28	14.52	14.20
	C.D. %	0.68	1.52	2.86	0.35	1.53	0.42	12.31	33.91

Note: bold figures for each character indicate maximum and minimum values

Table – 19: PCA scores of 50 genotypes of cotton (*Gossypium hirsutum* L.).

S.No.	GENOTYPE	PCA I X Vector	PCA II Y Vector	PCA III Z Vector
1	CSH 612	20.12	19.06	28.86
2	TSH 9908	19.84	14.87	29.86
3	RS 2525	18.37	19.92	32.036
4	TCH 1716	21.62	17.09	29.22
5	CPD 801	18.64	19.12	32.62
6	GJHV 448	20.44	18.74	26.81
7	KH 140	19.91	18.66	28.61
8	F 2168	20.01	19.05	30.99
9	CNH 1104	18.29	19.32	30.90
10	NDLH 1938	18.74	21.75	32.83
11	LH 2123	20.36	19.74	32.02
12	L 604	19.25	19.05	29.86
13	BS 51	20.06	18.01	31.54
14	CCH 2623	18.98	20.71	30.57
15	CSH 3129	19.59	19.09	33.87
16	CCH 4474	18.09	19.38	32.58
17	F 2170	19.84	19.99	34.22
18	GISV 216	21.32	20.50	27.92
19	HS 283	16.68	20.38	31.15
20	RAH 336	19.81	21.27	27.99
21	RS 2527	17.46	18.22	30.53
22	BS 41	19.55	18.74	32.23
23	RS 2013	20.14	17.73	33.33
24	LH 2132	19.94	19.98	33.56

Cont……..

25	P 1752	17.75	20.39	31.91
26	BIHANI 251	18.89	20.57	30.17
27	SCS 415	19.12	20.83	32.27
28	L 801	18.49	17.29	29.34
29	HAG 1015	19.56	19.12	31.57
30	F 1861	21.44	20.09	31.70
31	GSHV 155	16.58	19.65	30.71
32	H 1360	18.09	20.67	33.16
33	CA 7	20.18	21.54	30.32
34	TCH 1715	19.72	17.88	29.52
35	CANDTS 55	18.42	19.87	30.23
36	NH 630	19.85	18.74	31.00
37	RAH 61	22.62	19.45	30.29
38	BS 277	20.62	17.96	32.85
39	CPD 1050	23.28	20.35	30.66
40	GISV 218	22.16	21.35	33.68
41	RHC 9854	22.84	19.75	30.71
42	BS 279	23.08	20.75	31.70
43	MCU 5	24.51	18.60	31.02
44	ARBH 225	22.17	17.64	32.26
45	CPD 1019	23.17	19.79	32.01
46	ARBH 813	22.97	19.88	30.13
47	P 57-6	22.40	20.56	33.83
48	RAH 216	22.53	19.76	32.56
49	SURABHI	22.73	18.88	30.45
50	LK 861	20.27	8.93	32.44

Table-7: Analysis of variance for yield and yield components in cotton (*Gossypium hirsutum* L .).

Source	d.f.	Plant height(cm)	Days to 50% flowering	No. of monopodia / plant	No. of sympodia / plant	No. of bolls / plant	Boll weight (g)	Ginning-out-turn (%)	Seed index (g)
Mean squares									
Replications	2	0.520	1.500	0.035	0.440	0.573	0.125	0.115	1.045
Treatments	49	235.662**	6.015**	0.718**	18.621**	175.494**	0.407**	5.688**	5.026**
Error	98	23.216	0.812	0.039	2.041	14.106	0.075	0.374	0.431

Source	d.f.	Lint index (g)	2.5% span length (mm)	Micronaire (10^{-6} g/in)	Bundle strength (g/tex)	Uniformity ratio	Oil content (%)	Lint yield /plant (g)	Seed cotton yield / plant (g)
Mean squares									
Replications	2	0.077	1.758	0.059	2.404	0.646	0.098	1.279	1.387
Treatments	49	2.004**	14.993**	0.454**	5.834**	10.423**	1.345**	395.332**	3456.769**
Error	98	0.177	0.884	0.048	0.893	3.133	0.069	57.797	438.199

*** = Significant at 5% level, ** = Significant at 1% level, d.f. =degrees of freedom**

Table - 9: Mean, genetic variability, heritability ($h^2_{(b)}$) and genetic advance as per cent of mean (GAM) for seed cotton yield and yieldcomponents in cotton (*Gossypium hirsutum* L.).

S.No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Plant height (cm)	123.64	101.40	137.86	7.84	6.80	75	12.16
2	Days to 50% flowering	57.48	53.66	61.00	2.77	2.29	68	3.89
3	No. of monopodia plant^{-1}	1.27	0.33	2.56	40.39	37.26	85	70.79
4	No. of sympodia plant^{-1}	15.62	12.60	22.53	17.61	15.04	73	26.49
5	No. of bolls plant^{-1}	40.60	19.80	56.86	20.29	18.06	79	33.12
6	Boll weight (g)	3.81	3.13	4.69	11.29	8.71	60	13.85
7	Ginning out-turn (%)	35.60	32.44	39.29	4.11	3.73	83	6.99
8	Seed index (g)	9.35	7.40	13.16	14.98	13.23	78	24.08
9	Lint index (g)	5.22	4.20	7.06	16.98	14.94	77	27.08
10	2.5% span length (mm)	27.37	23.70	35.41	8.63	7.92	84	14.97
11	Micronaire (10^{-6}g/in)	4.15	2.52	4.72	10.33	8.85	73	15.63
12	Bundle strength(g/tex)	22.63	19.66	28.20	7.04	5.67	65	9.40
13	Uniformity ratio	49.62	42.83	52.56	4.75	3.14	44	4.27
14	Oil content (%)	20.53	18.35	21.83	3.42	3.17	86	6.06
15	Lint yield plant^{-1} (g)	52.33	20.83	78.50	24.93	20.26	66	33.93
16	Seed cotton yield plant^{-1} (g)	147.34	59.16	225.70	25.79	21.52	70	37.01

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

Table-10: Phenotypic (above diagonal) and genotypic (below diagonal) correlations among 16 characters in 50 cotton (*Gossypium hirsutum* L.) genotypes.

Character	Plant height	Days to 50% flowering	No. of mono-podia Plant^{-1}	No. of sympodia Plant^{-1}	No. of bolls plant^{-1}	Boll weight	Ginning out-turn	Seed index	Lint index	2.5% span-length	Uniformity ratio	Micronaire (10-6g/Inch)	Bundle strength (g/Tex)	Oil content (%)	Lint yield Plant^{-1}	Seed cotton yield Plant^{-1}
Plant height	--	0.0912	0.0085	0.3248**	0.3764**	0.1321	-0.0144	-0.0085	0.0248	-0.0588	-0.0233	0.1297	-0.0338	0.2877**	0.3889**	0.3726**
Days to 50% flowering	0.1270	--	0.1243	0.2163**	-0.0758	-0.1954*	-0.0190	-0.0322	-0.0544	0.1045	-0.1738*	-0.1430	0.2915**	-0.2189**	-0.1158	-0.1097
No. of monopodia plant^{-1}	0.0120	0.1379	--	0.0083	-0.0153	-0.1828*	0.0145	-0.0860	-0.0739	0.2288**	-0.2135**	-0.2066*	0.1630*	-0.0501	-0.1119	-0.1003
No. of sympodia plant^{-1}	0.3859**	0.3147**	0.0597	--	0.4656**	0.1200	-0.1792*	-0.0992	-0.1748*	-0.0197	-0.3389**	0.0671	0.2449**	0.0779	0.4526**	0.4669**
No. of bolls plant^{-1}	0.4687**	-0.0946	0.0017	0.5644**	--	0.0303	-0.3737**	-0.0749	-0.2440**	-0.1569	-0.1392	0.2259**	-0.0251	0.2174**	0.8706**	0.9015**
Boll weight	0.2115**	-0.2515**	-0.2792**	0.1833*	0.1236	--	0.0804	0.2487**	0.2475**	-0.1006	0.0312	0.1922*	0.0005	0.2665**	0.3911**	0.3626**
Ginning outturn	-0.0196	-0.0533	0.0635	-0.2379**	-0.4544**	0.0293	--	-0.0429	0.3457**	-0.0774	0.1395	0.0550	-0.1072	0.0944	-0.1433	-0.2937**
Seed index	-0.0130	-0.0492	-0.1125	-0.1764*	-0.0900	0.2893**	-0.0625	--	0.8392**	0.0204	0.2449**	0.1038	0.1316	0.1855*	0.0037	0.0111
Lint index	-0.0047	-0.0550	-0.0987	-0.2979**	-0.3115**	0.2234**	0.3822**	0.8986**	--	-0.0601	0.3053**	0.1104	0.0203	0.1740*	-0.0909	-0.1414
2.5% span length	-0.0805	0.1576	0.2837**	-0.0182	-0.2327**	-0.1544	-0.1128	0.0154	-0.0702	--	-0.4409**	-0.6159**	0.6584**	-0.1252	-0.1537	-0.1420
Uniformity ratio	-0.0827	-0.3186**	-0.3224**	-0.6309**	-0.1175	0.2164**	0.2460**	0.4028**	0.5219**	-0.6387**	--	0.3972**	-0.4169**	0.1644*	-0.1248	-0.1402
Micronaire	0.1995*	-0.2590**	-0.2306**	0.0908	0.3465**	0.2827**	0.0832	0.1875*	0.2172**	-0.7635**	0.6465**	--	-0.4641**	0.2841**	0.2369**	0.2197**
Bundle strength	0.0199	0.4362**	0.2438**	0.4168**	-0.0674	0.0262	-0.1349	0.1312	-0.0157	0.8098**	-0.6582**	-0.6640**	--	-0.1007	-0.0157	-0.0014
Oil content (%)	0.3566**	-0.2474**	-0.0573	0.1037	0.2714**	0.3728**	0.1179	0.2462**	0.2578**	-0.1450	0.2031*	0.3365**	-0.1274	--	0.2936**	0.2726**
Lint yield plant^{-1}	0.5290**	-0.1513	-0.1335	0.5837**	0.9109**	0.4884**	-0.2642**	-0.0066	-0.1649*	-0.2597**	-0.0861	0.4055**	-0.0225	0.4032**	--	0.9870**
Seed cotton yield plant^{-1}	0.4943**	-0.1328	-0.1250	0.5888**	0.9385**	0.4484**	-0.4208**	0.0015	-0.2213**	-0.2306**	-0.1176	0.3669**	-0.0001	0.3663**	0.9854**	--

***,** Significant at 5% and 1% level respectively.**

Table-11: Direct and indirect effects (phenotypic) between seed cotton yield per plant and yield components in 50 genotypes of cotton (*Gossypium hirsutum* L.).

