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

By

KRISHNA KISHORE DHANAVAT
B.Sc.,(Ag.)

THESIS SUBMITTED TO
THE ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY
IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE OF

MASTER OF SCIENCE IN AGRICULTURE

DEPARTMENT OF GENETICS AND PLANT BREEDING
AGRICULTURAL COLLEGE, BAPATLA
ACHARYA N.G.RANGA AGRICULTURAL UNIVERSITY
RAJENDRA NAGAR, HYDERABAD- 500030

2010

CERTIFICATE

Mr. D.KRISHNA KISHORE has satisfactorily prosecuted the course of research and that the thesis entitled "GENETIC DIVERGENCE IN UPLAND COTTON (*Gossypium hirsutum* L.)" submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that the thesis or part there of has not been previously submitted by him for a degree of any university.

Date:

(M. GOPINATH)
Major Advisor
Principal Scientist (Breeding)
RARS, Warangal

CERTIFICATE

This is to certify that the thesis entitled **"GENETIC DIVERGENCE IN UPLAND 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 bonafide research work carried out by **Mr. D. KRISHNA KISHORE** under our guidance and supervision. The subject of thesis has been approved by the Student's Advisory Committee.

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

(M. GOPINATH)
Chairman of the Advisory Committee

Thesis Approved by the Student's Advisory Committee

Chairman:	Dr. M. GOPINATH Principal Scientist (Breeding) RARS, Warangal	______________
Member:	Dr.V. SATYANARAYANA RAO Associate Professor Department of Genetics and Plant Breeding Agricultural College, Bapatla.	______________
Member:	Dr. V. SRINIVASA RAO Associate Professor & Head Department of Statistics and Mathematics Agricultural College, Bapatla.	______________

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF SYMBOLS AND ABBREVIATIONS

AICCIP	All India Coordinated Cotton Improvement Project
ANOVA	Analysis of Variance
ARS	Agricultural Research Station
CICR	Central Institute of Cotton Research
GAM	Genetic Advance as per cent of Mean
GAU	Gujarat Agricultural University
GCV	Genotypic coefficient of variation
HAU	Haryana Agricultural University
JNKVV	Jawaharlal Nehru Krishi Vishwa Vidhyalaya
MAU	Maharashtra Agricultural University
NS	Non Significant
PAU	Punjab Agricultural University
PCV	Phenotypic coefficient of Variation
RARS	Regional Agricultural Research Station
RAU	Rajasthan Agricultural University
S	Significant
TNAU	Tamilnadu Agricultural University
UAS	University of Agricultural Sciences
%	Per cent
°C	Degree Centigrade
df	Degrees of freedom
et al.	and coworkers
g	Grams
g/in	Grams per inch
g/tex	Grams per tex
kg/ha	Kilogram per hectare
No	Number
viz.,	Namely

ACKNOWLEDGEMENTS

Accomplishment of this thesis is the result of benevolence of Almighty. I am thankful to Good Yohava holy father living Good God Jesus Christ and good parishuddatma for giving me strength, from so many troubles, problems and depression which I have undergone during my Post Graduation study and finally saved me.

I deem this unique opportunity to express my abysmal sense of gratitude indebtedness and whole heartful and sincere thanks to the Chairman of my Advisory Committee ***Dr. M. Gopinath****, Principal Scientist (Breeding), Regional Agricultural Research Station, Warangal for his aurulent guidance, sustained interestable supervision with valuable suggestions and steady encouragement to bring out this thesis.*

I am extremely grateful to the members of my advisory committee, ***Dr. V. Satyanarayana Rao****, Associate Professor, Department of Genetics and Plant Breeding and* ***Dr. V. Srinivasa Rao,*** *Associate Professor and Head, Department of Statistics and Mathematics, Agricultural College, Bapatla for their constant encouragement, timely suggestions and advice during the course of investigation and preparation of thesis.*

I am extremely thankful to ***Dr. C. Panduranga Rao****, Professor and Head Department of Genetics and Plant Breeding, Agricultural College, Bapatla and equally owe my deep sense of gratitude for his valuable advice, valuable suggestions, Scholarly guidance and constant encouragement, kind help and wholehearted cooperation through out the course of this investigation and also bringing out this thesis.*

I am sincerely, faithfully, extremely thankful to ***Dr. M. Lal Ahamed****, Assistant Professor, Department of Genetics and Plant Breeding,* ***Dr. J. S. V. Sambamurthy****, Professor, Department of Genetics and Plant Breeding,* ***Dr. P.V. Rama Kumar****, Professor, Department of Genetics and Plant Breeding who have been a constant source of inspiration and saved me from so many difficulties during my research work and course of study.*

I am greatly beholden of vocabulary and owe a deep sense of honour to my beloved parents who gave me this life are ***Dhanavat Radhamma,*** *and* ***Raghupathi Naik*** *B.Sc.,(Ag.) Department of Agriculture Assistant Director of Agriculture, for their love, dedicated efforts in shaping my career since childhood and who have been a constant source of inspiration.*

I am greatly beholden beyond words to express my warmest thanks and inexplicable affection to Brother ***Dr.K.Chandra Sekhar****, Associate Professor, Department of Agronomy, Sister* ***Deepa*** *and children,* ***K. David Keerthan*** *and* ***K.Evangiline*** *without those support and affection and source of inspiration this study would be difficult to complete.*

I am extremely thankful to my classmates, ***P.Kirankumar, G.Eswar Rao, B.Purushotham, G.Chittibabu, T.Abhishekgowda, Mihir Ranjan Mohanthy, Samartlaha, V. Sitaram Babu, M.Sirisha, Phani Madhavi, A. Padmavathi, P.Padmavathi, Y.Pushpareni, Annie Sardus, J.Swapna*** *and* ***A.B.M. Sirisha*** *for their help and valuable suggestions and advices given to me during my research work.*

I acknowledge ***ANGRAU*** *for providing financial assistance in the form of stipend during my postgraduate study.*

Place: **(KRISHNA KISHORE)**
Date:

DECLARATION

I, Mr. **D. KRISHNA KISHORE** here by declare that the thesis entitled **"GENETIC DIVERGENCE IN UPLAND COTTON (*Gossypium hirsutum* L.)"** submitted to the Acharya N.G. Ranga Agricultural University for the degree of Master of Science in Agriculture in the field of **Genetics and Plant Breeding** is the result of the original research work done by me. I also declare that the thesis or any part there of has not been published earlier in any manner.

Date :
Place : Bapatla

(D. KRISHNA KISHORE)

ABSTRACT

Name of the Author	:	**KRISHNA KISHORE DHANAVAT**
Title of the thesis	:	**GENETIC DIVERGENCE IN UPLAND COTTON (*Gossypium hirsutum* L.)**
Faculty	:	Agriculture
Degree to which it is submitted	:	Master of Science in Agriculture
Major field of study	:	Genetics and Plant Breeding
Chairman	:	**Dr. M. GOPINATH**
University	:	Acharya N.G. Ranga Agricultural University
College	:	Agricultural College, Bapatla
Year of submission	:	**2010**

The present investigation was carried out during *kharif*, 2007 at Regional Agricultural Research Station, Lam Farm, Guntur with 60 genotypes of cotton (*Gossypium hirsutum* L.) to study the 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 in respect of 11 characters *viz*., plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed index (g), lint index (g), ginning out-turn (%), 2.5% span length (mm), uniformity ratio and seed cotton yield per plant (g).

The genotypic coefficient of variation for all the characters studied were lesser than phenotypic coefficient of variation indicating the masking effect of the environment. Number of monopodia per plant, number of bolls per plant, seed index, lint index and seed cotton yield per plant showed high variability while plant height, number of sympodia per plant, boll weight and ginning out-

turn recorded moderate variability. High heritability coupled with high genetic advance was noted for plant height, number of bolls per plant, boll weight, seed index, lint index, ginning out-turn and seed cotton yield per plant. This indicates the predominance of additive gene action and direct selection for these traits may be rewarding. High heritability coupled with moderate genetic advance was observed for number of sympodia per plant and uniformity ratio revealing the role of additive and non-additive gene action. The trait 2.5% span length showed moderate heritability and low genetic advance indicating the operation of non-additive gene action.

The correlation studies revealed that plant height, number of bolls per plant and boll weight had significant positive association with seed cotton yield per plant. The path coefficient analysis revealed that number of bolls per plant, boll weight, lint index and uniformity ratio exerted direct positive effects on seed cotton yield per plant. Selection based on these attributes may be helpful in evolving high yielding varieties of upland cotton.

The results of multivariable analysis revealed that the distribution of 60 cotton genotypes into 10 clusters in case of D^2 analysis and into eight clusters in case of cluster analysis was at random indicating the absence of relation between genetic diversity and geographical diversity. Based on D^2 values the intra-and inter –cluster distances among the groups, suggestions were made to attempt crosses after confirming their general combining ability between cluster 8 (H-1246) and cluster 10 (GIHV-53, GJHV-99 / 307and KH-140) followed by cluster 9 (L-604) and cluster 10 (GIHV-53, GJHV-99 / 307 and KH-140) to obtain better and desirable segregants. Using Mahalanobis' D^2 statistic, it could be inferred that the seed index contributed maximum towards genetic divergence followed by seed cotton yield per plant, plant height, boll weight and number of bolls per plant.

Principal Component analysis identified four principal components (PCs) which contributed 91.69 per cent of cumulative variance. The population with high PC_1 values were characterized by seed index and plant height where as, population with high PC_2 values were characterized by seed cotton yield per plant and number of bolls per plant. In PC_3 characters like boll weight and plant height showed maximum weightage.

Based on the cluster analysis Euclidian distance, the crosses between the clusters 3 (CWROK-165, CPD-787, ICMF-230, NDLH-1754, TSH-9727, RS-2169, SES-21 and H-1246) and 6 (CCH-18, MCU-2 and KH-140); 2 (MCU-5, SCS-95, L-761, CNH-3003, LK-861, SRT-1, MCU-9, ARB-9009, Abhadita, L-604, NH-100, ACP-738, GMP-5 and L-603) and 6 (CCH-18, MCU-2 and KH-140) and 1(NA 1325, RS 2141, ARB 8906, SCS-51, L-769, ARB-2005and RAH-3) and 8 (L-864, ARB-784, SCS-101 and Surabhi) may generate transgressive segregants in the next generations.

Therefore, major emphasis should be laid on more number of bolls per plant and simultaneous selection of other traits *viz.*, boll weight, lint index and uniformity ratio in selection process for realizing higher seed cotton yield.

CHAPTER – I

INTRODUCTION

Upland Cotton (*Gossypium hirsutum* L.) is an important commercial crop cultivated in India since ages. It is predominantly a fibre yielding crop that is having potential to offer livelihood security to millions of people. The genus, *Gossypium* belongs to family Malvaceae and includes 44 species out of which *viz.*, *Gossypium arboreum* L., *Gossypium herbaceum* L., *Gossypium hirsutum* L. and *Gossypium barbadense* L. are cultivated. However the American cotton (*Gossypium hirsutum* L.) predominates in cultivation with 90% area.

During 2008-09 in India cotton was cultivated over 93.7 lakh hectares producing 290 lakh bales (170 Kg each) of lint that has accounted for an average productivity of 526 Kg lint/ha (Ministry of Textile, Government of India, 2008-9). It is estimated that by 2010 about 350 lakh bales of cotton lint is required. At the present rate of progress in cotton area, production and productivity levels it could be difficult to reach the demand unless the productivity level of new hybrids is increased substantially.

To produce high yielding hybrids the parents involved in the cross must be genetically diverse with good combining ability. The quantification of degree of divergence present in the population is of immense value in identifying diverse genotypes for recombination breeding programmes to generate desirable recombinants in the progeny. Mahalonobis's D^2 statistic is a powerful tool for quantifying genetic divergence in a given population with respect to characters considered together.

Keeping this in view, present investigation was undertaken to study the genetic divergence present in 60 cotton germplasm accessions with the following objectives.

Objectives

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

ii. To study the association of yield and yield attributing characters among themselves.

iii. To estimate direct and indirect effects of component characters on yield.

iv. To estimate genetic divergence in available germplasm through D^2, PCA, Cluster analysis and to find out the important characters contributing to the genetic divergence.

CHAPTER - II

REVIEW OF LITERATURE

The literature on the main objectives of the present study has been comprehensively reviewed and presented under the following headings.

2.1. Genetic variability

2.2. Heritability and genetic advance 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 different quantitative and qualitative traits in any crop species plays a vital role while formulating an efficient breeding programme. 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 components with the help of genetic parameters like genotypic coefficient of variation.

The literature on genetic variability studies on cotton is reviewed and presented in Table-1.

Table- 1: Review of literature on genetic variability in cotton.

Sl. No.	Character	Wider genetic variability	Narrow genetic variability
1.	Plant height (cm)	Neelam and Potdukhe (2002) Laxman and Ganesh (2003) Patnaik *et al.* (2004) Neelima *et al.* (2005) Tuteja *et al.* (2006)	Sangeetha (1998) Deshpande and Baig (2003) Leela Pratap (2006) Vijayalaxmi (2008) Neelima *et al.* (2008)
2.	No. of monopodia per plant	Neelam and Potdukhe (2002) Altaher and Singh (2003b) Kaushik *et al.* (2003) Sivaprasad *et al.* (2004 b) Karunakar Raju (2005) Tuteja *et al.* (2006) Verma *et al.* (2006) Vijayalaxmi (2008) Neelima *et al.* (2008)	Ahuja and Tuteja (2000) Gururajan (2000) Girase and Mehetre (2002)
3	No. of sympodia per plant	Gururajan (2000) Neelam and Potdukhe (2002) Tuteja *et al.* (2003) Deshpande and Baig (2003) Tuteja *et al.* (2006) Neelima *et al.* (2008)	Girase and Mehetre (2002) Laxman and Ganesh (2003) Vijayalaxmi (2008)
4.	No. of bolls per plant	Laxman and Ganesh (2003) Gururajan and Sundar (2004) Narisireddy and Ratnakumari (2004) Sivaprasad *et al.* (2004 b) Neelima *et al.* (2005) Tuteja *et al.* (2006) Leela Pratap (2006) Neelima *et al.* (2008)	Girase and Mehetre (2002) Vijayalaxmi (2008)
5.	Boll weight (g)	Kaushik *et al.* (2003) Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Sivaprasad *et al.* (2004 b) Tuteja *et al.* (2006) Kale *et al.* (2006) Gitte *et al.* (2007)	

Contd..

Sl. No.	**Character**	**Wider genetic variability**	**Narrow genetic variability**
		Waqas Ahmed *et al.* (2008)	Reddy (2001) Altaher and Singh (2003b) Vijayalaxmi (2008) Neelima *et al.* (2008)
6.	Ginning out- turn (%)	Sambamurthy *et al.* (1994) Laxman and Ganesh (2003) Tuteja *et al.* (2003) Muthuswamy *et al.* (2003) Patnaik *et al.* (2004) Neelima *et al.* (2005) Kale *et al.* (2006) Tuteja *et al.* (2006)	Sumathi and Nadarajan (1996) Reddy (2001) Rao and Reddy (2001) Neelima (2002) Muraleedhar (2005) Vijayalaxmi (2008) Neelima *et al.* (2008)
7.	Seed index (g)	Sambamurthy *et al.* (1994) Meena (2001) Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Patnaik *et al.* (2004) Ravikumar (2004) Sivaprasad *et al.* (2004 b)	Rao and Reddy (2001) Reddy (2001) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Laxman and Ganesh (2003) Vijayalaxmi (2008) Neelima *et al.* (2008)
8.	Lint index (g)	Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Patnaik *et al.* (2004) Gururajan and Sundar (2004) Sivaprasad *et al.* (2004 b) Neelima *et al.* (2005)	Rao and Reddy (2001) Altaher and Singh (2003b) Vijayalaxmi (2008) Neelima *et al.* (2008)
9.	2.5% Span length (mm)	Muthuswamy *et al.* (2003) Patnaik *et al.* (2004) Naphade *et al.* (2004) Gururajan and Sundar (2004)	Reddy (2001) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Neelima *et al.* (2005) Tuteja *et al.* (2006)
10.	Uniformity ratio	Patnaik *et al.* (2004) Neelima *et al.* (2005)	Neelima (2002) Altaher and Singh (2003b) Muraleedhar (2005) Leela Pratap (2006) Karunakar Raju (2005) Vijayalaxmi (2008) Neelima *et al.* (2008) Eswar (2008)

Sl. No.	Character	Wider genetic variability	Narrow genetic variability
11.	Seed cotton yield per plant (g)	Sambamurthy *et al.* (1994) 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) Neelima *et al.* (2005) Karunakar Raju (2005) Kumari and Chamundeswari (2005) Leela Pratap (2006) Verma *et al.* (2006) Kale *et al.* (2006) Gitte *et al.* (2007) Vijayalaxmi (2008) Neelima *et al.* (2008)	--

Out of 10 studies made on plant height five each reported wider and narrow genetic variability. For number of monopodia per plant, nine out of twelve studies reported wider genetic variability where as three out of nine studies reported narrow genetic variability for number of sympodia per plant. Wider variability was reported for number of bolls per plant in eight out of ten studies. Similarly, out of fourteen studies ten reported wider variability for boll weight (g) and the rest are narrow. Out of 16 studies reviewed, 8 each reported wider and narrow genetic variability for ginning out turn (%) while, for seed index (g) seven studies each reported wider and narrow genetic variability. For lint index (g), four out of 11 studies revealed narrow genetic variability. Incase of 2.5% span length and uniformity ratio out of 10 studies each reviewed four and two studies respectively reported wider genetic variability. Out of 22 studies reviewed on seed cotton yield per plant none reported narrow genetic variability.

2.2. HERITABILITY ($h^2_{(b)}$) AND GENETIC ADVANCE AS PER CENT OF MEAN (GAM)

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 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) and genetic advance (GA) is presented in Table-2.

2.3. CHARACTER ASSOCIATION

Yield is a polygenically controlled character and highly influenced by the environment. Selection merely based on yield is not effective. Selection based on its components increases yield. Correlation studies will establish the extent of association between yield and yield components, which forms the basis for selection of genotypes for effective improvement. Yield component characters show association among themselves and with yield. Unfavourable associations between the desired attributes under selection may limit genetic advance. Hence, a sound knowledge of associations between the yield components is essential for planning effective selection programme.

The available literature on the association of component characters with seed cotton yield and among themselves is presented in Table-3 & 4.

2.4. PATH COEFFICIENT ANALYSIS

Path coefficient analysis devised by Wright (1921) is a standardized partial regression coefficient, which helps in partitioning the correlation coefficient into direct and indirect effects of independent variables on dependent variables. 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 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 planning a successful breeding programme. It has been well known that greater the genetic variability in the plant population greater will be the chance of obtaining 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 Mahalanobis' D^2 statistic was assessed among 62 varieties of upland cotton by Singh and Gill (1984) in 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.

There were wide differences between colour linted and white linted genotypes in view of their position in separate D^2 clusters.

Sambamurthy *et al.* (1995) assessed 50 cultivars of (*Gossypium hirsutum* L.) with the help of D^2 statistic. The genotypes were grouped into nine clusters. No. of bolls / plant followed by ginning percent contributed most of the total genetic divergence. The inter-cluster distance between cluster VIII & IX was the highest.

Kowsalya and Raveendran (1996) assessed genetic divergence among 28 genotypes of cotton. The genotypes were grouped into eight clusters irrespective of geographic divergence, indicating the absence of parallelism. number of sympodia and number of bolls had negligible role in genetic diversity.

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.

Amudha *et al.* (1997) used 10 coloured linted cotton genotypes, including two green and eight brown types for variability studies and genetic analysis.

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 contributed maximum 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 these, 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 *et al.* (2004) reported maximum contributing characters are bundle strength followed by seed cotton yield, number of sympodia per plant, 2.5% span length and uniformity ratio towards divergence.

Pushpam *et al.* (2004) reported 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.

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 geographical diversity is not always necessarily associated with 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 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.

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

Gopinath *et al.* (2009) evaluated 6o cotton genotypes of (*Gossypium hirsutum* L.) for genetic divergence using Mahalanobis D^2 statistics. Nine characters were evaluated for their contribution to total divergence. These 60 genotypes were grouped into eight clusters. The characters boll weight, boll number and 2.5% span length contributed maximum divergence. Genotypes in cluster V & VI could be utilized in the improvement of breeding programme.

Satish *et al.* (2009) assessed 70 genotypes (*Gossypium hirsutum* L.) using D^2 statistics. These genotypes were grouped into l5 clusters. The distribution of genotypes indicated that geographical diversity and genetic diversity were not related. The inter-cluster distance values were greater than intra-cluster distance values.

2.5.2 Principal component analysis and cluster analysis

Principal component analysis was carried out to transform the interdependent traits into a set of independent traits as well as to reduce the dimensionality 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 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 (*Gossypium hirsutum* L.) 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 (*Gossypium hirsutum* L.). 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 (*Gossypium hirsutum* L.). PCA identified seven principle components which contributed 87.47% of cumulative variance. The population with high PC_1 values were characterized by more number of bolls per plant, where as population with high PC_2 values were characterized by boll weight.

Table- 2: Review of literature on heritability ($h^2_{(b)}$) and genetic advance (GA) in cotton.

Sl.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) Kale *et al*. (2006) Sakthi *et al.*(2007) Preetha and Raveendran (2007)	Verma *et al.(*2006) Vijayalaxmi (2008)	---	Kumari & Chamundeswari (2005)
2.	No. of monopodia per plant	Girase and Mehetre (2002) Kaushik *et al.* (2003) Karunakar Raju (2005) Leela Pratap (2006) Verma *et al.* (2006) Kale *et al*.(2006) Gitte *et al.*(2007) Vijayalaxmi (2008)	Reddy (2001) Tuteja *et al.* (2004)	Neelima (2002) Sivaprasad *et al.* (2004a)	Rao and Reddy (2001)
3.	No. of sympodia per plant	Neelam and Potdukhe (2002) Girase and Mehetre (2002) Kaushik *et al.* (2003) Verma *et al.* (2006) Kale *et al*.(2006) Sakthi *et al.*(2007) Gitte *et al.*(2007) Preetha & Raveendran (2007)	Gururajan (2000) Reddy (2001) Tuteja *et al.* (2004) Vijayalaxmi (2008)	----	Rao and Reddy (2001) Sivaprasad *et al.* (2004a)

Contd..

Sl.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
4.	No. of bolls per plant	Krishna Rao & Mary (1990) Rao and Reddy (2001) Reddy (2001) Girase and Mehetre (2002) Neelam and Potdukhe (2002) Kaushik *et al.* (2003) Sivaprasad *et al.* (2004a) Leela Pratap (2006) Kale *et al*.(2006) Kale *et al*.(2007) Preetha and Raveendran (2007) Sakthi *et al.* (2007) Vijayalaxmi (2008)	Gururajan and Sundar (2004)	----	-----
5.	Boll weight (g)	Krishna Rao & Mary (1990) Neelam and Potdukhe (2002) Neelima (2002) Kaushik *et al.* (2003) Narisireddy and Ratnakumari (2004) Karunakar Raju (2005) Verma *et al.* (2006) Kale *et al*.(2006) Kale *et al*.(2007) Sakthi *et al.*(2007)	Gururajan (2000) Gururajan and Sundar (2004) Tuteja *et al.* (2004)	Sivaprasad *et al.* (2004a)	-----

Contd..