Character	**Plant height**	**Days to 50% flowering**	**No. of mono-podia plant^{-1}**	**No. of sympodia Plant^{-1}**	**No. of bolls plant^{-1}**	**Boll weight**	**Ginning out-turn**	**Seed index**	**Lint index**	**2.5% span-length**	**Uniformity ratio**	**Micronaire**	**Bundle strength**	**Oil content (%)**	**Lint yield Plant^{-1}**
Plant height	**-0.0093**	-0.0008	-0.0001	-0.0030	-0.0035	-0.0012	0.0001	0.0001	-0.0002	0.0005	0.0002	-0.0012	0.0003	-0.0027	-0.0036
Days to 50% flowering	0.0000	**0.0003**	0.0000	0.0001	0.0000	-0.0001	0.0000	0.0000	0.0000	0.0000	-0.0001	0.0000	0.0001	-0.0001	0.0000
No. of monopodia plant^{-1}	0.0001	0.0013	**0.0105**	0.0001	-0.0002	-0.0019	0.0002	-0.0009	-0.0008	0.0024	-0.0022	-0.0022	0.0017	-0.0005	-0.0012
No. of sympodia plant^{-1}	0.0018	0.0012	0.0000	**0.0054**	0.0025	0.0007	-0.0010	-0.0005	-0.0009	-0.0001	-0.0018	0.0004	0.0013	0.0004	0.0025
No. of bolls plant^{-1}	0.0103	-0.0021	-0.0004	0.0127	**0.0274**	0.0008	-0.0102	-0.0020	-0.0067	-0.0043	-0.0038	0.0062	-0.0007	0.0060	0.0238
Boll weight	0.0009	-0.0014	-0.0013	0.0009	0.0002	**0.0071**	0.0006	0.0018	0.0018	-0.0007	0.0002	0.0014	0.0000	0.0019	0.0028
Ginning out-turn	0.0021	0.0028	-0.0021	0.0265	0.0553	-0.0119	**-0.1480**	0.0063	-0.0512	0.0114	-0.0206	-0.0081	0.0159	-0.0140	0.0212
Seed index	-0.0001	-0.0002	-0.0006	-0.0007	-0.0005	0.0017	-0.0003	**0.0068**	0.0057	0.0001	0.0017	0.0007	0.0009	0.0013	0.0000
Lint index	-0.0001	0.0003	0.0004	0.0009	0.0012	-0.0012	-0.0017	-0.0041	**-0.0049**	0.0003	-0.0015	-0.0005	-0.0001	-0.0009	0.0004
2.5% Span length	0.0005	-0.0010	-0.0021	0.0002	0.0015	0.0009	0.0007	-0.0002	0.0006	**-0.0093**	0.0041	0.0057	-0.0061	0.0012	0.0014
Uniformity ratio	-0.0001	-0.0005	-0.0006	-0.0010	-0.0004	0.0001	0.0004	0.0007	0.0009	-0.0012	**0.0028**	0.0011	-0.0012	0.0005	-0.0004
Micronaire	-0.0012	0.0013	0.0019	-0.0006	-0.0021	-0.0018	-0.0005	-0.0010	-0.0010	0.0057	-0.0037	**-0.0093**	0.0043	-0.0026	-0.0022
Bundle strength	0.0001	-0.0007	-0.0004	-0.0006	0.0001	0.0000	0.0003	-0.0003	-0.0001	-0.0016	0.0010	0.0011	**-0.0025**	0.0002	0.0000
Oil content (%)	0.0017	-0.0013	-0.0003	0.0005	0.0013	0.0015	0.0005	0.0011	0.0010	-0.0007	0.0010	0.0016	-0.0006	**0.0058**	0.0017
Lint yield plant^{-1}	0.3657	-0.1089	-0.1052	0.4256	0.8188	0.3678	-0.1348	0.0035	-0.0855	-0.1445	-0.1174	0.2228	-0.0148	0.2761	**0.9405**
Correlation with seed cotton yield plant^{-1}	**0.3726****	**-0.1097**	**-0.1003**	**0.4669****	**0.9015****	**0.3626****	**-0.2937****	**0.0111**	**-0.1414**	**-0.1420**	**-0.1402**	**0.2197****	**-0.0014**	**0.2726****	**0.9870****

*** Significant at 5% level, ** Significant at 1% level, Residual effect = 0.042, Bold and diagonal values indicate direct effects**

Table-12: Direct and indirect effects (genotypic) between seed cotton yield per plant with yield components in 50 genotypes of cotton

(*Gossypium hirsutum* L.).

Character	Plant height	Days to 50% flowering	No. of monopodia plant^{-1}	No. of sympodia plant^{-1}	No. of bolls plant^{-1}	Boll weight	Ginning out-turn	Seed index	Lint index	2.5% span length	Uniformity ratio	Micronaire	Bundle strength	Oil content	Lint yield Plant^{-1}
Plant height	**0.0024**	0.0003	0.0000	0.0009	0.0011	0.0005	0.0000	0.0000	0.0000	-0.0002	-0.0002	0.0005	0.0000	0.0009	0.0013
Days to 50% flowering	0.0022	**0.0176**	0.0024	0.0055	-0.0017	-0.0044	-0.0009	-0.0009	-0.0010	0.0028	-0.0056	-0.0046	0.0077	-0.0044	-0.0027
No. of monopodia plant^{-1}	-0.0001	-0.0012	**-0.0090**	-0.0005	0.0000	0.0025	-0.0006	0.0010	0.0009	-0.0026	0.0029	0.0021	-0.0022	0.0005	0.0012
No. of sympodia plant^{-1}	-0.0015	-0.0013	-0.0002	**-0.0040**	-0.0023	-0.0007	0.0010	0.0007	0.0012	0.0001	0.0025	-0.0004	-0.0017	-0.0004	-0.0023
No. of bolls plant^{-1}	0.0938	-0.0189	0.0003	0.1130	**0.2002**	0.0247	-0.0910	-0.0180	-0.0624	-0.0466	-0.0235	0.0694	-0.0135	0.0543	0.1823
Boll weight	0.0134	-0.0159	-0.0176	0.0116	0.0078	**0.0631**	0.0019	0.0183	0.0141	-0.0097	0.0137	0.0178	0.0017	0.0235	0.0308
Ginning out-turn	0.0004	0.0012	-0.0014	0.0054	0.0102	-0.0007	**-0.0225**	0.0014	-0.0086	0.0025	-0.0055	-0.0019	0.0030	-0.0027	0.0059
Seed index	-0.0033	-0.0127	-0.0290	-0.0454	-0.0232	0.0745	-0.0161	**0.2576**	0.2315	0.0040	0.1038	0.0483	0.0338	0.0634	-0.0017
Lint index	0.0013	0.0145	0.0261	0.0786	0.0822	-0.0590	-0.1009	-0.2372	**-0.2639**	0.0185	-0.1377	-0.0573	0.0042	-0.0680	0.0435
2.5% spanlength	0.0013	-0.0025	-0.0044	0.0003	0.0036	0.0024	0.0018	-0.0002	0.0011	**-0.0156**	0.0099	0.0119	-0.0126	0.0023	0.0040
Uniformity ratio	0.0022	0.0084	0.0085	0.0166	0.0031	-0.0057	-0.0065	-0.0106	-0.0137	0.0168	**-0.0263**	-0.0170	0.0173	-0.0053	0.0023
Micronaire	-0.0048	0.0062	0.0055	-0.0022	-0.0083	-0.0068	-0.0020	-0.0045	-0.0052	0.0183	-0.0155	**-0.0239**	0.0159	-0.0080	-0.0097
Bundle strength	-0.0007	-0.0156	-0.0087	-0.0149	0.0024	-0.0009	0.0048	-0.0047	0.0006	-0.0289	0.0235	0.0237	**-0.0357**	0.0045	0.0008
Oil content (%)	0.0049	-0.0034	-0.0008	0.0014	0.0037	0.0051	0.0016	0.0034	0.0036	-0.0020	0.0028	0.0046	-0.0018	**0.0138**	0.0056
Lint yield plant^{-1}	0.3830	-0.1096	-0.0966	0.4226	0.6595	0.3536	-0.1913	-0.0048	-0.1194	-0.1880	-0.0623	0.2936	-0.0163	0.2919	**0.7240**
Correlation with seed cotton yield plant^{-1}	**0.4943****	**-0.1328**	**-0.1250**	**0.5888****	**0.9385****	**0.4484****	**-0.4208****	**0.0015**	**-0.2213****	**-0.2306****	**-0.1176**	**0.3669****	**-0.0001**	**0.3663****	**0.9854****

* = Significant at 5% level, ** = Significant at 1% level, Residual effect = 0.04, Bold and diagonal values indicate direct effects

Table -13: Contribution of different characters towards genetic divergence in 50 cotton (*Gossypium hirsutum* L.) **genotypes.**

S. No.	Character	Contribution towards divergence (%)	Times ranked first
1	Plant height (cm)	5.80	71
2	Days to 50%flowering	2.94	36
3	No. of monopodia plant^{-1}	13.71	168
4	No.of sympodia plant^{-1}	6.86	84
5	No.of bolls plant^{-1}	3.59	44
6	Boll weight (gm)	1.96	24
7	Ginning out turn(%)	15.92	195
8	Seed index (g)	10.12	124
9	Lint index (g)	3.27	40
10	2.5% span length (mm)	14.86	182
11	Uniformity ratio	0.00	0
12	Micronaire (10-6g/inch)	3.10	38
13	Bundle strength (g/tex)	1.06	13
14	Oil content (%)	14.12	173
15	Lint yield plant^{-1} (g)	0.08	1
16	Seed cotton yield plant^{-1} (g)	2.61	32

Table-14 : Average intra-and inter-cluster D^2 values among eight clusters in 50 cotton (*Gossypium hirsutum* L.) **genotypes.**

Cluster No	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**
I	**15.99** **(3.99)**	28.13 (5.30)	29.34 (5.41)	27.66 (5.259)	40.01 (6.32)	33.47 (5.78)	61.00 (7.81)	133.50 (11.55)
II		**19.05** **(4.36)**	42.79 (6.54)	38.93 (6.23)	38.91 (6.23)	55.02 (7.41)	62.92 (7.93)	151.93 (12.32)
III			**35.02** **(5.91)**	43.54 (6.59)	51.90 (7.20)	55.64 (7.44)	55.99 (7.48)	153.15 (12.37)
IV				**0.00** **(0.00)**	38.39 (6.19)	64.01 (8.00)	85.65 (9.25)	105.36 (10.26)
V					**39.67** **(6.29)**	66.59 (8.16)	64.92 (8.05)	96.47 (9.82)
VI						**0.00** **(0.00)**	108.44 (10.41)	175.43 (13.24)
VII							**0.00** **(0.00)**	180.30 (13.42)
VIII								**0.00** **(0.00)**

Note: Bold and diagonal values indicate intra-cluster D^2 distance; figures in parentheses are D values

Table-15: The nearest and the farthest cluster from each cluster based on D^2 values.