Sl.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
		Kale *et al*.(2007) Gitte *et al*.(2007) Vijayalaxmi (2008)			
6.	Ginning out- turn (%)	Gururajan and Sundar (2004) Kale *et al*.(2006)	Gururajan (2000) Rao and Reddy (2001) Neelam and Potdukhe (2002) Karunakar Raju (2005) Leela Pratap (2006) Verma *et al.(*2006) Kale *et al*.(2006) Vijayalaxmi (2008)	----	Sivaprasad *et al.* (2004a)
7.	Seed index (g)	Sambamurthy *et al.* (1994) Rao and Reddy (2001) Karunakar Raju (2005) Vijayalaxmi (2008)	Gururajan (2000) Neelam and Potdukhe (2002) Sivaprasad *et al.* (2004a)	----	Reddy (2001) Gururajan and Sundar (2004)
8.	Lint index (g)	Reddy (2001) Neelima (2002) Karunakar Raju (2005) Sambamurthy *et al.*(2006) Vijayalaxmi (2008)	Rao and Reddy (2001) Neelam and Potdukhe (2002) Sivaprasad *et al.* (2004a)	----	----
9.	2.5% Span length (mm)	Rao and Reddy (2001) Reddy (2001) Gururajan and Sundar (2004)	Tuteja *et al.* (2005a) Verma *et al.* (2006) Vijayalaxmi (2008)	----	----

Contd..

Sl.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
10.	Uniformity ratio	----	Neelima (2002) Karunakar Raju (2005)	----	Sivaprasad *et al.* (2004a) Muraleedhar (2005)
11.	Seed cotton yield/plant (g)	Ahuja and Tuteja (2000) Rao and Reddy (2001) Neelam and Potdukhe (2002) Girase and Mehetre (2002) Kaushik *et al.* (2003) Sivaprasad *et al.* (2004a) Kumari & Chamundeswari (2005) Kale *et al*.(2006) Preetha & Raveendran (2007) Karunakar Raju (2005) Tuteja *et al.* (2006) Leela Pratap (2006) Verma *et al.(*2006) Sambamurthy *et al.*(2006) Vijayalaxmi (2008)	Gururajan and Sundar (2004)	----	----

High heritability and high genetic advance was reported by several studies for all the characters reviewed except uniformity ratio. Low heritability and high genetic advance was reported for number of monopodia per plant and boll weight (g) only.

Table -3: Review of literature on the association of component characters with seed cotton yield in cotton.

Sl. No	Character	Association	S/NS	Reference
1.	Plant height(cm)	Positive	S	Dhanda *et al.*(1984) Samanc and Ozkaynak (2000) Altaher and Singh (2003b) Tuteja *et al.* (2006) Ganapathy *et al.*(2006) Sakthi *et al.*(2007)
			NS	Sumathi and Nadarajan (1995)
		Negative	S	Neelima *et al.* (2005)
			NS	Pradeep and Sumalini (2005) Vijayalaxmi (2008)
2.	No. of monopodia per plant	Positive	S	Ladole and Meshram (2000) Altaher and Singh (2003b) Kaushik *et al.* (2003)
			NS	Neelam and Potdukhe (2002) Altaher and Singh (2003b) Pradeep and Sumalini (2005) Vijayalaxmi (2008)
		Negative	NS	Reddy (2001) Karunakar Raju (2005) Waqas Ahmed *et al.*(2008)
3.	No. of sympodia per plant	Positive	S	Neelima (2002) Altaher and Singh (2003b) Muthu *et al.* (2004) Neelima *et al.* (2005) Tuteja *et al.* (2006) Ganapathy *etal.*(2006) Leela Pratap *et al.* (2007) Sakthi *et al.* (2007) Kale *et al.* (2007) Vijayalaxmi (2008) Kalpande *et al.* (2008)

Contd..

Sl. No	Character	Association	S/NS	Reference
				Ladole and Meshram (2000)
			NS	Neelam and Potdukhe (2002) Pradeep and Sumalini (2005) Karunakar Raju (2005)
4.	No.of bolls/plant	Positive	S	Dhanda *et al.*(1984) Tyagi (1994) Kaushik *et al.*(2003) Altaher & Singh (2003b) Sivaprasad (2003) Muthu *et al.* (2004) Gururajan and Sundar (2004) Neelima *et al.* (2005) Karunakar Raju (2005) Ganapathy *et al. (2006)* Tuteja *et al.* (2006) Verma *et al.* .(2006) Preetha and Raveendran (2007) Kale *et al.(2007)* Leela Pratap *et al.* (2007) Sakthi *et al.(2007)* Vijayalaxmi (2008)
			NS	Pradeep and Sumalini (2005)
		Negative	S	Patil *et al.* (1991)
5.	Boll weight (g)	Positive	S	Tyagi (1994) Altaher and Singh (2003b) Sivaprasad (2003) Gururajan and Sundar (2004) Muthu *et al.* (2004) Neelima *et al.* (2005) Karunakar Raju (2005) Sambamurthy *et al.* (2006) Preetha and Raveendran (2007) Kale *et al. (2007)* Sakthi *et al. (2007)*
			NS	Ladole and Meshram (2000) Reddy (2001) Kaushik *et al.* (2003) Vijayalaxmi (2008)

Contd..

Sl. No	Character	Association	S/NS	Reference
		Negative	S	Gururajan (2000)
				Rao *et al.* (2001)
			NS	Pradeep and Sumalini (2005)
6.	Ginning out - turn (%)	Positive	NS	Rao *et al.* (2001)
				Neelam and Potdukhe (2002)
			S	Tyagi (1994)
				Gururajan (2000)
				Ganapathy (2001)
				Reddy (2001)
				Neelima (2002)
				Sivaprasad (2003)
				Tuteja *et al.* (2005a)
		Negative	S	Mandloi *et al.* (2003)
				Muthuswamy and Vivekanandan (2004)
			NS	Karunakar Raju (2005)
				Vijayalaxmi (2008)
7	Seed index (g)	Positive	S	Neelam and Potdukhe (2002)
				Sivaprasad (2003)
				Muthu *et al.* (2004)
				Gururajan and Sundar (2004)
				Neelima *et al.* (2005)
				Sambamurthy *et al.* (2006)
			NS	Reddy (2001)
				Vijayalaxmi (2008)
		Negative	NS	Karunakar Raju (2005)
				Rao *et al.* (2001)
				Ladole and Meshram (2000)
				Mandloi *et al.* (2003)
8.	Lint index (g)	Positive	S	Tyagi (1994)
				Reddy (2001)
				Neelima (2002)
				Neelam and Potdukhe (2002)
				Sivaprasad (2003)
				Muthu *et al.* (2004)
				Karunakar Raju (2005)
				Neelima *et al.* (2005)
				Sambamurthy *et al.* (2006)

Contd..

Sl. No	Character	Association	S/NS	Reference
				Sakthi *et al.* (2007)
			NS	Rao *et al.* (2001) Vijayalaxmi (2008)
		Negative	NS	Ladole and Meshram (2000) Mandloi *et al.* (2003)
9.	2.5% span length (mm)	Positive	NS	Rao *et al.* (2001) Reddy (2001) Neelima (2002) Mandloi *et al.* (2003) Sakthi *et al.* (2007)
		Negative	S	Gururajan and Sundar (2004)
			NS	Neelam and Potdukhe (2002) Pankaj Rathore *et al.* (2004) Tuteja *et al.* (2005a) Karunakar Raju (2005) Vijayalaxmi (2008)
		Negative	S	Rao *et al.* (2001) Altaher and Singh (2003b) Sivaprasad (2003) Muthu *et al.* (2004)
10.	Uniformity ratio (%)	Positive	S	Sivaprasad (2003) Neelima *et al.* (2005)
			NS	Neelima (2002) Karunakar Raju (2005)
		Negative	S	Vijayalaxmi (2008)
			NS	Dedaniya and Pethani (1994) Tuteja *et al.* (2005 a,b)
11.	Seed cotton yield / plant(g)	Positive	S	Mandloi *et al.* (2003) Deshpande and Baig (2003) Leela Pratap *et al.* (2007) Vijayalaxmi (2008)

S: Significant NS: Non-significant

Table -4: Review of literature on association among the yield component characters in cotton.

Sl. No	Character	Association	S/NS	Reference
I: Plant height with				
1.	No. of monopodia per plant	Positive	S	Neelam and Potdukhe (2002)
		Negative	NS	Sangeetha (1998)
				Pradeep and Sumalini (2005)
				Vijayalaxmi (2008)
2.	No. of sympodia per plant	Positive	S	Samanc and Ozkaynak (2000)
				Muthu *et al.* (2004)
				Tuteja *et al.* (2006)
				Leela Pratap *et al.* (2007)
				Verma *et al.*(2006)
				Vijayalaxmi (2008)
			NS	Pradeep and Sumalini (2005)
3.	No. of bolls/plant	Positive	S	Samanc and Ozkaynak (2000)
				Muthu *et al.* (2004)
				Tuteja *et al.* (2006)
				Vijayalaxmi (2008)
			NS	Sangeetha (1998)
		Negative	NS	Sharad Bahtnagar (1995)
				Pradeep and Sumalini (2005)
4.	Boll weight (g)	Positive	NS	Pradeep and Sumalini (2005)
				Vijayalaxmi (2008)
		Negative	NS	Tyagi (1994)
				Sharad Bhatnagar (1995)
				Sangeetha (1998)
5.	Ginning out- turn (%)	Positive	NS	Vijayalaxmi (2008)
		Negative	NS	Kowsalya and Raveendran (1996)
				Sangeetha (1998)
			S	Tyagi (1994)
				Sharad Bhatnagar (1995)

Contd..

Sl. No	Character	Association	S/NS	Reference
6.	Seed index (g)	Positive	S	Muthu *et al.* (2004)
			NS	Sumathi and Nadarajan (1995)
				Sangeetha (1998)
				Vijayalaxmi (2008)
				Sharad Bhatnagar (1995)
		Negative	NS	Tyagi (1994)
			S	Leela Pratap *et al.* (2007)
7.	Lint index (g)	Positive	NS	Sumathi and Nadarajan (1995)
				Vijayalaxmi (2008)
		Negative	NS	Sangeetha (1998)
				Sharad Bhatnagar (1995)
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)

II. No. of monopodia per plant with

1.	No.of sympodia per plant	Positive	NS	Ladole and Meshram (2000)
				Reddy (2001)
				Neelima (2002)
				Kaushik *et al.* (2003)
			S	Leela Pratap *et al.* (2007)
		Negative	S	Verma *et al.* (2006)
				Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002)
				Pradeep and Sumalini (2005)
2.	No.of bolls/plant	Positive	S	Ladole and Meshram (2000)
				Kaushik *et al.* (2003)
				Leela Pratap *et al.* (2007)
				Verma *et al.*(2006)
				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)

Contd..

Sl. No	Character	Association	S/NS	Reference
		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) Reddy (2001) Neelima (2002)
		Negative	NS	Neelam and Potdukhe (2002) Chengareddy *et al.* (2008)
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.	Uniformity ratio	Negative	NS	Sangeetha (1998) Neelima (2002)
			S	Vijayalaxmi (2008)
		Positive	S	Altaher and Singh (2003b)
			NS	Karunakar Raju (2005)

Contd..

Sl. No	Character	Association	S/NS	Reference
III. 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)
		Positive	NS	Ladole and Meshram (2000) Ganapathy (2001) Kaushik *et al.* (2003) Pradeep and Sumalini (2005)
		Negative	NS	Karunakar Raju (2005) Vijayalaxmi (2008) Ganapathy *et al.* (2006)
2.	Boll weight (g)	Positive	S	Neelima (2002) Altaher and Singh (2003b) Neelima *et al.* (2005)
			NS	Vijayalaxmi (2008)
		Negative	S	Paramasivan and Udayasoorian (1989) Rao *et al.* (2001) Leela Pratap *et al.* (2007)
			NS	Pradeep and Sumalini (2005)
3.	Ginning out-turn (%)	Positive	S	Muthu *et al.* (2004) Muthuswamy and Vivekanandan (2004) Neelima *et al.* (2005)
			NS	Dhanda *et al.*(1984) 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	Dhanda *et al.* (1984) Ladole and Meshram (2000) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Muthu *et al.* (2004) Neelima *et al.* (2005)

Contd..

Sl. No	Character	Association	S/NS	Reference
			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)
			NS	Dhanda *et al.*(1984) Reddy (2001) Vijayalaxmi (2008)
		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.	Uniformity ratio	Negative	NS	Neelima (2002)
		Positive	S	Karunakar Raju (2005) Vijayalaxmi (2008)
IV. 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 *et al.* (2001) Karunakar Raju (2005) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Reddy (2001) Kaushik *et al.* (2003) Pradeep and Sumalini (2005)
2.	Plant Height	Positive	S	Dhanda *et al.* (1984)
3.	Ginning out-turn (%)	Positive	S	Ganapathy (2001) Muthu *et al.* (2004) Leela Pratap *et al.* (2007)

Contd..

Sl. No	Character	Association	S/NS	Reference
			NS	Dhanda *et al.* (1984)
				Vijayalaxmi (2008)
		Negative	NS	Sangeetha (1998)
			S	Karunakar Raju (2005)
4.	Seed index (g)	Positive	S	Dhanda *et al.* (1984)
				Neelima (2002)
				Muthu *et al.* (2004)
				Neelam and Potdukhe (2002)
				Neelima *et al.* (2005)
			NS	Reddy (2001)
		Negative	S	Rao *et al.* (2001)
				Muraleedhar (2005)
				Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000)
5.	Lint index (g)	Positive	S	Dhanda *et al.* (1984)
				Neelima (2002)
				Neelam and Potdukhe (2002)
				Muthu *et al.* (2004)
				Neelima *et al.* (2005)
			NS	Reddy (2001)
		Negative	S	Murthy (1997)
				Karunakar Raju *et al.* (2005)
				Vijayalaxmi (2008)
			NS	Neelima (2002)
				Ladole and Meshram (2000)
				Rao *et al.* (2001)
				Neelam and Potdukhe (2002)
6.	2.5% span length (mm)	Positive	NS	Ladole and Meshram (2000)
				Rao *et al.* (2001) Reddy (2001)
				Neelam and Potdukhe (2002)
		Negative	NS	Neelima (2002)
				Vijayalaxmi (2008)
			S	Tyagi (1994)
				Muraleedhar (2005)
7.	Uniformity ratio	Negative	NS	Sangeetha (1998)
				Neelima (2002)
			S	Vijayalaxmi (2008)
		Positive	S	Muthu *et al.* (2004)
V. Boll weight (g) with				
1.	Ginning out-turn (%)	Positive	S	Dhanda *etal.* (1984)
				Reddy (2001)
				Muthuswamy and Vivekanandan (2004)

Contd..

Sl. No	Character	Association	S/NS	Reference
				Karunakar Raju (2005)
			NS	Neelima (2002)
		Negative	NS	Murthy (1997) Ladole and Meshram (2000) Vijayalaxmi (2008)
2.	Seed index (g)	Positive	S	Dhanda *et al.* (1984) Ladole and Meshram (2000) Neelima (2002) Altaher and Singh (2003b) Sivaprasad (2003) Muthu *et al.* (2004) Neelima *et al.* (2005) Karunakar Raju (2005) 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) 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) Chengareddy *et al.* (2008)
		Negative	NS	Neelima (2002)
5.	Uniformity ratio	Negative	S	Neelima (2002) Muraleedhar (2005)
			NS	Vijayalaxmi (2008)
VI. Ginning out turn (%) with				
1	Seed index (g)	Positive	NS	Dhanda *et al.*(1984) Reddy (2001) Neelima (2002) Mandloi *et al.* (2003) Altaher and Singh (2003b) Chengareddy *et al.*(2008)
		Negative	S	Leela Pratap *et al.* (2007)
			NS	Ladole and Meshram (2000) Rao *et al.* (2001) Neelam and Potdukhe (2002)

Contd..

Sl. No	Character	Association	S/NS	Reference
				Vijayalaxmi (2008)
2.	Lint index (g)	Positive	S	Dhanda *et al.* (1984)
				Reddy (2001)
				Neelima (2002)
				Altaher and Singh (2003b)
				Mandloi *et al.* (2003)
				Muthu *et al.* (2004)
				Karunakar Raju (2005)
				Leela Pratap *et al.* (2007)
				Vijayalaxmi (2008)
			NS	Rao *et al.* (2001)
				Neelam and Potdukhe (2002)
3.	2.5% span length (mm)	Positive	S	Sivaprasad (2003)
				Chengareddy *et al.* (2008)
			NS	Ladole and Meshram (2000)
				Rao *et al.* (2001)
				Reddy (2001)
				Neelima (2002)
		Negative	S	Muthu *et al.* (2004)
			NS	Mandloi *et al.* (2003)
				Neelam and Potdukhe (2002)
				Vijayalaxmi (2008)
4.	Uniformity ratio	Positive	S	Muthu *et al.* (2004)
				Karunakar Raju (2005)
			NS	Sangeetha (1998)
		Negative	S	Altaher and Singh (2003b)
			NS	Neelima (2002)
				Vijayalaxmi (2008)
VII. 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)
				Vijayalaxmi (2008)
				Chengareddy *et al.* (2008)
			NS	Neelam and Potdukhe (2002)
2.	2.5% span length (mm)	Positive	S	Rao *et al.* (2001)
				Karunakar Raju (2005)
				Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002)

Contd..

Sl. No	Character	Association	S/NS	Reference
		Negative	NS	Neelima (2002) Mandloi *et al.* (2003) Ladole and Meshram (2000)
3.	Uniformity ratio	Negative	S	Neelima (2002) Muraleedhar (2005)
			NS	Sangeetha (1998) Vijayalaxmi (2008)
VIII. Lint index (g) with				
1.	2.5% span length (mm)	Positive	S	Muthu *et al.* (2004) Sambamurthy *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.	Uniformity ratio	Negative	S	Muthu *et al.* (2004)
			NS	Sangeetha (1998) Neelima (2002)
		Positive	NS	Karunakar Raju (2005) Vijayalaxmi (2008)
		Negative	S	Rao *et al.* (2001)
IX. 2.5% span length with				
1.	Uniformity ratio	Positive	NS	Neelima (2002)
			S	Sivaprasad (2003)
		Negative	S	Altaher and Singh (2003b) Karunakar Raju (2005) Leela Pratap *et al.* (2007) Vijayalaxmi (2008)
			NS	Muthu *et al.* (2004) Tuteja *et al.* (2005b)

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

Table- 5: Review of literature on direct effects of component characters on yield in cotton.

Sl.No	Character	Positive Direct effect	Negative Direct effect
1.	Plant height (cm)	Reddy (2001) Neelima (2002) Neelam *et al.* (2002) Altaher and Singh (2003a) Sivaprasad (2003) Muthu *et al.* (2004)	Ladole and Meshram (2000) Karunakar Raju (2005) Verma *et al.* (2006) Vijayalaxmi (2008)
2.	No. of monopodia per plant	Gururajan (2000) Reddy (2001) Neelam *et al.* (2002) Kaushik *et al.* (2003) Altaher and Singh (2003a) Muthu *et al.* (2004) Vijayalaxmi (2008)	Ladole and Meshram (2000) Neelima (2002) Sivaprasad (2003) Karunakar Raju (2005) Tuteja *et al.* (2006) Verma *et al.* (2006)
3.	No. of sympodia per plant	Ladole and Meshram (2000) Rao *et al.* (2001) Neelima (2002) Neelam *et al.* (2002) Kaushik *et al.* (2003) Neelima *et al.* (2005) Verma *et al.* (2006) Leela Pratap *et al.* (2007) Vijayalaxmi (2008)	Sumathi and Nadarajan (1995) Gururajan (2000) Reddy (2001) Sivaprasad (2003) Muthu *et al.* (2004) Karunakar Raju (2005) Tuteja *et al.* (2006)
4.	No. of bolls/plant	Krishnarao and Mary (1990) Sharad Bhatnagar (1995) Altaher and Singh (2003a) Sivaprasad (2003) Muthu *et al.* (2004) Gururajan and Sundar (2004) Karunakar Raju (2005) Neelima *et al.* (2005) Ganapathy *et al.* (2006) Leela Pratap *et al.* (2007) Verma *et al.* (2006) Vijayalaxmi (2008)	Kaushik *et al.* (2003) Tuteja *et al.* (2006)
5.	Boll weight (g)	Krishnarao and Mary (1990) Sharad Bhatnagar (1995) Neelima (2002) Kaushik *et al.* (2003) Altaher and Singh (2003a) Muthu *et al.* (2004) Gururajan and Sundar (2004) Karunakar Raju (2005) Vijayalaxmi (2008)	Ladole and Meshram (2000) Verma *et al.* (2006)

Sl.No	Character	Positive Direct effect	Negative Direct effect
6.	Ginning out-turn (%)	Sharad Bhatnagar (1995) Gururajan (2000) Reddy (2001) Muthu *et al.* (2004) Tuteja *et al.* (2006) Verma *et al.* (2006) Leela Pratap *et al.* (2007)	Ladole and Meshram (2000) Neelima (2002) Altaher and Singh (2003b) Sivaprasad (2003) Gururajan and Sundar (2004) Karunakar Raju (2005) Vijayalaxmi (2008)
7.	Seed index (g)	Sharad Bhatnagar (1995) Gururajan (2000) Rao *et al.* (2001) Reddy (2001) Sivaprasad (2003) Sambamurthy *et al. (*2006) Vijayalaxmi (2008)	Ladole and Meshram (2000) Neelima (2002) Altaher and Singh (2003a) Gururajan and Sundar (2004) Karunakar Raju (2005)
8.	Lint index (g)	Reddy (2001) Neelima (2002) Altaher and Singh (2003a) Gururajan and Sundar (2004) Neelima *et al.*(2005) Karunakar Raju (2005) Vijayalaxmi (2008)	Sivaprasad (2003) Muthu *et al.* (2004) Leela Pratap *et al.* (2007)
9.	2.5% span length (mm)	Ladole and Meshram (2000) Muthu *et al.* (2004) Karunakar Raju (2005) Tuteja *et al.* (2006)	Reddy (2001) Neelima (2002) Sivaprasad (2003) Gururajan and Sundar (2004) Verma *et al.* (2006) Vijayalaxmi (2008)
10.	Uniformity ratio	Sivaprasad (2003) Karunakar Raju (2005) Sambamurthy *et al.* (2006) Vijayalaxmi (2008)	Neelima (2002) Muthu *et al.* (2004) Leela Pratap *et al.* (2007)

CHAPTER – III

MATERIALS AND METHODS

The present investigation entitled as “Genetic divergence in upland cotton (*Gossypium hirsutum* L.)” was taken up during *Kharif* 2007 at Regional Agricultural Research Station, Lam Farm, Guntur. The site of 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 comprised of 60 genotypes obtained from all over India. The source of origin of these genotypes has been presented in Table 6.

3.2 METHODS

3.2.1 Experimental technique

The detailed experimental technique for the present investigation has been furnished in the Table 7 .

3.2.2 Record of observations

Five plants of each genotype in each replication were chosen at random and labelled for recording observations. The mean of the five plants was used for statistical analysis. The data on the following yield and yield component traits and quality parameters were recorded.