Cluster No.	Nearest cluster with D^2 values	Farthest cluster with D^2 values
I	IV (27.66)	VIII (133.50)
II	I (28.13)	VIII (151.93)
III	I (29.34)	VIII (153.15)
IV	I (27.66)	VIII (105.36)
V	IV (38.39)	VIII (96.47)
VI	I (33.47)	VIII (175.43)
VII	III (55.99)	VIII (180.30)
VIII	V (96.47)	VII (180.30)

Note: Values in parentheses indicate D^2 values

Table -16: Clustering pattern of 50 cotton (*Gossypium hirsutum* L.) **genotypes by Tocher's method.**

Cluster No.	No. of genotypes	Name of the genotype
I	13	F-2170, LH-2132, CSH-3129, HAG-1015, LH-2123, SCS-415, F-2168, RS-2525, HIHANI-251, L-604, BS-51, NH-630, CPD-801
II	12	RHC-9854, ARBH-813, RAH-61, SURABHI, RAH-216, CPD-1050, CPD-1019, ARBH-225, BS-279, GISV-218, F-1861, P-57-6
III	17	HS-283, P-1752, GSHV-155, CNH-1104, CANDTS-55, CCH-4474, CCH-2623, RS-2527, NDLH-1938, RAH-336, CA-7, KH-140, CSH-612, TCH-1715, L-801, BS-41, GISV-216
IV	1	RS-2013
V	4	TSH-9908, TCH-1716, MCU-5, BS-277
VI	1	H-1360
VII	1	GJHV-448
VIII	1	LK-861

Table -17: Mean values of eight clusters estimated by Tocher's method from 50 genotypes of cotton (*Gossypium hirsutum* L.).

Cl No	**Plant height (cm)**	**Days to 50% flowering**	**No. of monopodia plant^{-1}**	**No.of sympodia plant^{-1}**	**No.of bolls plant^{-1}**	**Boll weight (g)**	**Ginning out-turn (%)**	**Seed index (g)**	**Lint index (g)**	**2.5% span length (mm)**	**Micronaire (10^{-6}g/in)**	**Bundle strength (g/tex)**	**Uniformity ratio**	**Oil content (%)**	**Lint yield Plant^{-1} (g)**	**Seed cotton yield Plant^{-1} (g)**
I	123.39	57.38	0.97	14.16	39.11	3.93	35.72	9.10	5.08	27.19	4.09	22.37	50.44	20.65	52.34	146.47
II	129.54	58.00	1.32	**19.11**	**49.42**	**3.94**	35.03	9.01	4.83	26.54	4.23	22.99	48.42	20.69	**65.61**	**187.13**
III	121.85	**56.72**	1.29	14.37	37.22	3.77	36.29	**10.22**	**5.93**	27.32	4.27	22.37	50.49	20.60	47.45	130.85
IV	**131.93**	57.00	1.40	13.93	40.83	3.33	**33.35**	9.06	4.53	31.37	3.69	23.53	46.66	**21.23**	45.60	136.66
V	122.43	58.58	1.83	16.45	41.74	3.46	34.55	8.53	4.49	29.11	3.82	22.83	48.11	19.82	48.01	140.06
VI	109.86	57.00	**0.33**	**13.33**	39.00	3.91	33.66	8.33	4.50	**24.47**	**4.70**	**20.00**	**52.56**	19.67	49.50	147.08
VII	**107.06**	58.33	**2.56**	13.66	29.23	3.65	**38.14**	**7.56**	4.73	24.53	4.62	21.40	51.20	21.09	34.02	89.58
VIII	113.60	**61.00**	1.66	16.53	**19.80**	**3.33**	35.20	8.03	**4.36**	**35.41**	**2.52**	**28.20**	**42.83**	**18.35**	**20.83**	**59.16**

Note: Bold figures are minimum and maximum values

Table-18: Eigen values, proportion of the total variance represented by first six principal components, cumulative percent variance and component loading of different characters in cotton (*Gossypium hirsutum* L.).

	PC_1	PC_2	PC_3	PC_4	PC_5	PC_6
Eigene Value (Root)	**3.53**	**3.27**	**1.98**	**1.50**	**1.16**	**0.91**
% variance Explained	**22.08**	**20.47**	**12.41**	**9.41**	**7.30**	**5.73**
cumulative per cent variance Explained	**22.08**	**42.55**	**54.96**	**64.37**	**71.67**	**77.41**
Plant height (cm)	0.24	0.16	0.08	0.35	0.19	0.00
Days to 50% flowering	0.10	-0.25	0.14	0.25	0.08	-0.68
No. of monopodia plant^{-1}	0.19	-0.13	-0.40	0.18	-0.45	0.03
No.of sympodia plant^{-1}	0.42	-0.09	0.01	0.17	0.08	-0.15
No.of bolls plant^{-1}	0.35	0.29	0.06	-0.11	-0.19	-0.17
Boll weight (g)	0.11	0.28	0.31	0.15	0.33	0.30
Ginning out-turn (%)	-0.10	-0.08	-0.53	0.31	0.05	0.23
Seed index (g)	-0.30	0.16	0.11	0.32	-0.12	-0.25
Lint index (g)	-0.45	0.00	-0.11	0.23	-0.01	-0.25
2.5% span length (mm)	-0.01	-0.40	0.11	0.14	-0.28	0.25
Micronaire (10g/Inch)	-0.01	0.43	-0.26	0.16	0.07	-0.17
Bundle strength (g/Tex)	0.37	-0.22	0.07	0.30	0.06	0.10
Uniformity ratio	-0.06	0.41	-0.02	-0.07	-0.22	0.00
Oil content (%)	-0.03	0.24	0.16	0.52	-0.23	0.27
Lint yield plant^{-1} (g)	-0.35	-0.21	0.29	0.16	0.23	0.13
Seed cotton yield plant^{-1} (g)	-0.04	0.02	0.45	-0.01	-0.55	-0.03

PC = Principal component

Table-20: Clustering pattern of 50 cotton (*Gossypium hirsutum* L.) genotypes by Ward's minimum variance method.

Cluster No.	No. of Genotypes	Name of the Genotypes
I	3	TSH-9908, TCH-1716, TCH-1715
II	3	CCH-2623, RAH-336, GJHV-448
III	13	KH-140, CA-7, GISV-216, F-2168, F-1861, LH-2123, L-604, BIHANI-251, CSH-612, BS-51, HAG-1015, NH-630, L-801
IV	8	RS-2525, SCS-415, F-2170, LH-2132, CSH-3129, CPD-801, H-1360, BS-277
V	6	CNH-1104, CANDTS-55, HS-283, P-1752, RS-2527, GSHV155
VI	4	NDLH-1938, CCH-4474, BS-41, RS-2013
VII	1	LK-861
VIII	12	RAH-61, SURABHI, RHC-9854, ARBH-813 , ARBH-225, CPD-1050, CPD-1019, GISV-218, RAH-216, BS-279, P-57-6, MCU-5

Table-21: Average intra- and inter-cluster Eucledian^2 values among eight clusters in 50 cotton (*Gossypium hirsutum* L.) genotypes.

Cluster No.	I	II	III	IV	V	VI	VII	VIII
I	**64.23**	139.86	101.99	156.79	135.00	146.51	248.16	136.78
II		**100.18**	120.09	174.46	122.18	166.90	556.96	148.22
III			**59.82**	86.97	86.93	126.91	405.80	96.74
IV				**69.74**	92.85	117.58	428.33	113.32
V					**56.79**	109.11	454.16	142.29
VI						**79.65**	438.34	135.75
VII							**0.00**	452.66
VIII								**59.75**

Note: Bold and diagonal values indicate intra-cluster distance

Table-22: Mean values of eight clusters estimated by Ward's minimum variance method from 50 genotypes of cotton (*Gossypium hirsutum* L.).

Cluster No	Plant height (cm)	Days to 50% flowering	No. of monopodia plant^{-1}	No.of sympodia plant^{-1}	No.of bolls plant^{-1}	Boll weight (g)	Ginning out-turn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Micronaire (10^{-6}g/in)	Bundle strength (g/tex)	Uniformity ratio	Oil content (%)	Lint yield Plant^{-1} (g)	Seed cotton yield Plant^{-1} (g)
I	125.06	58.33	**2.11**	**13.68**	34.36	3.60	36.12	9.03	5.10	30.33	3.64	23.10	49.18	19.94	41.61	115.13
II	128.22	57.33	1.87	14.68	33.38	4.04	**37.96**	9.61	6.04	**25.85**	**4.64**	**21.82**	**51.07**	21.03	45.93	121.25
III	120.61	**56.43**	1.17	14.39	40.82	3.69	36.10	8.64	4.88	27.06	4.16	22.14	50.02	20.30	51.48	142.60
IV	121.78	57.70	**0.75**	14.53	37.67	**4.09**	35.01	9.17	4.99	26.46	4.20	22.12	50.89	20.58	51.13	146.14
V	119.36	57.94	1.11	13.89	35.40	3.59	36.00	**11.00**	**6.47**	26.20	4.27	21.88	50.88	20.33	43.17	120.06
VI	123.20	56.58	1.25	15.06	40.74	3.78	**34.69**	10.99	5.84	30.49	4.05	23.78	48.91	**21.49**	51.63	148.75
VII	**113.60**	**61.00**	1.66	16.53	**19.80**	**3.33**	35.20	**8.03**	**4.36**	**35.41**	**2.52**	**28.20**	**42.83**	**18.35**	**20.83**	**59.16**
VIII	**129.80**	58.05	1.43	**19.37**	**49.96**	3.91	34.86	8.98	4.80	26.84	4.22	23.10	48.24	20.73	**65.76**	**188.36**

Note: Bold figures are minimum and maximum values

CHAPTER - V

DISCUSSION AND CONCLUSIONS

The results obtained for 16 quantitative and qualitative characters in 50 genotypes of cotton for different genetic parameters are discussed character-wise and presented hereunder the following headings.

5.1 Genetic variability, heritability and genetic advance as per cent of mean

5.2 Character association

5.3 Path coefficient analysis

5.4 Genetic divergence

5.1 Genetic variability, heritability and genetic advance as per cent of mean

The success of any breeding programme depends upon the quantum of genetic variability present in the material for exploitation. Most of the quantitative characters are highly influenced by the environment. Hence, the phenotypic variability among the genotypes does not give a true picture of the heritable and non-heritable components of variation.

Burton (1952) and Swarup and Chaugle (1962) indicated that the genetic variability together with the heritability would give a better idea on the amount of genetic advance expected from selection. The magnitude of heritable variability is the most important aspect of genetic contribution of the breeding material, which has a close relationship on its response to selection (Panse, 1957).

Fifty cotton genotypes studied in the present investigation differed statistically for all the characters. The results obtained on the genetic variability, heritability and genetic advance as per cent of mean are discussed here under.

5.1.1 Plant height (cm)

The estimates of phenotypic and genotypic coefficient of variation were low for plant height and similar results were observed by Sangeetha (1998), Deshpande and Baig 2003) ,Leela Pratap (2006), Eswararao (2008), Neelima *et al*. (2008) and Vijayalaxmi (2008). High heritability coupled with moderate genetic advance as per cent of mean indicated the presence of both additive and non-additive gene action in the inheritance of this trait. The above findings are in broad agreement with Sangeetha (1998), Neelam and Potdukhe (2002), Roy (2006), Preetha and Raveendran (2007), Sakthi *et al.(*2007) and Padmavathi (2008).

5.1.2 Days to 50% flowering

This character exhibited low phenotypic and genotypic coefficients of variation. These results are in conformity with the findings of Reddy (2001), Neelam and Potdukhe (2002), Altaher and Singh (2003b), Narisireddy and Ratnakumari (2004), Karunakar Raju (2005), Prasad *et al*. (2005), Leela Pratap (2006) ,Eswararao (2008), Neelima *et al*. (2008), Padmavathi (2008) and

Vijayalaxmi (2008). High heritability coupled with low genetic advance as per cent of mean revealed the predominance of non-additive type of gene action in the inheritance of this trait. Sangeetha (1998), Reddy (2001), Muraleedhar (2005), Roy (2006) and Padmavathi (2008) also noted similar results.

5.1.3 Number of monopodia per plant

The PCV and GCV values were high for number of monopodia per plant. Similar findings were reported by Neelam and Potdukhe (2002), Altaher and Singh (2003b), Kaushik *et al.* (2003), Ravikumar (2004), Sivaprasad *et al.* (2004 b), Karunakar Raju (2005), Prasad *et al.* (2005), Kumari and Chamundeswari (2005), Tuteja *et al.*(2006), Verma *et al.* (2006), Gitte *et al.* (2007), Eswararao(2008), Kalpande *et al.*(2008), Neelima *et al.*(2008), Padmavathi (2008), and Vijayalaxmi (2008). High heritability coupled with high genetic advance as per cent of mean was observed for this trait, indicating the role of additive gene action (Girase and Mehetre, 2002; Kaushik *et al,* 2003; Karunakar Raju, 2005; Leela Pratap, 2006; Verma, *et al,* 2006; Eswararao, 2008; Padmavathi, 2008 and Vijayalaxmi, 2008).

5.1.4 Number of sympodia per plant

The estimates of PCV and GCV were moderate for number of sympodia per plant. High heritability coupled with high genetic advance as per cent of mean revealed predominance of additive type of gene action in the inheritance of this trait. These results are in agreement with the findings of Gururajan (2000), Reddy (2001), Kiran (2003) and Vijayalaxmi (2008).

5.1.5 Number of bolls per plant

The estimates of PCV and GCV were high and moderate, respectively. The results are in broad agreement with the results reported by Laxman and Ganesh (2003), Gururajan and Sundar (2004), Narisireddy and Ratnakumari (2004), Sivaprasad *et al.* (2004 b), Kale *et al.* (2006), Leela Pratap (2006), Tuteja *et al.* (2006), Gitte *et al.* (2007), Reddy and Reddy (2007) and Padmavathi (2008). High heritability coupled with high genetic advance as per cent of mean for this trait revealed the presence of additive gene action. Similar findings were earlier reported by Rao and Reddy (2001), Reddy (2001), Girase and Mehetre (2002), Neelam and Potdukhe (2002), Kaushik *et al.* (2003), Ravikumar (2004), Sivaprasad *et al.* (2004a), Leela Pratap (2006), Roy (2006), Padmavathi (2008) and Vijayalaxmi (2008).

5.1.6 Boll weight (g)

The estimates of PCV and GCV were moderate and low respectively. The results are in broad agreement with the results reported by Reddy (2001), Altaher and Singh (2003b), Eswararao (2008), Neelima *et al*. (2008) and Vijayalaxmi (2008). Moderate heritability coupled with moderate genetic advance as per cent of mean was recorded for this trait, indicating the role of both additive and non-additive gene action. The above findings are in broad agreement with Gururajan (2000) and Gururajan and Sundar (2004).

5.1.7 Ginning-out turn (%)

Low estimates of phenotypic and genotypic coefficients of variation were observed for ginning out-turn. Reddy (2001), Rao and Reddy (2001), Muraleedhar (2005), Prasad *et al.* (2005),Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008) also reported similar findings for this trait. High heritability and low genetic advance as per cent of mean were recorded for this trait revealed the presence of non-additive gene action. Similar findings were earlier reported by Gururajan (2000), Rao and Reddy (2001), Neelam and Potdukhe (2002), Karunakar Raju (2005), Leela Pratap (2006), Verma *et al. (*2006), Vijayalaxmi (2008) and Do Thi Ha An *et al.* (2008) .

5.1.8 Seed index (g)

The estimates of PCV and GCV were moderate for seed index. These results are in broad agreement with those reported by Rao and Reddy (2001), Reddy (2001), Neelam and Potdukhe (2002), Altaher and Singh (2003b), Laxman and Ganesh (2003), Neelima *et al.* (2008) and Vijayalaxmi (2008). High heritability and high genetic advance as per cent of mean indicated the predominance of additive type of gene action. Hence, direct selection would be effective for this trait. Rao and Reddy (2001), Ravikumar (2004), Karunakar Raju (2005), Padmavathi (2008) and Vijayalaxmi (2008) reported similar findings.

5.1.9 Lint index (g)

The estimates of PCV and GCV were moderate However, the results are in broad agreement with those reported by Laxman and Ganesh (2003), Muthuswamy *et al.* (2003), Patnaik *et al.* (2004), Gururajan and Sundar (2004) and Sivaprasad *et al.* (2004b). High heritability coupled with high genetic advance was observed for this character suggesting the role of additive gene action in governing the inheritance of this trait. Thus, direct selection is effective for this trait. Similar results were reported by Reddy (2001), Neelima (2002), Karunakar Raju (2005), Murthy *et al.* (2006), Padmavathi (2008) and Vijayalaxmi (2008).

5.1.10 2.5% span length (mm)

The estimates of PCV and GCV were low for this trait. Reddy (2001), Neelam and Potdukhe (2002), Altaher and Singh (2003b), Prasad *et al.* (2005), Leela Pratap (2006), Tuteja *et al.* (2006), Verma *et al.* (2006), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008) also reported similar findings in their studies for this trait. High heritability coupled with moderate genetic advance as per cent of mean was observed for this trait indicating the presence of both additive and non-additive genes and offers the best possibility of improvement through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects. Similar results were reported by Murthy *et al.* (1994), Siddiqui (1996), Ravi Kumar (2004) and Vijayalaxmi (2008).

5.1.11 Micronaire (10^{-6} g/in)

Moderate and low estimates of PCV and GCV were recorded for this trait. However, the results are in broad agreement with those reported by Reddy (2001), Altaher and Singh (2003b), Prasad *et al.* (2005), Vijayalaxmi (2008) and Eswararao (2008). High heritability coupled with moderate genetic advance as per cent of mean was recorded for this trait, indicating the role of both additive and non-additive gene action (Ravikumar, 2004; karunakar Raju, 2005; Leela Pratap, 2006 and Vijayalaxmi, 2008).

5.1.12 Bundle strength (g/tex)

This trait recorded low phenotypic and genotypic coefficients of variation. Similar results were earlier reported by Reddy (2001), Rao and Reddy (2001), Neelam and Potdukhe (2002), Girase and Mehetre (2002), Altaher and Singh (2003b), Karunakar Raju (2005), Prasad *et al*. (2005), Leela Pratap (2006), Eswararao (2008), Neelima *et al*. (2008), Padmavathi (2008) and Vijayalaxmi (2008). High heritability coupled with low genetic advance as per cent of mean was recorded for this trait indicating the operation of non-additive gene action. Similar results were reported by Rao and Reddy (2001) and Kiran (2003).

5.1.13 Uniformity ratio

For uniformity ratio, low phenotypic and genotypic coefficients of variation were observed. Similar results were earlier reported by Altaher and Singh (2003b), Muraleedhar (2005), Prasad *et al*. (2005), Leela Pratap (2006), Karunakar Raju (2005), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008). Moderate heritability along with low genetic advance as per cent of mean was recorded indicating the importance of non-additive gene action. However, Sangeetha (1998), Neelima (2002), Kiran (2003) and Karunakar Raju (2005) observed high heritability with low genetic advance.

5.1.14 Oil content (%)

For oil percentage, low phenotypic and genotypic coefficients of variation were observed. The above findings are in conformity with the results reported by Agarwal *et al*. (2003) and Nagarajan (1997). High heritability coupled with low genetic advance as per cent of mean was observed in this trait which revealed the importance of non-additive gene action. Similar findings were earlier reported by Nagarajan (1997).

5.1.15 Lint yield per plant (g)

The estimates of phenotypic and genotypic coefficients of variation were high for this trait. Similar results were earlier reported by Dedaniya and Pethani (1994), Deshpande and Baig (2003), Patnaik *et al.* (2004), Leela Pratap (2006), Padmavathi (2008) and Vijayalaxmi (2008). High heritability with high genetic advance as per cent of mean was showed for this trait indicating the involvement additive gene action and operating relatively low environmental and dominance components of the phenotypic variation for this trait. Simple selection for this trait would be more fruitful for further improvement of lint yield. These results were of similar with that of Leela Pratap (2006), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008).

5.1.15 Seed cotton yield per plant

High phenotypic and genotypic coefficients of variation were observed for seed cotton yield per plant (Rao and Reddy, 2001; Reddy, 2001; Neelam and Potdukhe, 2002; Tuteja *et al*, 2003; Muthuswamy *et al*, 2003; Laxman and Ganesh, 2003; Kaushik *et al*, 2003; Sivaprasad *et al*, 2004 b; Gururajan and Sundar, 2004; Narisireddy and Ratnakumari, 2004; Karunakar Raju, 2005; Kumari and Chamundeswari, 2005; Leela Pratap, 2006; Verma *et al*, 2006; Gitte *et al*, 2007; Reddy and Reddy, 2007; Padmavathi, 2008 and Vijayalaxmi, 2008). High heritability coupled with high genetic advance as per cent of mean revealed the importance of additive gene action in the inheritance of this trait. These results are in conformity with the findings of Ahuja and Tuteja (2000), Rao and Reddy (2001), Neelam and Potdukhe (2002), Girase and Mehetre (2002), Pandey *et al.* (2002), Kaushik *et al.* (2003), Sivaprasad *et al.* (2004a), Karunakar Raju (2005), Kumari and Chamundeswari(2005), Kale *et al*. (2006), Leela Pratap

(2006), Murthy *et al.* (2006), Tuteja *et al.* (2006), Verma *et al. (*2006), Preetha and Raveendran (2007), Reddy and Reddy (2007), Roy (2006), Padmavathi (2008) and Vijayalaxmi (2008).

Thus, in the present study, wide genetic variability in terms of PCV and GCV were recorded for the characters number of monopodia per plant, lint yield per plant and seed cotton yield per plant. While, variability was moderate for number of sympodia per plant, seed index and lint index. Low variability was recorded for plant height, days to 50% flowering, ginning out-turn, 2.5% span length, bundle strength, uniformity ratio and oil percentage. High PCV and moderate GCV was recorded for the character number of bolls per plant. Moderate PCV and low GCV was recorded for the characters boll weight and micronaire.