3.2.2.1 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.

3.2.2.2 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 were counted at maturity stage.

3.2.2.3 Number of bolls per plant

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

3.2.2.4 Boll weight (g)

The boll weight in grams was obtained by taking the average weight of 10 randomly collected bolls from each selected plant.

3.2.2.5 Seed index (g)

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

3.2.2.6 Lint index (g)

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

3.2.2.7 Ginning percentage

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

$$\text{Ginning percentage} = \frac{\text{Weight of lint}}{\text{Weight of seed cotton}} \times 100$$

3.2.2.8 2.5% span length (mm)

In the laboratory, 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.

3.2.2.10 Uniformity ratio (%)

It was determined by Fibrograph model 430. It is the ratio of 2.5% span length and 50% span length.

3.2.2.11 Seed cotton yield per plant (g)

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

3.2.3 Statistical analysis

The details of various statistical methods followed are furnished below.

3.2.3.1 Analysis of variance

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

$$Yij = \mu + bi + tj + eij$$

Where

Yij = Performance of the ith block in the jth genotype

μ = general mean

bi = effect of ith block

tj = effect of jth genotype

eij = random error associates with ith block and jth 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	$M'_r = \sigma^2_r + 6^2_e$	M'_r / M'_e
Treatments (Genotypes)	t-1	TrSS	$M'_t = \sigma^2_e + \sigma^2_g$	M'_t / M'_e
Error	(r-1) (t-1)	ESS	$M'_e = \sigma^2_e$	
Total	(rt-1)	TSS		

Where,

r = Number of replications

t = Number of genotypes

d.f = 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

The test of significance was carried out using ‘F’ table values given by Fisher and Yates (1963).

3.2.3.2 Estimation of genetic parameters

1) Coefficient of variation

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

Phenotypic standard deviation

$$(\sigma p) = \sqrt{\sigma^2 p} = \sqrt{\sigma^2 g + \sigma^2 e}$$

$$\text{PCV} = \frac{\text{Phenotypic standard deviation } (\sigma p)}{\text{General Mean } (\bar{X})} \times 100$$

Genotypic Standard deviation

$$(\sigma g) = \sqrt{\sigma^2 g} = \sqrt{(\text{MS due to genotypes} - \text{EMSS})/r}$$

$$\text{GCV} = \frac{\text{Genotypic standard deviation } (\sigma g)}{\text{General Mean } (\overline{X})} \text{ X } 100$$

As suggested by Sivasubramanian and Menon (1973), GCV and PCV were categorised into

Low = Less than 10%

Moderate = 10-20%

High = More than 20%

(2) Heritability in Broad Sense [h^2(b)]

Heritability in broad sense was estimated as per Allard (1960)

$$h^2(b) = \frac{\text{Genotypic variance } (\sigma^2 g)}{\text{Phenotypic variance } (\sigma^2 p)} \text{ X } 100$$

As suggested by Johnson *et al.* (1955), h^2 (b) estimates were categorized into

Low = 0 – 30%

Moderate = 31-60%

High = 61% and above

(3) Genetic advance (GA)

This was estimated as per the formula proposed by Lush (1940) and Johnson *et.al.* (1955)

$$GA = K \text{ x } \sigma p \text{ x } h^2(b)$$

Where

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

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

σp = Phenotypic standard deviation

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

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

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%

3.2.3.3 Correlation studies

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

Phenotypic coefficients of correlation (γ_P)

$$\gamma(x_i.x_j)P = \frac{Cov\,(x_i.x_j)P}{V(x_i)P.V(x_j)P}$$

Where,

$\gamma(x_i.x_j)p$ = Phenotypic correlation between ith and jth character

$Cov(x_i.x_j)p$ = Phenotypic covariance between ith and jth character

$V(x_i)p$ = Phenotypic variance of ith character

$V(x_j)p$ =Phenotypic variance of jth character

Genotypic coefficients of correlation (γ_g)

$$\gamma(x_i.x_j)g = \frac{Cov(x_i.x_j)g}{\sqrt{V(x_i)g.V(x_j)g}}$$

$\gamma(x_i.x_j)g$ = genotypic correlation between ith and jth character

$Cov\ (x_i.x_j)g$ = genotypic covariance between ith and jth character

$V(x_i)g$ = genotypic variance of ith character

$V(x_j)g$ = genotypic variance of jth character

3.2.3.3.1 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 paired observations used in the calculation.

3.2.3.4 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

$$\gamma_{1y} = P_{1y} + P_{12} + P_{2y} + P_{13}\, P_{3y} + \ldots\ldots + P_{1k}\, P_{ky}$$

$$\gamma_{2y} = \gamma_{21}\, P_{1y} + P_{2y} + \gamma_{23}\, P_{3y} + \ldots\ldots + \gamma_{2k}\, P_{ky}$$

$$\gamma_{iy} = \gamma_{i1}\, P_{1y} + P_{i2}\, P_{2y} + \gamma_{i3}\, P_{3y} + \ldots\ldots + \gamma_{ik}\, P_{ky}$$

$$\gamma_{ky} = \gamma_{k1}\, P_{1y} + P_{k2}\, P_{2y} + \gamma_{i3}\, P_{3y} + \ldots\ldots + \gamma_{kk}\, P_{ky}$$

Where,

γ_{1y} to γ_{ky} = Coefficient of correlation between casual factors 1 to k and dependant character y.

γ_{12} to γ_{k-1}, K = Coefficient of correlation among casual 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

$$\begin{bmatrix} \gamma_{1y} \\ \gamma_{2y} \\ \cdot \\ \cdot \\ \cdot \\ \gamma_{ky} \end{bmatrix} \begin{bmatrix} 1 & \gamma_{12} & \gamma_{13} & \cdot & \cdot & \cdot & \gamma_{1} \\ \gamma_{2y} & 1 & \gamma_{23} & \cdot & \cdot & \cdot & \gamma_{2} \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \gamma_{k1} & \gamma_{ky} & \gamma_{ky} & \cdot & \cdot & \cdot & 1 \end{bmatrix} \begin{bmatrix} p_{1y} \\ p_{2y} \\ \cdot \\ \cdot \\ \cdot \\ p_{ky} \end{bmatrix}$$

Then

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

Then direct effects were calculated as follows

$$P_{1y} = \sum_{i-1}^{k} C_{1i} \,.\, \gamma_{iy}$$

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

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

3.2.3.4.1. Residual effect

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 a role of other possible independent variables which were not included in the study on the dependent variable. The residual effect was estimated with the help of direct effects and simple correlation coefficients.

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

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

3.2.3.5 Genetic divergence

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

D^2 value between ijth genotypes for 'P' characters was calculated as

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

Where

Y_{it} is uncorrelated mean value of ith genotype for 't' characters

Y_{jt} is uncorrelated mean value of jth genotype for 't' characters

$D^2{}_{ij}$ is D^2 between ith and jth genotype

3.2.3.5.1 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, 1957). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for difference 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 and error + variety, variance – covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using the following relationship.

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

Where

$\wedge$ = Wilk’s criterion

(E) = Determinant of error matrix and

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

V (Stat) = $-m \log^{\wedge}_{e} = -(n- \frac{P+Q+1}{2}) \log_{e} {}^{‘\wedge’}$

Where,

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

n = degrees of freedom for error

+ varieties and $\log_{e} {}^{‘\wedge’} = 2.3026 \log_{10} {}^{‘\wedge’}$

P = number of varieties or characters

Q = number of variables -1 (or d.f / or populations)

V (Stat) is distributed as α^2 with PQ degrees of freedom.

Transformation of correlated variables

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

3.2.3.5.2 Computation of D^2 values

For the given combination of i and j genotype, the mean deviation i.e. Y_{it} - Y_{jt} for t=1, 2 … P variables are computed and the D^2 values were calculated as

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

Where,

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

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

$D^2{}_{ij}$ is D^2 between i^th^ and j^th^ genotypes.

3.2.3.5.3 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of α^2 and is tested against the tabulated value of α^2 for P degrees of freedom where P is the number of characters considered.

3.2.3.5.4 Contribution of individual characters towards divergence

In all combinations each character was ranked based on their contribution towards divergence between two entries (di =Y_{it}-Y_{jt}). Rank 1 is given to the highest mean difference and rank P to the lowest difference, where, P is the total number of characters. Percentage contribution towards genetic divergence was calculated using the following formula.

Percentage contribution of character

$$= X = \frac{N X 100}{M}$$

Where

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

M = All possible combinations of number of genotypes considered.

3.2.3.5.5 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 should 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 than eliminated and the rest were treated in a similar way. This procedure was continued until all the genotypes were included into one or other cluster.

3.2.3.5.6 Average intra-cluster distance

For the measurement of intra-cluster distance, 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.

3.2.3.5.7 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 same of D^2 values between the members of one cluster to each of the members of the other cluster divided by the product of number of genotypes in both the clusters under consideration.

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

Where n_1 and n_2 are number of genotypes of two clusters.

3.2.3.5.8 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, there by removing the effects of scale (Jackson, 1991).

3.2.3.5.8.1 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.

$$\text{Per cent variance explained for PC1} = \frac{\text{Eigen value (PC1)}}{\text{Sum of eigen values}}$$

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

The principal components were identified by following procedure.

The j^{th} principal component (Y_j) of the observations 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

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

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 or 3D (dimensional) scatter plot of individuals.

3.2.3.5.8.2 Cluster analysis

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

1. Obtaining data matrix

PCA scores for 60 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. 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 60 genotypes were taken in data matrix therefore resemblance coefficient was computed for a total of 1770 combinations *i.e.*, ${}^{60}C_2$ 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.*, 60

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

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

3. 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 with in cluster sum of squares is minimized over all partitions obtained by combining 2 clusters from previous stage.

3.2.3.5.8.3 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, 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,

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.

Table 6: Source of upland Cotton genotypes under study

S. No.	Genotype	Source
1	NA-1325	RARS, Nandyal
2	L-604	(ANGRAU) Lam (Andhra Pradesh)
3	NDLH -1678	RARS, Nandyal
4	CWROK -165	CICR, Coimbatore
5	MCU - 5	TNAU, Coimbatore
6	L - 761	(ANGRAU) Lam Farm, Guntur (Andhra Pradesh)
7	L - 765	(ANGRAU) Lam Farm, Guntur (Andhra Pradesh)
8	L - 763	RARS, Lam Farm, Guntur
9	LK -861	RARS, Lam Farm, Guntur
10	L- 603	RARS, Lam Farm, Guntur
11	RAH -3	UAS, Raichur
12	SRT - 1	GAU, Surat
13	NH - 100	Nanded, Maharashtra
14	CCH - 5104	HAU, Hissar
15	SCS - 95	UAS, Siriguppa
16	ARB - 8906	UAS, Arbhavi
17	SCS - 51	UAS, Siriguppa
18	CPD - 787	UAS, Dharwad
19	ARB - 9009	UAS, Arbhavi
20	MCU - 7	TNAU, Coimbatore
21	KH - 140	JNKVV, Khandwa
22	L - 769	RARS, Lam Farm, Guntur
23	L - 768	RARS, Lam Farm, Guntur
24	L - 864	RARS, Lam Farm, Guntur
25	RHH - 7553	UAS, Raichur
26	Abhadita	UAS, Dharwad
27	ARB - 760	UAS, Arbhavi
28	GJHV- 392	GAU, Surat
29	GIHV- 53	NAU, Surat
30	LRK-5166	CICR, Coimbatore

S. No.	Genotype	Source
31	SCS -101	UAS, Siriguppa
32	RS- 2141	RAU, Sri Ganga Nagar
33	GJHV- 99/307	NAU, Surat
34	TSH -9727	Tamilnadu Agricultural University (TNAU) Srivilli Puttur (Tamilnadu)
35	CCH - 18	HAU, Hissar, Haryana
36	MCU - 2	TNAU, Coimbatore
37	PKV Rajat	PKV, Akola
38	Surabhi	CICR, Coimbatore
39	TCH - 1542	TNAU, Coimbatore
40	GMP - 5	HAU, Hissar, Haryana
41	HAG - 785	ARS, Hagari
42	Khandwa-2MB	JNKVV, Khandwa
43	HS – 271	HAU, Hissar, Haryana
44	ICMF – 230	Indian Cotton mills federation, Coimbatore
45	RS – 2169	RAU, Sri Ganga Nagar
46	ICMF – 1542	TNAU, Coimbatore
47	CNH – 3003	CICR, Nagpur
48	ACS – 738	Arbhavi
49	MCU – 12	TNAU, Coimbatore
50	NDLH – 1754	RARS, Nandyal
51	ARB – 784	UAS, Arbhavi
52	SES – 21	UAS, Siriguppa
53	Krishna	RARS, Lam Farm, Guntur
54	BUSP – 13	RARS, Lam Farm, Guntur
55	ADB - 39	ARS, Adilabad
56	H - 1246	HAU, Hissar, Haryana
57	HD - 328	HAU, Hissar, Haryana
58	ARB - 2005	UAS, Arbhavi
59	RCH - 1594	Rasi Seeds Guntur
60	MCU - 9	TNAU, Coimbatore

Table 7: Experimental details of present investigation.