High heritability coupled with high genetic adavance as per cent of mean observed in case of number of monopodia per plant, number of sympodia per plant, number of bolls per plant, seed index, lint index, lint yield per plant and seed cotton yield per plant indicated the importance of additive gene action governing in the inheritance of the above traits. Paul (1978) also reported that, if heritability in broad sense is mainly due to additive gene effects then only it associates with high genetic gain. If the heritability in broad sense is mainly due to non-additive gene effects (dominance and/or epistasis), the genetic gain will be low as observed in case of days to 50% flowering, ginning out-turn, bundle strength, and Oil percentage as indicated by their moderate heritability and low to moderate genetic advance as per cent of mean. The influence of environment on the expression of other traits *viz.,* plant height, boll weight, 2.5% span length, micronaire and uniformity ratio. Which ultimately limits progress under selection. Selection would be rewarding for those traits which show high heritability coupled with high genetic advance as per cent of mean. However, the characters which are governed by non-additive gene action need to be exploited by cyclic hybridization, heterosis breeding, diallel selective mating system and biparental mating system duly adopting standard selection procedures.

5.2 CHARACTER ASSOCIATION

Seed cotton yield is a polygenically controlled complex character resulting from multiplicative interaction of yield components. The cumulative effects of such characters determine the dependent variable yield. These characters play an important role in modifying the system of seed cotton yield as a whole in magnitude as well as in direction. Further, the direct selection for seed cotton yield is not effective as it is a complex quantitative character and much influenced by the environment. The change in one character brings about a series of changes in other characters, since they are interrelated. Therefore, the correlation between yield and yield components are of considerable importance in selection programmes.

In the present study, correlation estimates were obtained for 16 characters in 50 genotypes of cotton and the results are discussed here under.

The perusal of Table -10 revealed that genotypic correlations are in general are higher than phenotypic correlations.This may be due to the relative stability of genotypes as majority of them were subjected to certain amount of selection (Johnson *et al.*,1955).

5.2.1 Plant height (cm)

Plant height recorded significant positive association with number of sympodia per plant, number of bolls per plant, oil percentage, lint yield per plant and seed cotton yield per plant at both genotypic and phenotypic levels, while, boll weight and micronaire at genotypic level only. These results indicated that, an increase in plant height would bring an increase in seed cotton yield per plant through increase in lint yield per plant and number of bolls per plant. These results are in accordance with Dedaniya and Pethani (1994), Samanc and Ozkaynak (2000), Muthu *et al.* (2004), Tuteja *et al.* (2006), Verma *et al*. (2006), Leela Pratap *et al.*(2007), Padmavathi (2008) and Vijayalaxmi (2008).

5.2.2 Days to 50% flowering

At both phenotypic and genotypic levels, days to 50%flowering showed significant positive association with number of sympodia per plant and bundle strength. Where as, it showed significant negative association with boll weight, uniformity ratio and oil percentage. In case of micronaire showed significant negative association at genotypic level only. Ladole and Meshram (2000), Siva Prasad (2003), Muraleedhar (2005), Karunakar Raju (2005), Leela Pratap *et al.* (2007), Padmavathi (2008) and Vijayalaxmi (2008) also noted the similar findings.

5.2.3 Number of monopodia per plant

At both genotypic and phenotypic levels, this trait exhibited significant and positive association with 2.5% span length and bundle strength. It showed significant negative association with boll weight, uniformity ratio and micronaire. These results are in conformity with the previous reports of Reddy (2001), Siva Prasad (2003), Muraleedhar (2005), Leela Pratap *et al.* (2007) and Vijayalaxmi (2008).

5.2.4 Number of sympodia per plant

Both genotypic and phenotypic levels, this trait revealed significant and positive association with number of bolls per plant, bundle strength, lint yield per plant and seed cotton yield per plant. It showed significant negative association with ginning out-turn, lint index and uniformity ratio. At genotypic level, this trait showed significant positive association with boll weight, while in negative direction significant association with seed index (Rao *et al,* 2001; Altaher and Singh, 2003b; Sivaprasad, 2003; Muthu *et al,* 2004; Muthuswamy and

Vivekanandan, 2004; Neelima *et al,* 2005; Muraleedhar, 2005; Tuteja *et al,* 2006; Leela pratap, 2007; Eswararao, 2008 and Padmavathi, 2008).

5.2.5 Number of bolls per plant

The character, number of bolls per plant exhibited highly significant and positive association with seed cotton yield per plant and lint yield per plant and significant positive association with oil content (%) and micronaire at both genotypic and phenotypic levels. While, in negative direction significant association was observed with ginning out-turn and lint index.

How ever, at genotypic level, this trait showed significant negative association with 2.5% span length. These results are in agreement with the earlier reports of Dedaniya and Pethani (1994), Murthy (1997), Reddy (2001), Neelima (2002), Altaher and Singh (2003b), Muthu *et al.* (2004), Karunakar Raju (2005), Leela Pratap *et al.*(2007), Sakthi *et al.*(2007), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008).

5.2.6 Boll weight (g)

This trait showed positive and significant association with seed cotton yield per plant, lint yield per plant, oil percentage (%), micronaire, lint index and seed index both at genotypic and phenotypic levels. It possessed significant positive association with uniformity ratio at genotypic level. Similar results are reported by Tyagi (1994a), Dedaniya and Pethani (1994), Ladole and Meshram

(2000), Neelima (2002), Altaher and Singh (2003b), Sivaprasad (2003), Muthu *et al.* (2004), Muthuswamy and Vivekanandan (2004), Neelima *et al.* (2005), Karunakar Raju (2005), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008).

5.2.7 Ginning out-turn (%)

Ginning out-turn recorded significant positive association with lint index where as significant negative association with seed cotton yield per plant at both the levels. It also showed significant positive association with uniformity ratio and significant negative association with lint yield per plant at genotypic level only. These findings are in accordance with Reddy (2001), Neelima (2002), Altaher and Singh (2003b), Mandloi *et al* (2003), Muthu *et al.* (2004), Karunakar Raju (2005), Leela pratap *et al*. (2007), Padmavathi (2008) and Vijayalaxmi (2008).

5.2.8 Seed index (g)

This trait exhibited significant positive association with lint index, uniformity ratio and oil percentage (%) at both the levels and significant positive association with micronaire at genotypic level only. These results are in conformity with the reports of Altaher and Singh (2003b), Mandloi *et al.* (2003), Muthu *et al.* (2004), Karunakar Raju (2005), Neelima *et al.* (2005), Hassan *et al.*

(2005), Leela Pratap *et al.* (2007), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008).

5.2.9 Lint index (g)

This trait possessed highly significant and positive association with uniformity ratio while, at significant level with oil percentage at both genotypic and phenotypic levels and significant positive association with micronaire at genotypic level.

This trait recorded significant negative association with lint yield per plant and seed cotton yield per plant at genotypic level. These results are in conformity with the reports of Reddy (2001), Neelam and Potdukhe (2002), Sivaprasad (2003), Muthu *et al.* (2004), Karunakar Raju (2005), Neelima *et al.* (2005), Murthy *et al.* (2006) and Padmavathi (2008).

5.2.10 2.5% span length (mm)

Both at genotypic and phenotypic levels, this trait showed significant positive association with bundle strength and significant negative association with uniformity ratio and micronaire. It also exhibited significant negative association with lint yield per plant and seed cotton yield per plant. These results are in agreement with the reports of Neelam and Potdukhe (2002), Mandloi *et al.* (2003), Altaher and Singh (2003b), Pankaj Rathore *et al.* (2004), Muthu *et al.*(2004), Muthuswamy and Vivekanandan (2004), Karunakar Raju (2005), Muraleedhar (2005), Tuteja *et al.* (2005b), Leela Pratap *et al.* (2007), Padmavathi (2008) and Vijayalaxmi (2008).

5.2.11 Micronaire (10^{-6} g/in)

This character, micronaire showed significant positive association with oil content (%), lint yield per plant and seed cotton yield per plant and negative association with bundle strength at both the levels. Karunakar Raju (2005), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008) also reported similar results.

5.2.12 Uniformity ratio

At both genotypic and phenotypic levels, this trait recorded significant positive association with micronaire and oil percentage. Where as, it exhibited significant negative association with bundle strength . These results are in conformity with reports by Sivaprasad (2003) and Neelima *et al*. (2005).

5.2.13 Oil content (%)

This trait exhibited significant and positive association with seed cotton yield per plant and lint yield per plant at both genotypic and phenotypic levels. These results are in conformity with the reports by Patel *et al*. (2003) and Hassan *et al*. (2005).

5.2.14 Lint yield per plant (g)

Lint yield per plant had strong positive association with seed cotton yield per plant at both the levels. This is in accordance with Mandloi *et al* (2003), Leela Pratap *et al.*(2007), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008).

Thus, character association studies indicated that plant height, number of sympodia per plant, number of bolls per plant, boll weight, micronaire, oil content (%) and lint yield per plant were found to have significant positive influence on seed cotton yield per plant based on phenotypic and genotypic correlations. Hence, improvement of seed cotton yield may be possible if these above characters are considered in selection programme.

5.3 PATH COEFFICIENT ANALYSIS

The observed correlation between yield and a particular yield component character is the net result of the direct effect of that component and indirect effects through other yield attributes. The total correlation coefficient between yield and its component characters may sometimes be misleading, as it may be an over or under estimate of its association with other characters. Hence, direct selection by correlated response may not prove fruitful. When many characters are affecting a given trait, it is necessary to separate the correlation into direct and indirect effects of cause as devised by Wright (1921) and utilized by Dewy and

Lu (1959) in selection programmes. If the correlation coefficients between causal factor and yield are equal to its direct effect, then the correlation explains the true relationship and direct selection of this trait will be effective. If the correlation coefficient is positive and its direct effect is negative or negligible, then the indirect effects seem to be the cause of correlations. Under such situations, the other factors have to be considered simultaneously.

Sometimes correlation coefficient may be negative, but the direct effect is positive and high. Under these conditions, a restricted simultaneous selection model has to be followed *i.e.,* restrictions are to be imposed to nullify the undesirable indirect effects, in order to make use of the direct effect (Singh and Chaudhary 1977).

The results obtained by path analysis in the present study for the fibre and other related components with the seed cotton yield and estimates of direct and indirect contributions towards yield are discussed character wise hereunder.

5.3.1 Plant height (cm)

Plant height exhibited low negative direct effect (-0.0093) and positive significant phenotypic correlation with seed cotton yield per plant (0.3726**). It had positive indirect effect mainly through lint yield per plant (0.3657). The negligible negative direct effect *via* micronaire (-0.0012) was nullified by high positive indirect effect *via* lint yield per plant and thus gave significant positive correlation with seed cotton yield per plant. Hence, selection could be exercised indirectly via lint yield per plant which exhibited positive indirect effect. These results are in conformity with the reports of Ladole and Meshram (2000), Karunakar Raju (2005), Verma *et al.*(2006), Padmavathi (2008) and Vijayalaxmi (2008).

5.3.2 Days to 50% flowering

Days to 50% flowering exerted low positive direct effect (0.0003) and negative phenotypic correlation with seed cotton yield per plant (-0.1097). It had positive indirect effect mainly through ginning out-turn (0.0028) and negative indirect effect mainly lint yield per plant (-0.1089). The positive direct effect and indirect effect through lint yield per plant, leaving a low negative correlation with seed cotton yield. The direct effect is positive and correlation is negative and non-significant. Further, selection could be done indirectly *via* the positive direct effect *i.e.,* ginning out-turn for seed cotton yield improvement. These results are in agreement with Sangeetha (1998), Tuteja *et al.* (2006), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008).

5.3.3 Number of monopodia per plant

Number of monopodia per plant exhibited positive direct effect (0.0105) and negative phenotypic correlation with seed cotton yield per plant (-0.1003). It had positive indirect effect mainly through micronaire (0.0019) and negative indirect effect mainly lint yield per plant (-0.1052). The positive direct effect and indirect effect through lint yield per plant, leaving a low negative correlation with seed cotton yield. The direct effect is positive and correlation is negative and non-significant. Further, selection could be done indirectly *via* the positive direct effect *i.e*. micronaire for seed cotton yield improvement. These findings were in agreement with the findings of Gururajan (2000), Reddy (2001), Kaushik *et al.* (2003), Altaher and Singh (2003a), Muthu *et al.* (2004) and Eswararao (2008).

5.3.4 Number of sympodia per plant

Number of sympodia per plant showed positive direct effect (0.0054) and positive significant phenotypic correlation with seed cotton yield per plant (0.4669**). The indirect effects mainly *via* plant height (-0.0030) and uniformity ratio (-0.0010) were low and negative. However, the indirect effect was mainly *via* lint yield per plant (0.4256) was high and positive. The positive direct and indirect effect through lint yield per plant nullified the negative indirect effects, leaving a high significant correlation with seed cotton yield per plant. Ladole and Meshram (2000), Rao *et al.* (2001), Neelima (2002), Kaushik *et al.* (2003), Neelima *et al.* (2005), Verma *et al*. (2006), Leela Pratap *et al.* (2007) and Vijayalaxmi (2008) also reported positive direct effect on seed cotton yield per plant.

5.3.5 Number of bolls per plant

Number of bolls per plant exhibited positive direct effect (0.0274) but significant positive phenotypic correlation with seed cotton yield per plant (0.9015**). It had high positive indirect effects *via* lint yield per plant (0.8188) and low positive indirect effect *via* ginning out-turn (0.0533). While, plant height (-0.0035) and micronaire (-0.0021) showed negative indirect effects. The negative indirect effect *via* plant height and micronaire were nullified by the positive direct and indirect effects *via* lint yield per plant and ginning out-turn leaving a significant positive correlation. The improvement can be aimed through the above traits which showed positive indirect effects. Similar results were reported by Altaher and Singh (2003b), Sivaprasad (2003), Ahuja *et al.*(2004), Muthu *et al.* (2004), Gururajan and Sundar (2004), Saeed *et al.*(2004), Karunakar Raju (2005), Neelima *et al.* (2005), Verma *et al*. (2006), Leela Pratap *et al.* (2007), Sakthi *et al.*(2007), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008).

5.3.6 Boll weight (g)

Boll weight had low positive direct effect (0.0071) but positive significant phenotypic correlation with seed cotton yield per plant (0.3626**). It had high positive indirect effect through lint yield per plant (0.3678) and low positive indirect effect *via.* seed index (0.0017). The indirect effects mainly *via* ginning out-turn (-0.0119) and number of monopodia per plant (-0.0019) were low and negative. The direct effect and indirect positive effects through lint yield per plant and seed index nullified the negative indirect effects through ginning out-turn and number of monopodia per plant leading to a high significant positive correlation with yield. Therefore, selection for improvement of this trait has to be done carefully by lowering the negative indirect effects contributed by ginning out-turn and number of monopodia per plant. Similar results were earlier reported by Neelima (2002), Kaushik *et al.* (2003), Altaher and Singh (2003b), Muthu *et al.* (2004), Gururajan and Sundar (2004), Karunakar Raju (2005), Sakthi *et al.*(2007) and Padmavathi (2008).

5.3.7 Ginning out turn (%)

Ginning out-turn exhibited negative direct effect (-0.1480) and significant negative phenotypic correlation with seed cotton yield per plant (-0.2937**). It showed positive low indirect effects mainly through 2.5% span length (0.0007) which were out weighted by the low negative indirect effects lint yield per plant (-0.1348), number of bolls per plant (-0.0102) and lint index (-0.0017) and thus gave significant negative correlation. Hence, selection for yield could be practiced by increasing the positive indirect effect *via* 2.5% span length. These results are in accordance with those of Ladole and Meshram (2000), Altaher and Singh (2003b), Sivaprasad (2003), Gururajan and Sundar (2004), Karunakar Raju (2005), Eswararao (2008) and Padmavathi (2008).

5.3.8 Seed index (g)

Seed index had low positive direct effect (0.0068) and positive phenotypic correlation with seed cotton yield per plant (0.0111). Positive low indirect effects were recorded *via* ginning out-turn (0.0063) and lint yield per plant (0.0035). The direct effect is positive and low and even correlation is non-significant. Hence seed index is of little importance in seed cotton yield improvement. The results were in agreement with the findings of Gururajan (2000), Rao *et al.* (2001), Reddy (2001), Sivaprasad (2003), Murthy *et al.*(2006), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008).

5.3.9 Lint index (g)

Lint index exhibited low negative direct effect (-0.0049) and negative phenotypic correlation with seed cotton yield per plant (-0.1414). Negative indirect effects mainly through ginning out-turn (-0.0512) and lint yield per plant (-0.0855) out weighted the positive indirect effects through seed index (0.0057) resulting in negative correlation with seed cotton yield per plant. The direct effect is low and correlation is negative and non-significant. So, lint index need not to be considered in seed cotton improvement programme. The results were in accordance with those of Sivaprasad (2003), Muthu *et al.* (2004), Leela Pratap *et al.* (2007) and Padmavathi (2008).

5.3.10 2.5% span length (mm)

2.5% span length exhibited low negative direct effect (-0.0093) and non-significant negative phenotypic correlation with seed cotton yield per plant (-0.1420). Negative indirect effects mainly through number of bolls per plant (-0.0043) and lint yield per plant (-0.1445) out weighted the positive indirect effects through ginning out-turn (0.0114) resulting in negative correlation with seed cotton yield per plant. The direct effect is low and correlation is negative and non-significant. So, 2.5% span length need not to be considered in seed cotton improvement programme. Similar results were also reported by Reddy (2001), Neelima (2002), Sivaprasad (2003), Gururajan and Sundar (2004), Verma *et al.*(2006), Eswararao (2008) and Padmavathi (2008).

5.3.11 Micronaire (10^{-6} g/in)

Micronaire showed low negative direct effect (-0.0093) and significant positive phenotypic correlation with seed cotton yield per plant (0.2197**). The low negative direct effect and low indirect effect mainly through ginning out-turn (-0.0081) were out weighted by the positive indirect effects of lint yield per plant (0.2228). The positive indirect effect mainly through lint yield per plant nullified the negative direct effect and indirect effects through ginning out-turn and there by leading to the positive significant correlation. Hence, selection should be exercised for the above characters which showed positive direct effects for seed cotton yield improvement. These results are in conformity with Dedaniya and Pethani (1994), Karunakar Raju (2005) and Eswararao (2008).

5.3.12 Bundle strength (g/tex)

Bundle strength exhibited low negative direct effect (-0.0025) and negative phenotypic correlation with seed cotton yield per plant (-0.0014). Negative indirect effects mainly through 2.5% span length (-0.0061) and lint yield per plant (-0.0148) out weighted the positive indirect effects through ginning out-turn (0.0159) resulting in negative correlation with seed cotton yield per plant. The direct effect is low and correlation is negative and non significant. So bundle strength need not to be considered in seed cotton improvement programme. Similar results were earlier reported by Muthu *et al.* (2004), Gururajan and Sundar (2004), Karunakar Raju (2005), Eswararao (2008) and Vijayalaxmi (2008).

5.3.13 Uniformity ratio

Uniformity ratio exerted positive low direct effect (0.0028) and negative non-significant phenotypic correlation with seed cotton yield per plant (-0.1420). It had low positive indirect effect mainly through 2.5% span length (0.0041) and negative indirect mainly lint yield per plant (-0.1174). The positive direct effect and indirect effect through lint yield per plant, leaving a low negative correlation with seed cotton yield. The direct effect is positive and correlation is negative and non-significant. Further, selection could be done indirectly *via* the positive direct effect *i.e.,* 2.5% span length for seed cotton yield improvement. These findings are in accordance with the results of Sivaprasad (2003), Karunakar Raju (2005), Murthy *et al. (*2006), Eswararao (2008) and Vijayalaxmi (2008).

5.3.14 Oil content (%)

Oil content showed low positive direct effect (0.0058) and positive significant phenotypic correlation with seed cotton yield per plant (0.2726**). The indirect effects mainly *via* ginning outturn (-0.0140) and plant height (-0.0027) were low and negative. However, the indirect effect mainly *via* lint yield per plant (0.2761) was high and positive. The positive direct and indirect effect through lint yield per plant nullified the negative indirect effects, leaving a significant correlation with seed cotton yield per plant. Similar results were earlier reported by Patel *et al*. (2003) and Punitha and Raveendran (2005).

5.3.15 Lint yield per plant (g)

Lint yield per plant showed high positive direct effect (0.9405) and significant positive phenotypic correlation with seed cotton yield per plant (0.9870**). It had positive indirect effects through number of sympodia per plant (0.0025), number of bolls per plant (0.0238), boll weight (0.0028), ginning out-turn (0.0212), lint index (0.0004), 2.5% span length (0.0014) and oil content (0.0017). As the correlation coefficient between seed cotton yield per plant and lint yield per plant is almost equal to its direct effect, this correlation explains true relationship and a direct selection through lint yield per plant will be effective for seed cotton yield improvement. These results are in agreement with Dedaniya and Pethani (1994), Leela Pratap *et al.* (2007), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008).

The path analysis indicated that number of bolls per plant and lint yield per plant showed direct positive effects and significant correlation with seed cotton yield per plant revealing their true relationship.

In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures the role of possible independent variables which were not included in the study of dependent variable. In the present study, the residual effect observed was very low both at genotypic and phenotypic levels (0.04 and 0.042). So the characters included in the study were clearly explained the direct and indirect effects on the dependent variable.

The present study revealed that major emphasis should be laid on selection process with lint yield per plant and number of bolls per plant without sacrificing desirable fibre quality by adopting restriction selection model.

5.4 GENETIC DIVERGENCE

In hybridization progammes, the diversity of parents is of prime importance, since the crosses made between the genetically divergent parents are likely to throw desirable recombinants in the progenies. It is a difficult task for plant breeder to choose most suitable parents unless provided with the information on genetic variability present in the material.