Season	:	*Kharif*, 2007
Design	:	Randomized block design
Replications	:	3
Genotypes	:	60
Number of rows/genotypes	:	1
Row length	:	6 m
Spacing	:	120 x 60 cm
Fertiliser dose	:	90 N + 45 P + 45 K Kg/ha.

CHAPTER - IV

RESULTS

The data collected on 11characters *viz.*, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed index (g), lint index (g), ginning out-turn (%), 2.5% span length (mm), uniformity ratio and seed cotton yield per plant (g) of 60 cotton (*Gossypium hirsutum* L.) genotypes evaluated during *kharif*, 2007 at Regional Agricultural Research Station, Lam Farm, Guntur were subjected to statistical analysis.

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

4.1. Analysis of variance

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

4.3 Character association

4.4 Path coefficient analysis

4.5 Genetic divergence

4.1 ANALYSIS OF VARIANCE

The analysis of variance revealed significant differences among the genotypes for all the 11 characters indicating the presence of genetic variability in the genotypes studied and are furnished in Table –8. The replication mean sum of squares were non-significant for all the characters.

4.2 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The mean values for different characters genotype wise are presented in Table-9. The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2_{(b)}$) and genetic advance as per cent of mean (GAM) were calculated and are presented in Table-10 and described character-wise here under.

4.2.1. Plant height (cm)

The range of variation for this character varied from 96.00 (L-604) to 194.67 (MCU-12) with a mean of 150.72cm. The estimates of PCV (13.57) and GCV (13.43) were moderate. High heritability (97.88) and high genetic advance as per cent of mean (27.36%) were observed for this trait.

4.2.2 Number of monopodia per plant

The number of monopodia per plant ranged from 1.00 (LK-861, MCU-7, PCM-1542 and SES-21) to 3.33 (NH-100) with a mean of 2.01. The estimates of PCV (13.38) and GCV (13.05) were moderate. High heritability (7.27) and low genetic advance as per cent of mean (7.25) were observed for this trait.

4.2.3. Number of sympodia per plant

The number of sympodia per plant ranged from 17.67 (L-604) to 32.33 (CPD-787) with a mean of 24.22. The estimates of PCV (13.48) and GCV (10.71) were moderate. High heritability (63.05) coupled with moderate genetic advance as per cent of mean (17.51) were recorded for this character.

4.2.4 Number of bolls per plant

The number of bolls per plant ranged from 36.00 (ICMF-230) to 83.33 (MCU-12) with a mean of 56.24. The estimates of PCV (23.79) and GCV (23.46) were high and high heritability (97.20) coupled with high genetic advance as per cent of mean (47.65) were observed.

4.2.5 Boll weight (g)

Boll weight ranged from 2.77 (L-603) to 6.32 (GJHV 392) with a mean of 4.40. The estimates of PCV (19.47) and GCV (19.11) were moderate. High heritability (96.34) coupled with high genetic advance as per cent of mean (38.64) were recorded for this trait.

4.2.6 Seed index (g)

Seed index was in the range of 5.70(RS-2141) to 13.37 (GJHV-99/307) with a mean of 9.19. The estimates of PCV (21.07) and GCV (20.93) were high. High heritability (98.69) coupled with high genetic advance as per cent of mean (42.84) were observed for this character.

4.2.7. Lint index (g)

The range of variation observed for this character was from 2.60 (SCS-51 and Krishna) to 6.47 (CWROK-165) with a mean of 4.27grams. The estimates of PCV (20.81) and GCV (19.94) were high and moderate, respectively. High heritability (91.87) coupled with high genetic advance as per cent of mean (39.37) was observed for lint index.

4.2.8 Ginning out-turn (%)

The range of variation among genotypes for this trait was 20.66 (GJHV99/307) to 41.00 (NA-1325, ARB-8906 and RS-2141) with a mean of 31.67. The estimates of PCV (16.98) and GCV (16.34) were moderate. High heritability (92.45) coupled with high genetic advance as per cent of mean (32.36) was recorded for this trait.

4.2.9. 2.5% span length (mm)

The 2.5% span length ranged from 22.91(KH-140) to 31.28 (MCU-5) with a mean of 26.53. The estimates of PCV (8.77) and GCV (5.49) were low. Moderate heritability (39.21) coupled with low genetic advance as per cent of mean (7.08) was observed for this trait.

4.2.10. Uniformity ratio

The range of variation was 37.53 (MCU-5) to 57.20 (PKV-Rajat) with a mean of 47.13. The estimates of PCV (7.55) and GCV (6.29) were low. High heritability (69.44) coupled with moderate genetic advance as per cent of mean (10.80) was observed for uniformity ratio.

4.2.11 Seed cotton yield per plant (g)

The range of variation was from 105.00 (H-1246) to 566.67 (KH-140) with a mean of 240.78. The estimates of PCV and GCV (31.31 and 30.96) were high. High heritability (97.79) coupled with high genetic advance as per cent of mean (63.07) was observed for seed cotton yield per plant.

4.3 CHARACTER ASSOCIATION

The phenotypic and genotypic correlation coefficients between seed cotton yield and other related component characters and among themselves were estimated and presented in (Table 11).

4.3.1. Plant height (cm)

At genotypic and phenotypic levels, this trait showed significant positive association with number of sympodia per plant (0.31** and 0.25**), boll weight (0.34** and 0.33**) and seed cotton yield per plant (0.26** and 0.25**). It also showed negative significant association with ginning out-turn (-0.19**and -0.18*) and lint index (-0.16* and -0.16*).

4.3.2. Number of monopodia per plant

Genotypic and phenotypic correlations revealed that this trait showed significant positive association only with number of bolls per plant (0.70** and 0.19**). While, ginning out-turn (0.35**), lint index (0.28**), 2.5% span length (0.46**) and seed cotton yield per plant (0.22**) showed positive significant association only at genotypic level. It also showed negative significant association with number of sympodia per plant (-0.50** and -0.16*) at genotypic and phenotypic levels and only at genotypic level for boll weight (-0.39**).

4.3.3. Number of sympodia per plant

At genotype level, this trait showed positive significant correlation with seed cotton yield per plant (0.14*) and negative correlation with seed index (-0.19*), lint index (-0.30**) and 2.5% span length (-0.21**). At phenotypic level, this trait recorded significant negative association with seed index (-0.15*) and lint index (-0.22**).

4.3.4. Number of bolls per plant

This trait showed positive significant association with number of monopodia per plant (0.70** and 0.19**) and seed cotton yield per plant (0.52** and 0.50**), while, significant negative association with boll weight (-0.30** and -0.29**) and uniformity ratio (-0.42** and -0.34**) at both genotypic and phenotypic levels.

4.3.5. Boll weight (g)

At genotypic level, this trait showed positive significant association with plant height (0.34**), uniformity ratio (0.16*) and seed cotton yield per plant (0.32**). It also showed negative association with number of monopodia per plant (-0.39**), number of bolls per plant (-0.30**) and 2.5% span length (-0.16*).

This trait showed significant positive association with plant height (0.33**) and seed cotton yield per plant (0.31**) and significant negative association with bolls per plant (-0.29**) at phenotypic level.

4.3.6. Ginning out - turn (%)

This trait showed positive significant association with lint index (0.58** and 0.58**) and uniformity ratio (0.21** and 0.16*) and negative significant association with seed index (-0.58** and -0.56**) and plant height (-0.19** and -0.18*) at genotypic and phenotypic levels, respectively, while, monopodia per plant showed significant positive association (0.35**) with ginning out-turn only at genotypic level.

4.3.7. Seed index (g)

This trait showed positive significant association with lint index (0.31* and 0.28**) and significant negative association with number of sympodia per plant (-0.19* and -0.15*), ginning out-turn % (-0.58** and -0.56**) at both genotypic and phenotypic levels, respectively.

4.3.8. Lint index (g)

This trait showed positive significant association with ginning out turn (0.58** and 0.58**), seed index (0.31* and 0.28**) and uniformity ratio (0.18* and 0.15*) and significant negative association with plant height (-0.16* and -0.16*) and number of sympodia per plant (-0.30**and -0.22**) at both genotypic and phenotypic levels, respectively.

4.3.9. 2.5% span length (mm)

This trait showed negative significant association with uniformity ratio (-0.37** and -0.21**) and seed cotton yield per plant (-0.25** and -0.16*) at both genotypic and phenotypic levels. This trait also showed significant positive association with monopodia per plant (0.46**) and significant negative association with number of sympodia per plant (-0.21**) and boll weight (-0.16) only at genotypic level.

4.3.10. Uniformity ratio

At both genotypic and phenotypic levels, this trait showed positive significant association with ginning out-turn (0.21** and 0.16*) and lint index (0.18* and 0.15*) and negative significant association with number of bolls per plant (-0.42** and -0.34**) and 2.5% span length (-0.37** and -0.21**). Boll weight at genotypic level showed positive significant association (0.16*) with uniformity ratio.

4.3.11. Seed cotton yield per plant (g)

This trait showed positive significant association with plant height (0.26** and 0.25**), number of bolls per plant (0.52** and 0.50**) and boll weight (0.32** and 0.31**) and negative significant association with 2.5% span length (-0.25* and -0.16*) at both genotypic and phenotypic levels, respectively. At genotypic level, it showed positive significant association with number of monopodia per plant (0.22**) and number of sympodia per plant (0.14*).

4.4 PATH COEFFICIENT ANALYSIS

The direct and indirect effects of different yield component traits on seed cotton yield were worked out through path analysis at phenotypic and genotypic levels and are presented in Tables 12 and 13 and Figures 1 and 2.

4.4.1 Plant height (cm)

The direct contribution of this character on seed cotton yield per plant was negative (-0.0549) at phenotypic level and positive (0.0916) at genotypic level.

The indirect effects *via* number of sympodia per plant (0.0367), number of bolls per plant (0.0760), boll weight (0.1721), ginning out-turn (0.0170), seed index (0.0002), 2.5% span length (0.0056) and uniformity ratio (0.0045) were positive, while, number of monopodia per plant (-0.0009) and lint index (-0.0021) were negative at phenotypic level. At genotypic level, indirect effects *via* bolls per plant (0.1497), boll weight (0.2296) and ginning out-turn (0.9680) were positive and were negative *via* seed index (-0.4766) and lint index (-0.7240).

This trait had positive correlation with seed cotton yield per plant (0.2541** and 0.2624**) both at phenotypic and genotypic levels, respectively.