The multivariate analysis using Mahalanobis' D^2 statistic provides a very useful statistical tool for measuring the amount of genetic diversity in a given germplasm with respect to the characters considered together (Panse and Sukhatme, 1978). Further, the problem of selecting divergent parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discrimination between populations.

The success and usefulness of Mahalanobis' D^2 analysis in quantifying genetic divergence has been studied by Rajarathinam *et al.* (1994), Sumathi and Nadarajan (1995) , Kalsy and Garg (1995), Murthy *et al.* (1995a,b), Kumar *et al.* (2000), Jain and Yadav (2001), Gururajan and Manickam (2002), Altaher and Sing (2003b), Kiran (2003), Ravikumar (2004), Pushpam *et al.* (2004), Muraleedhar (2005), Eswararao (2008), Padmavathi (2008) Vijayalaxmi (2008) and Gopinath *et al.* (2009).

The data collected on sixteen yield contributing characters from fifty genotypes of cotton were subjected to multivariate analysis. Genetic divergence was estimated by using Mahalanobis' D^2 statistic and grouped them into eight clusters. The magnitude of D^2 values suggested that there was considerable variability in the material, which leads to high genetic diversity. The distribution of genotypes in to various clusters was at random revealing that genetic diversity and geographical diversity were not related. This suggests that forces other than geographical separation such as exchange of breeding material, unidirectional selection, genetic drift and variation in recombinants were also responsible for diversity. Similar conculsions were earlier drawn by Sing and Gill (1984), Rajarathinam and Nadarajan (1993), Sumathi and Nadarajan (1995), Kalsy and Garg (1995), Murthy *et al.* (1995a,b), Kumar *et al.* (2000), Jain and Yadav (2001), Gururajan and Manickam (2002), Altaher and Sing (2003b), Kiran (2003), Ravikumar (2004), Pushpam *et al*. (2004), KarunakarRaju *et al.* (2005) Muraleedhar (2005), Eswararao (2008), Padmavathi (2008) Vijayalaxmi (2008) and Gopinath *et al.* (2009).

The results obtained with respect to estimation contribution of various characters towards genetic divergence indicated that ginning out-turn (15.92), 2.5% span length (14.86), oil content (%) (14.12), number of monopodia per plant (13.71), seed index (10.12), number of sympodia per plant (6.86), plant height (5.80), number of bolls per plant (3.59), lint index (3.27), micronaire

(3.10), days to 50% flowering (2.94), seed cotton yield per plant (2.61) and boll weight (1.96), while remaining characters contributed less than one per cent towards genetic divergence. These results are in broad agreement with the earlier findings of Rajarathinam and Nadarajan (1993), Rajarathinam *et al.* (1994), Murthy *et al.* (1995a,b), Kiran (2003), KarunakarRaju *et al.* (2005), Padmavathi (2008) and Gopinath *et al.* (2009).

The relative importance of yield components contributing towards divergence can be judged by comparing the group means of sixteen characters. Cluster II recorded high mean values for seed cotton yield per plant (187.13), lint yield per plant (65.61), boll weight (3.94), number of bolls per plant (49.42) and number of sympodia per plant (19.11); cluster III recorded high mean values for seed index (10.22) and lint index (5.93); cluster IV recorded high mean for plant height (131.93) and oil percentage (21.23); cluster VI recorded high mean for micronaire (4.70) and uniformity ratio (52.56); cluster VII recorded high mean for number monopodia per plant (2.56) and ginning out-turn (38.14) and cluster VIII recorded high mean for days to 50% flowering (61.00), 2.5% span length (35.41) and bundle strength (28.20) .

It can be inferred from the results that, inter cluster D^2 values were greater than intra-cluster D^2 values. Intra-cluster D^2 values ranged from 0.000 (cluster IV, VI,VII and VIII) to 39.678 (cluster V) . The intra-cluster distance indicated the greater diversity among the genotypes grouped in that cluster.

5.4.1 Mahalanobis' D^2 analysis

In the present investigation, 50 accessions of cotton were considered for the assessment of nature of genetic diversity through Mahalanobis' D^2 analysis. Based on the D^2 values for all 1225 pairs of genotypes, 50 genotypes were grouped into eight clusters which indicated that there was considerable genetic diversity in the material studied.

Cluster III was the largest and comprising of 17 genotypes. Cluster I was the second largest with 13 genotypes followed by cluster II with 12 genotypes and cluster V with 4 genotypes which also exhibited similar types of diversity .It could be seen from the results that cluster IV, VI,VII and cluster VIII were solitary clusters. The formation of distinct solitary clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes must be responsible for this genetic diversity.

Genotypes grouped in to the same cluster presumably differ little from one another as the aggregate of characters measured. General notion exists that the larger is the divergence between the genotypes, the higher will be the heterosis (Falconer, 1964). Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters forgetting highly heterotic crosses which are likely to yield a wide range of segregants on which selection can be practiced.

In the present study, inter-cluster distances were worked out considering 16 characters and these distances ranged from 27.66 (between cluster I and IV) to 180.30 (between cluster VII and VIII).

The inter-cluster distance was maximum between cluster VII and VIII (180.30) followed by cluster VI and VIII (175.43), cluster III and VIII (153.15), cluster II and VIII (151.93), cluster I and cluster VIII (133.50) and cluster VI and cluster VII (108.44). This suggested that there is wide genetic diversity between the clusters. Based on these studies, crosses can be made between genotypes of these clusters to obtain desirable transgressive segregants.

Choice of the particular cluster and selection of particular genotype from selected cluster are the two important points to be considered before initiating the crossing programme. Before effecting crosses, the worth of the parents from above mentioned clusters may be established through combining ability studies.

5.4.2 Principal Component Analysis

Results obtained from PCA on the correlation matrix of the traits reduce the dimensionality of the data set by creating six significant principal components having eigen value more than one. The PCA scores for individual genotypes were used for clustering the genotypes as suggested by Anderberg (1993). Results of PCA and cluster analysis are discussed here under.

The first six principal components with eigen value more than one contributed to 77.41 per cent of the variability among 50 genotypes evaluated for 16 traits. Other principal components with eigen values less than one, which were considered non-significant and hence ignored as they are unlikely to have any practical significance. These results are in accordance with the reports of Altaher and Singh (2003a) where six principal components were formed to describe the maximum variance of the data set.

First principal component (PC_1) described maximum variability (22.081%). The characters viz., number of sympodia per plant (0.42), bundle strength (0.37), number of bolls per plant (0.35) and plant height (0.24) and negative loadings of lint index (-0.45), lint yield per plant (-0.35) and seed index(-0.30) explained the maximum variance in the first principal component. The characters viz., number of sympodia per plant, bundle strength and number of bolls per plant had a greatest positive weight on first principal component (PC_1) where as lint index had a substantial negative weight.

The second principal component (PC_2) described 20.47 per cent of total variance and it reflected significant loading of micronaire (0.43), uniformity ratio (0.41), 2.5% span length (-0.40), number of bolls per plant (0.29), boll weight (0.28), days to 50% flowering (-0.25) and oil content (%) (0.24).

The third principal component (PC_3) was characterized by 12.415 per cent contribution towards the total variability. The characters viz., ginning out-turn (-

0.53), seed cotton yield per plant (0.45), number of monopodia per plant (-0.40), boll weight (0.31), lint yield per plant (0.291) and micronaire (-0.26) showed the maximum variance in this principal component.

The fourth principal component (PC_4) was characterized by high loading of oil content% (0.52), plant height (0.35), seed index (0.32), ginning out-turn (0.31), bundle strength (0.30) and days to 50% flowering (0.25) which were positively correlated. Number of bolls per plant (-0.11) was negatively correlated. Contribution of this principal component towards the total variability was 9.41 per cent.

Similarly, principal components fifth (PC_5) and sixth (PC_6) contributed 7.30 per cent and 5.73 per cent respectively towards total variability. High loading value of seed cotton yield per plant (-0.55), number of monopodia per plant (-0.45), number of bolls per plant (0.33), 2.5% span length (-0.28) and oil content (-0.23) in PC_5 and days to 50% flowering (-0.68), boll weight (0.30), oil content (0.27), seed index (-0.25), lint index (-0.25) and 2.5% span length (0.25) in PC_6 was observed.

The analysis thus identified the maximum contributing *i.e.,* days to 50% flowering, seed cotton yield per plant, ginning out-turn, oil percentage, number of monopodia per plant, lint index, micronaire and number of simpodia per plant. It is important for studying the variance as the relative contributions are more important than the signs (indicative of direction) in principal component analysis.

The PCA scores for 50 cotton genotypes were plotted in graph to get the 2D and 3D scattered diagram. These graphs showed wide divergence between the genotypes GSHV-155 and HS-283 from MCU-5 and CPD-1050 signifying their usefulness in cotton breeding.

5.4.3 Hierarchical cluster analysis

The principal component scores of genotypes were used as input for clustering procedures in order to group the genotypes into various clusters and to confirm the results of principal component analysis.

Hierarchical clustering (Ward's minimum variance) method was followed to create the tree like structure called dendrogram based on Euclidean^2 distance (dissimilarity coefficients). Fifty genotypes were grouped into eight clusters and distribution of various genotypes into various clusters were at random indicating the geographical diversity and genetic diversity were not related. Among all the clusters, cluster III was the largest one containing 13 genotypes followed by cluster VIII with 12 genotypes, cluster IV with 8 genotypes, cluster V with 6 genotypes, cluster VI with 4 genotypes, cluster I and cluster II with 3 genotypes each and cluster VII with 1 genotype.

Of the eight clusters formed, maximum intra-cluster distance Euclidean^2 distance was recorded in cluster II (100.18) followed by cluster VI (79.65) and cluster IV (69.74).

The maximum inter-cluster distance was observed between cluster II and cluster VII (556.96) followed by cluster V and cluster VII (454.16) and cluster VII and cluster VIII (452.66). This suggested that there is a wide genetic diversity between these clusters. Based on these studies, crosses can be made between genotypes of these clusters to obtain better and desirable segregants.

Results of the cluster analysis based on PCA scores were compared with the results of the principal component analysis on a visual aid in desecrating clusters in the 2D and 3D scattered diagrams. The genotypes falling in same cluster are plotted closer to each other in scattered diagram.

Brown (1991), Altaher and Singh (2003a), Karunakar Raju *et al.* (2005) Muraleedhar *et al.* (2005), Eswararao (2008), Padmavathi (2008) and Vijayalaxmi (2008) also studied the utilization of principal component analysis combined with clustering of Ward's method in genetic divergence of cotton.

Among eight clusters, cluster VIII recorded high mean value for plant height (129.80), number of sympodia per plant (19.37), number of bolls per plant (49.96), lint yield per plant (65.76) and seed cotton yield per plant (188.36). Where as cluster VII recorded low mean value for plant height (113.6), number of bolls per plant (19.80), lint yield per plant (20.83) and seed cotton yield per plant (59.16). So, the genotypes from these clusters can be used for cotton yield improvement. Among the quality attributes, high mean values for 2.5% span length (35.41) and bundle strength (28.2) recorded in cluster VII. Cluster II recorded high mean values for ginning out-turn (37.96), micronaire (4.64) and uniformity ratio (51.07). Seed index (11.00) and lint index (6.47) recorded high mean value for cluster V. So, the genotypes following in these clusters can be used for cotton fibre improvement. Cluster II recorded low mean value for 2.5% span length and bundle strength. Cluster VII recorded low mean value for seed index, lint index, micronaire and uniformity ratio. So, the crosses between these two distant clusters (Cluster VII and cluster II, cluster II and cluster VII and cluster V and cluster VII) may produce transgressive segregants for 2.5% span length, bundle strength, micronaire, uniformity ratio, seed index and lint index. As far as oil percentage is concerned, cluster VI and cluster VII recorded high and low mean values.

5.4.4 Comparative study of D^2 analysis, principal component analysis and cluster analysis

The grouping of clusters using D^2 analysis, principal component analysis and cluster analysis was compared and the implications are discussed and presented here under.

All the three methods of grouping revealed a single concept of non correspondence of genetic divergence and geographical diversity. In D^2 analysis the intra-and inter-cluster distances are low while in the cluster analysis the distances are high. The same is with the utilization of correlation matrix in principal component analysis derived from covariance matrix. The standardization made the principal component analysis to support the cluster analysis.

Mahalanobis' D^2 statistic and Jackson's principal component analysis are the tools for analyzing multivariate data. The advantage of PCA over D^2 analysis is that it reduces the dimensionality of the data set by creating significant principal components which contributed towards maximum variability of the genotypes. In PCA, standardization of data made attributes to contribute equally towards the divergence studies irrespective of the units taken.

The principal component analysis sorted only significant principal components out of the total 16 attributes. The contribution of the main characters for variance easily identified by the characters loaded on the PC_1 with high loading values. PCA facilitates the in depth analysis for genetic diversity. In D^2 analysis, ginning out-turn, 2.5% span length, oil content, number of monopodia per plant, seed index, number of sympodia per plant, plant height, number bolls per plant, lint index, micronaire and days to 50% flowering contributed maximum for the divergence. While, in PCA characters *viz.*, ginning out-turn in $PC_{3,}$ lint index PC_1 and micronaire in PC_2 significantly contributed towards variability. It can be concluded that the characters which contributed more towards divergence in D^2 analysis were loaded in $PC_{1,}$ PC_2 and $PC_{3.}$

Both D^2 analysis and PCA grouped the 50 cotton genotypes into eight clusters. In D^2 analysis, cluster III is the largest with 17 genotypes followed by cluster I (13 genotypes) and cluster II (12 genotypes) where as in Ward's method, the cluster III is the largest comprising of 13 genotypes followed by cluster VII (12 genotypes) and cluster IV (8 genotypes).

The pattern of distribution of genotypes into different clusters was at random. Furthermore, the two clustering methods grouped differently and clustering pattern for genotypes are not same. There was one solitary cluster formed in Ward's minimum variance method, where as in case of D^2 analysis cluster IV, cluster VI, cluster VII and cluster VIII represent solitary clusters. Genetic diversity was the outcome of several factors along with geographic diversity. Hence, the selection for hybridization should be more based on genetic diversity rather than geographic diversity.

Ward's minimum variance dendrogram (cluster analysis) created sub groups with in a cluster, so relative position of the genotypes within the clusters can be examined by seeing the dendrogram distance. In case of D^2 analysis, we can only know the intra-cluster distance but not the genotypes relative position in the respective cluster.

Of 50 genotypes in general multivariate analysis revealed divergence among the parents GSHV-155, GJHV-448 and LK-861. These parents may be involved in crossing programmes to get heterotic hybrids and / or isolation of superior recombinants in the segregating generations.

CONCLUSIONS

- The analysis of variance revealed significant differences among the genotypes for all the characters studied, indicating that data generated from the above diverse material will yield reliable information.
- From the studies of genetic variability, it revealed that high variability was recorded for number of monopodia per plant, lint yield per plant and seed cotton yield per plant.
- High heritability coupled with high genetic advance as per cent of mean was observed for the characters viz., number of monopodia per plant, number of sympodia per plant, number of bolls per plant, seed index, lint index, lint yield per plant and seed cotton yield per plant. This indicates the predominance of additive gene action and hence, selection may be fruitful to some extent. Where as the other traits viz., days to 50% flowering, ginning out-turn, bundle strength, uniformity ratio and oil content showed moderate to high heritability with low genetic advance indicating the role of non-additive gene action. It may be exploited through heterosis breeding, cyclic hybridization, biparental mating and diallel selective mating system.
- Correlation studies and path analysis indicated strong positive true relationship among number of bolls per plant, oil content and lint yield per plant with seed cotton yield per plant. So improvement of seed cotton yield

may be made through the above traits with desirable fibre qualities by adopting restriction selection model. There is scope for improvement of oil content through cyclic hybridization.

- The results of multivariate analysis revealed the presence of considerable divergence among fifty genotypes. These genotypes were grouped into eight clusters both in the case of D^2 analysis and in Ward's minimum variance method. Clustering pattern suggested that geographical distance may not be the only factor causing genetic divergence in the genotypes. The characters ginning out-turn, 2.5% span length, oil percentage, number of monopodia per plant, seed index and number of sympodia per plant contributed maximum towards genetic divergence among the genotypes.
- Crosses may be planned between genotypes falling under cluster VII (GJHV-448) and cluster VIII (LK-861) followed by cluster VI (H-1360) and cluster VIII (LK-861) to exploit heterosis as well as for recovery of superior recombinants for improvement of seed cotton yield, oil content and fibre quality as per the Mahalanobis' D^2 statistic studies.
- 2D and 3D PCA graphs showed wide divergence between (GSHV-155 and HS-283) and (MCU-5and CPD-1050) signifying their usefulness in cotton breeding to develop high heterotic combinations for seed cotton yield and desirable fibre quality.

- Principal component analysis identified six principal components (PCS), which contributed (77.41) per cent of cumulative variance. The population with high (PC_1) values were characterized by lint index and number of sympodia per plant. Where as, population with high (PC_2) values were characterized by micronaire and uniformity ratio, in (PC_3) characters like ginning out-turn and seed cotton yield per plant showed maximum weightage.

- Agglomerative cluster analysis revealed that wide genetic distance exists between cluster II (CCH-2623, RAH-336 and GJHV-448) and VII (LK-861) followed by cluster V (CNH-1104, CANDTS-55, HS-283, P-1752 , RS-2527 and GSHV-155) and VII (LK-861). Therefore during hybridization programme, selection of parents from these clusters will produce superior segregants for improvement of seed cotton, lint yield and oil content.

- In general, multivariate analysis revealed maximum genetic divergence among GSHV-155, GJHV-448 and LK-861 revealing the scope for exploitation of heterosis with high seed cotton yield and desirable fibre quality.

CHAPTER VI

SUMMARY

The present investigation was carried out during *kharif*, 2008 at Regional Agricultural Research Station, Lam Farm, Guntur with 50 genotypes of cotton (*Gossypium hirsutum* L.).

The mean, genetic variability, heritability, genetic advance as per cent of mean, genetic divergence, character association and the magnitude of direct and indirect effects of yield component traits with seed cotton yield were studied for 16 characters viz., plant height (cm), days to 50% flowering, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), ginning out-turn (%), seed index (g), lint index (g), 2.5% span length (mm), micronaire (10^{-6}g/in), bundle strength (g/tex), uniformity ratio, oil content (%), lint yield per plant (g) and seed cotton yield per plant (g).

The analysis of variance revealed significant differences among the genotypes for all the characters indicating the existence of genetic variability for exploitation. The genotypic coefficients of variation for all the characters were lesser than the phenotypic coefficients of variation indicating the masking effects of the environment. High variability was recorded for number of monopodia per plant, lint yield per plant and seed cotton yield per plant.

High heritability coupled with high genetic advance as per cent of mean was observed for the characters viz., number of monopodia per plant, number of

sympodia per plant, number of bolls per plant, seed index, lint index, lint yield per plant and seed cotton yield per plant. This indicates the predominance of additive gene action and hence, selection may be fruitful to some extent. Where as the other traits viz., uniformity ratio, days to 50% flowering, ginning out-turn, bundle strength, and oil content were showed moderate to high heritability with low genetic advance indicating the role of non-additive gene action. It might be exploited through heterosis breeding, cyclic hybridization, biparental mating and diallel selective mating system.

Correlation studies indicated that the plant height, number of sympodia per plant, number of bolls per plant, boll weight, micronaire, oil percentage and lint yield per plant had significant positive association with seed cotton yield per plant. There is scope for improvement in oil content through cyclic hybridization.

The path analysis indicated considerable positive direct effects of number of bolls per plant and lint yield per plant on seed cotton yield together with significant positive correlation revealing their true relationship. So improvement of seed cotton yield may be aimed *via* number of bolls per plant, oil content and lint yield per plant by preferring these characters during selection.

The results of multivariate analysis revealed that the presence of considerable divergence among fifty genotypes studied. These genotypes were grouped into eight clusters both in case of D^2 analysis and also in Ward's minimum variance method. Clustering pattern suggested that geographical distance may not be the only factor causing genetic divergence in the genotypes studied.

It could be inferred from Mahalanobis' D^2 statistic that ginning out-turn, 2.5% span length, oil percentage, number of monopodia per plant, seed index and number of sympodia per plant contributed maximum towards the divergence. Based on intra and inter-cluster distance among the groups, suggestions were made to attempt crosses for confirming the general combining ability between cluster VII (GJHV-448) and cluster VIII (LK-861) followed by cluster VI (H-1360) and cluster VIII (LK-861) to obtain better and desirable segregants for improvement of seed cotton yield, oil content and fibre quality.

Principal component analysis identified six principal components (PCS), which contributed (77.41) per cent of cumulative variance. The population with high (PC_1) values were characterized by lint index and number of sympodia per plant. Where as, population with high (PC_2) values were characterized by micronaire and uniformity ratio, in (PC_3) characters like ginning out-turn and seed cotton yield per plant showed maximum weightage.2D and 3D PCA graphs showed wide divergence between GSHV-155 and HS-283 and MCU-5 and CPD-1050 signifying their usefulness in the cotton breeding to develop high heterotic combinations for seed cotton yield and desirable fibre quality.

Agglomerative cluster analysis revealed that wide genetic distance exists between cluster II (CCH-2623, RAH-336 and GJHV-448) and VII (LK-861) followed by cluster V (CNH-1104, CANDTS-55, HS-283, P-1752 , RS-2527 and GSHV-155) and VII (LK-861). Therefore, selection of parents from these clusters will produce superior segregants through the process of hybridization for improvement of seed cotton yield, lint yield and oil content.

In general, multivariate analysis revealed that divergence existed among GSHV-155, GJHV-448 and LK-861 revealing the scope for exploitation of heterosis with high seed cotton yield and desirable fibre quality.

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