4.4.2 Number of monopodia per plant

The direct contribution of this character on seed cotton yield per plant was positive (0.0248) at phenotypic level and negative (-0.5183) at genotypic level.

The indirect effects *via* plant height (0.0020), number of bolls per plant (0.1391) and lint index (0.0011) were positive, while, number of sympodia per plant (-0.0229), boll weight (-0.0423), ginning out- turn (-0.0103), seed index (-0.0001), 2.5% span length (-0.0073) and uniformity ratio (-0.0051) were negative at phenotypic level. At genotypic level, indirect effects *via* number of bolls per plant (0.9690), seed index (0.4395) and lint index (0.1.2510) were positive, while, were negative for boll weight (-0.2642) and ginning out-turn (-1.7273).

This trait had positive correlation with seed cotton yield per plant (0.0791 and 0.2230) both at phenotypic and genotypic levels.

4.4.3. Number of sympodia per plant

The direct contribution of this character on seed cotton yield per plant was positive (0.1420) at phenotypic level and negative (-0.1256) at genotypic level.

The phenotypic indirect effects *via* number of bolls per plant (0.0121), ginning out-turn (0.0047), 2.5% span length (0.0061) and uniformity ratio (0.0082) were positive, while, indirect effects through plant height (-0.0142), number of monopodia per plant (-0.0040), boll weight (-0.0355), seed index (-0.0003) and lint index (-0.0030) were negative. The indirect effects through monopodia per plant (0.2593), ginning out-turn (0.5055) and seed index (0.8068) were positive on seed cotton yield per plant at genotypic level.

This trait had positive correlation with seed cotton yield per plant (0.1161 and 0.1447) both at phenotypic and genotypic levels, respectively.

4.4.4 Number of bolls per plant

The direct contribution of this character on seed cotton yield per plant was positive (0.7080 and 1.3734) both at phenotypic and genotypic levels.

The phenotypic indirect effects *via* number of monopodia per plant (0.0049), number of sympodia per plant (0.0024) and 2.5% span length (0.0013) were positive. While, plant height (-0.0059), boll weight (-0.1535), ginning out-turn (-0.0033), seed index (-0.0002), lint index (-0.0015) and uniformity ratio (-0.0432) were negative. At genotypic level, indirect effects *via* seed index (0.4958) was positive and were negative through monopodia per plant (-0.3657), boll weight (-0.2047), ginning out-turn (-0.1743) and lint index (-0.5144).

This trait had significant positive correlation with seed cotton yield per plant (0.5090** and 0.5268**) at both phenotypic and genotypic levels, respectively.

4.4.5 Boll weight (g)

The direct contribution of this character on seed cotton yield per plant was positive (0.5205 and 0.6663) both at phenotypic and genotypic levels, respectively.

The phenotypic indirect effects *via* ginning out-turn (0.0063), seed index (0.0002), lint index (0.0003), 2.5% span length (0.0067) and uniformity ratio (0.0167) were also positive. While plant height (-0.0181), number of monopodia per plant (-0.0020), number of sympodia per plant (-0.0097) and number of bolls per plant (-0.2088) were negative at phenotypic level. The indirect effects on seed cotton yield per plant at genotypic level were positive through monopodia per plant (0.2056) and ginning out-turn (0.3296) and were negative *via* bolls per plant (-0.4219) and seed index (-0.6039).

This trait had positive significant correlation with seed cotton yield per plant (0.3121** and 0.3214**) both at phenotypic and genotypic levels, respectively.

4.4.6. Ginning out-turn (%)

The direct contribution of this character on seed cotton yield per plant was negative (-0.0923 and -4.9298) both at phenotypic and genotypic levels, respectively.

The phenotypic indirect effects *via* plant height (0.0101), number of monopodia per plant (0.0028); number of bolls per plant (0.0250), lint index (0.0076), 2.5% span length (0.0012) and uniformity ratio (0.0207) were positive. While, number of sympodia per plant (-0.0073), boll weight (-0.0356) and seed index (-0.0009) were negative.

. The indirect effects on seed cotton yield per plant at genotypic level were positive through seed index (2.4546) and lint index (2.5375) while negative through monopodia per plant (-0.1817).

This trait had negative correlation with seed cotton yield per plant (-0.0687 and -0.0788) both at phenotypic and genotypic levels, respectively.

4.4.7. Seed index (g)

The direct contribution of this character on seed cotton yield per plant was positive (0.0016) at phenotypic level and negative (-4.9298) at genotypic level.

The indirect effects *via* boll weight (0.0715), ginning out–turn (0.0518) and lint index (0.0038) were positive. While, indirect effects were negative through plant height (-0.0060), number of monopodia per plant (-0.0010), number of sympodia per plant (-0.0223), number of bolls per plant (-0.0828), 2.5% span length (-0.0030) and uniformity ratio (-0.0116).

The indirect effects on seed cotton yield per plant at genotypic level were positive through ginning out-turn (2.8684) and lint index (1.3412) and were negative *via* bolls per plant (-0.1614).

This trait had positive correlation with seed cotton yield per plant (0.0022 and 0.0015) both at phenotypic and genotypic levels, respectively.

4.4.8. Lint index (g)

The direct contribution of this character on seed cotton yield per plant was positive (0.0131 and 4.3150) both at phenotypic and genotypic levels, respectively.

The indirect effects *via* plant height (0.0088), number of monopodia per plant (0.0021), boll weight (0.0103), seed index (0.0005) and uniformity ratio (0.0191) were positive. While, indirect effects through number of sympodia per plant (-0.0324), number of bolls per plant (-0.0791), ginning out turn (-0.0536) and 2.5% span length (-0.0036) were negative.

The indirect effects on seed cotton yield per plant at genotypic level were negative through monopodia per plant (-0.1503), bolls per plant (-0.1637), ginning out-turn (-2.8986) and seed index (-1.3110).

This trait had negative correlation with seed cotton yield per plant (-0.1147 and -0.1265) both at phenotypic and genotypic levels, respectively.

4.4.9 2.5% span length (mm)

The direct contribution of this character on seed cotton yield per plant was negative (-0.0672) at phenotypic level and positive (0.1011) at genotypic level.

The indirect effects *via* plant height (0.0046), number of monopodia per plant (0.0027), ginning out turn (0.0017), seed index (0.0001) and lint index

(0.0007) were positive. While, indirect effects were negative through number of sympodia per plant (-0.0129), number of bolls per plant (-0.0137), boll weight (-0.0521) and uniformity ratio (-0.0266). The indirect effects on seed cotton yield per plant at genotypic level were positive through ginning out-turn (0.1440) and lint index (0.3307) and were negative through monopodia per plant (-0.2394), boll weight (-0.1071) and seed index (-0.3870).

This trait had negative significant correlation with seed cotton yield per plant (-0.1628* and -0.2599**) both at phenotypic and genotypic levels, respectively.

4.4.10. Uniformity ratio

The direct contribution of this character on seed cotton yield per plant was positive (0.1248 and 2033) both at phenotypic and genotypic levels, respectively.

The indirect effects *via* number of sympodia per plant (0.0093), boll weight (0.0696), lint index (0.0020) and 2.5% span length (0.0143) were positive and were negative through plant height (-0.0020), number of monopodia per plant (-0.0010), number of bolls per plant (-0.2453), ginning out-turn (-0.0153) and seed index (-0.0001).

The indirect effects on seed cotton yield per plant at genotypic level were positive through boll weight (0.1107), seed index (0.4563) and lint index (0.8059) and were negative through bolls per plant (-0.5891) and ginning out-turn (-1.0594).

This trait had negative correlation with seed cotton yield per plant (-0.0437 and -0.0507) both at phenotypic and genotypic levels, respectively.

Residual effect determines how best the causal factors account for the variability of the dependent factor. In the present investigation, the residual effects at phenotypic and genotypic levels were 0.6800 and 0.6102.

4.5 GENETIC DIVERGENCE

The quantitative assessment of genetic divergence was carried out for 60 genotypes for all the 11 contributing characters studied in the present investigation using Mahalanobis D^2 Statistic, principal component analysis and cluster analysis.

4.5.1. Mahalanobis' D^2 Analysis

4.5.1.1 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 differ significantly when all the characters were considered simultaneously.

4.5.1.2 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 1770 combinations and the corresponding D^2 values were obtained.

The per cent contribution towards genetic divergence by all the 11contributing characters is presented in Table-14. The maximum contribution towards genetic divergence was by seed index (36.50) followed by seed cotton yield per plant (20.45), plant height (18.64), boll weight (11.02), number of bolls per plant (9.44), ginning out-turn (2.99), lint index (0.62), number of sympodia per plant (0.17) and uniformity ratio (0.17). There was no contribution towards genetic divergence for the characters number of monopodia per plant and 2.5% span length.

4.5.1.3 Grouping of genotypes into various clusters

The 60 genotypes were grouped into ten 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 distribution of genotypes into 10 clusters was presented in Table-15. The mutual relationships between the clusters were represented diagrammatically by taking average intra and inter cluster D values. The tree like structure called dendrogram (Fig.-3) was constructed based on clustering by Tocher's method.

4.5.1.4. Average intra-and inter-cluster-D^2 values

The average intra-and inter-Cluster D^2 values estimated as per the procedure given by Singh and Chowdary (1977) are presented in Table -16. The proximity and divergence among ten clusters are indicated in Table - 17.

The maximum intra cluster distance was 275.158 for cluster 10 followed by 161.599 for cluster 4, 95.272 for cluster 3, 82.306 for cluster 2 and 61.130 for cluster 1, while, it was zero for clusters 5, 6, 7, 8 and 9.

Cluster1 was close to cluster 8 (91.206) followed by cluster 5 (107.418) and cluster 6 (109.452) and it is farthest from cluster 10 (450.365) followed by cluster 4 (211.179) and cluster 2 (157.599).

Cluster 2 was close to cluster 7 (146.748) followed by cluster 1(157.599) and cluster 6 (165.346) and it is farthest from cluster 8 (323.816) followed by cluster 9 (258.136) and cluster 4 (254.295).

Cluster 3 was nearer to cluster 1(145.664) followed by cluster 9 (182.675) and cluster 8 (187.228) and it is farthest from cluster 10 (479.329) followed by cluster 7 (364.127) and cluster 6 (321.673).

Cluster 4 was nearer to cluster 1(211.179) followed by cluster 3 (218.835) and cluster 2 (254.295) and it is farthest from cluster 5 (420.093) followed by cluster 10 (409.855) and cluster 9 (362.338).

Cluster 5 was nearer to cluster 7(91.552) followed by cluster 1 (107.418) and cluster 8 (120.553) and it is farthest from cluster 10 (584.264) followed by cluster 4 (420.093) and cluster 3 (275.771).

Cluster 6 was nearer to cluster 7 (37.302) followed by cluster 1 (109.452) and cluster 5 (128.533) and it is farthest from cluster 10 (411.508) followed by cluster 3 (321.673) and cluster 4 (290.809).

Cluster 7 was nearer to Cluster 6 (37.302) followed by cluster 5 (91.552) and cluster 1(137.982) and it is farthest from cluster 10 (385.248) followed by cluster 3 (364.127) and cluster 4 (338.489).

Cluster 8 was nearer to cluster 1 (91.206) followed by cluster 5 (120.553) and cluster 3 (187.228) and it is farthest from cluster 10 (702.395) followed by cluster 2 (323.816) and cluster 4 (278.522).

Cluster 9 was nearer to cluster 1(129.090) followed by cluster 5 (167.474) and cluster 3 (182.675) and it is farthest from cluster 10 (655.924) followed by cluster 4 (362.338) and cluster 7 (287.456).

Cluster 10 was nearer to cluster 2 (224.989) followed by cluster 7 (385.248) and cluster 4 (409.855) and it is farthest from cluster 8 (702.395) followed by cluster 9 (655.924) and cluster 5 (584.264).

4.5.1.5. Cluster Mean Values

The cluster mean values for 11characters are presented in Table -18. The data indicated a wide range of mean values between the characters.

Plant height had a range of 96.00 for cluster 9 to 182.44 for cluster 10; number of monopodia per plant ranged from 1.00 for cluster 8 to 2.33 for clusters 5 and 7; number of sympodia per plant varied from 17.67 for cluster 9 to 27.22 for cluster 10; number of bolls per plant ranged from 35.67 for cluster 6 to 70.78 for cluster 10; boll weight ranged from 3.22 for cluster 8 to 5.52 for cluster 4; ginning out turn varied from 22.33 for cluster 6 to 37.33 for cluster 8; seed index varied from 7.55 for cluster 4 to 12.77 for cluster 7; lint index ranged from 3.60 for cluster 6 to 6.47 for cluster 5; 2.5% span length varied from 24.38 for cluster 9 to 29.59 for cluster 5; uniformity ratio ranged from 44.73 for cluster 6 to 51.00 for cluster 8 and seed cotton yield per plant varied from 105.00 for cluster 8 to 404.56 for cluster 10.

4.5.2. Application of Principal Component analysis in genetic divergence

In principal component analysis on correlation matrix the standardization of columns (characters) created 11 new variables for 60 genotypes without changing their relative positions. These 11 new variables are the principal components (PC_1,

PC_2,------PC_{11}). Each principal component is a linear contribution of the 11 attributes of data matrix. The loading values are scaled or standardized in such a manner that the sum of square of loadings with in 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, subject to the constraint that PC_1, and PC_2 are uncorrelated. The process was continued to create 11 principal components, but PC's having eigen value less than one are not having any practical significance (Legendre and Legendre, 1984).

Principal components (eigen value greater than one), eigen values (Latent Root), per cent variability, Cumulative percent variability and component loading of different characters are presented in Table-19.

In the present study, the first four principal components with eigen values more than one contributed 91.690 per cent towards 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 four principal components.

The first principal component (PC_1) contributed maximum towards variability (35.175%) and it reflected significant positive loading of seed index (0.774), plant height (0.362), boll weight (0.284), lint index (0.281) and seed cotton yield per plant (0.265). The second principal component (PC_2) contributed 30.844 per cent of total variance. The characters *viz*., seed cotton yield per plant (0.750), number of bolls per plant (0.428), seed index (-0.340) and plant height (0.282) explained the maximum variance in the second principal component (PC_2) and signifying their importance in yield. Positive loading values were observed among seed cotton yield per plant number of bolls per plant and plant height, while, seed index showed negative loading value. The third principal component (PC_3) was characterized by 17.468 per cent contribution towards the total variability characters *viz.*, boll weight (0.585), plant height (0.494), number of bolls per plant (-0.504) and seed index (-0.297) showed the maximum variance in this principal component. Boll weight and plant height were reloaded positively where as, number of bolls per plant and seed index were negatively loaded. The fourth principal component (PC_4) was characterized by 8.202 per cent contribution towards the total variability. Characters *viz*., plant height (0.711), boll weight (-0.477) and seed cotton yield per plant (-0.398) showed maximum variance in this component. Plant height, monopodia per plant, sympodia per plant and bolls per plant loaded positively where as, other remaining characters were negatively loaded.

The PCA scores for 60 cotton genotypes in the first three principal components were computed. Principal Components 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-20.

These three PCA scores for 60 genotypes were plotted in graph to get two dimensional and three dimensional scatter diagrams (Fig. 4 and 5).

4.5.3. Cluster analysis

To group the 60 genotypes into various clusters, agglomerative hierarchical cluster analysis was followed. Principal component scores for genotypes were used as input for clustering in Ward's minimum variance method. The Tree like structure called dendrogram (Fig-6) was constructed based on Euclidean ^{2} distance computed from PCA scores of genotypes.

The 60 genotypes were grouped into 8 clusters. The distribution of genotypes into 8 clusters was presented in Table-21. The mutual relationship between clusters was represented diagrammatically (Fig-7) by taking average intra- and inter-clusters 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-22.

By Ward's method, the 60 genotypes were grouped into 8 clusters of the 8 clusters formed. Cluster 1 had minimum intra cluster Euclidean^2 distance value of 131.780 followed by cluster 3 (162.241), cluster 8 (166.394), cluster 4 (193.039), cluster 2 (202.055), cluster 5 (206.285), cluster 7 (269.426) and cluster 6 (498.419).

The inter cluster Euclidean^2 distance varied from 346.895 (between cluster 1 and cluster 2) to 1671.909 (cluster 3 and cluster 6). All the inter-cluster Euclidean^2 values were lying between these values.

Cluster 1 was composed of 7 genotypes. It was nearest to cluster 2 (346.895) followed by cluster 5 (361.039) and farthest from cluster 8 (1209.205) followed by cluster 7 (985.312).

Cluster 2 was composed of 14 genotypes. It was nearest to cluster1 (346.895) followed by cluster 5 (371.340) and farthest from cluster 6 (1291.112) followed by cluster 8 (771.988).

Cluster 3 was composed of 8 genotypes. It was nearest to cluster 8(396.225) followed by cluster 2 (429.835) and farthest from cluster 6 (1671.909) followed by cluster 7 (806.818).

Cluster 4 was composed of 6 genotypes. It was nearest to cluster 5 (395.411) followed by cluster 1 (556.547) and farthest from cluster 7 (959.224) followed by cluster 6 (923.151).

Cluster 5 was composed of 9 genotypes. It was nearest to cluster 1 (361.039) followed by cluster 2 (371.340) and farthest from cluster 6 (784.706) followed by cluster 7 (561.042).

Cluster 6 was composed of 3 genotypes. It was nearest to cluster 5 (784.706) followed by cluster 7 (821.444) and farthest from cluster 3 (1671.909) followed by cluster 8 (1241.931).

Cluster 7 was composed of 9genotypes. It was nearest to cluster 8 (417.024) followed by cluster 5 (561.042) and farthest from cluster 1 (985.312) followed by cluster 4 (959.224).

Cluster 8 was composed of 4 genotypes. It was nearest to cluster 3 (396.225) followed by cluster 7 (417.024) and farthest from cluster 6 (1241.931) followed by cluster 1 (1209.205).

4.5.3.2. Cluster means

Cluster means were computed for the 11characters studied on pooled basis and are presented in Table –23.

Cluster 1 recorded high mean value for seed cotton yield per plant (258.00) and plant height (143.762), but showed low mean value for number of monopodia per plant (2.238) and lint index (3.733)

Cluster 2 recorded high mean value for seed cotton yield per plant (210.595) and plant height (129.024), but showed low mean value for number of monopodia per plant (2.143) and boll weight (3.810).

Cluster 3 recorded high mean value for seed Cotton yield per plant (154.33) and plant height (144.167), but showed low mean value for number of monopodia per plant (1.708) and boll weight (4.109).

Cluster 4 recorded high mean value for seed cotton yield per plant (234.278) and plant height (161.556), but showed low mean value for number of monopodia per plant (1.667) and lint index (4.122).

Cluster 5 recorded high mean value for seed cotton yield per plant (224.111) and plant height (165.00), but showed low mean value for number of monopodia per plant (2.00) and lint index (3.70).

Cluster 6 recorded high mean value for seed cotton yield per plant (432.111) and plant height (181.778), but showed low mean value for number of monopodia per plant (2.222) and lint index (4.033).

Cluster 7 recorded high mean value for seed cotton yield per plant (315.407) and plant height (158.778), but showed low mean value for number of monopodia per plant (2.074) and lint index (4.533).

Cluster 8 recorded high mean value for seed cotton yield per plant (225.00) and plant height (162.167), but showed low mean value for number of monopodia per plant (2.000) and lint index (4.358).

Table-8: Analysis of variance for yield and yield components in cotton (*Gossypium hirsutum* L .).

Sl. No.		**Source of variation**		
		Replications	**Genotypes**	**Error**
	Degrees of freedom	**2**	**59**	**118**
	Characters	**Mean squares**		
1	Plant height(cm)	17.89	1237.48**	8.89
2	No. of monopodia / plant	0.03	1.551**	0.03
3	No. of sympodia / plant	1.44	112.22**	6.80
4	No. of bolls / plant	6.54	112.22**	6.81
5	Boll weight (g)	0.01	2.15**	0.03
6	Seed index (g)	0.02	11.15**	0.05
7	Lint index (g)	0.02	2.23**	0.06
8	Ginning-out-turn (%)	0.91	19.51**	1.14
9	2.5% span length (mm)	0.34	9.66**	3.29
10	Uniformity ratio	0.31	30.25**	3.87
11	Seed cotton yield / plant (g)	154.26	1710.01**	121.26

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

Table 9: Mean performance of 60 genotypes of cotton for 11 characters.

Sl. No	Genotypes	Plant height (cm)	Monopodia/ plant	Sympodia/ plant	Bolls/ plant	Boll weight (g)	Ginning outturn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Uniformity ratio	Seed cotton yield/ plant (g)
1	NA-1325	142.00	2.66	21.66	72.66	4.06	41.00	6.43	4.60	25.61	43.40	320.00
2	L-604	96.00	2.00	17.66	46.00	5.05	32.00	9.60	4.63	24.38	49.36	220.00
3	NDLH- 1678	154.00	2.33	22.00	56.33	4.76	30.00	12.36	5.23	23.87	47.56	305.00
4	CWROK -165	135.66	2.33	26.00	46.33	3.26	35.66	11.60	6.46	29.59	48.43	158.33
5	MCU – 5	144.66	2.33	25.00	64.00	2.92	32.66	8.60	4.26	31.27	37.53	216.66
6	L – 761	142.00	2.66	22.00	72.66	4.15	36.00	9.60	5.40	26.37	45.66	149.33
7	L – 765	165.00	3.00	22.33	64.00	4.56	33.00	11.53	5.76	26.36	49.13	291.66
8	L – 763	144.33	1.66	24.00	72.33	4.92	33.33	10.40	5.23	26.92	45.33	340.00
9	LK -861	125.66	1.00	22.00	56.00	4.15	30.33	9.33	4.20	23.30	46.96	236.66
10	L -603	123.66	1.66	25.00	66.00	2.77	39.00	7.23	4.70	27.25	44.13	182.00
11	RAH-3	142.33	1.66	23.66	66.00	4.41	33.66	6.40	3.33	27.73	40.83	223.66
12	SRT - 1	124.00	2.66	21.66	56.33	3.65	39.00	8.60	5.56	25.47	47.73	228.00
13	NH - 100	126.33	3.33	24.33	60.33	3.33	28.33	8.20	3.26	27.19	48.40	216.66
14	CCH - 5104	143.00	2.33	22.00	66.00	4.34	25.33	12.60	4.30	25.14	47.10	300.33
15	SCS - 95	152.00	1.33	23.66	60.66	3.57	31.00	9.26	4.20	25.35	49.26	205.00
16	ARB - 8906	115.00	2.33	23.33	64.00	4.56	41.00	6.76	4.73	25.26	47.66	289.66

Contd…

Sl. No	Genotypes	Plant height (cm)	Monopodia/ plant	Sympodia/ plant	Bolls/ plant	Boll weight (g)	Ginning outturn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Uniformity ratio	Seed cotton yield/ plant (g)
17	SCS - 51	152.00	2.00	26.00	65.33	3.56	28.33	6.46	2.60	23.42	47.50	235.00
18	CPD - 787	132.33	1.3333	32.3333	42.00	3.85	29.66	11.30	4.76	26.59	47.05	164.00
19	ARB - 9009	135.66	2.66	24.33	55.33	4.22	37.66	8.60	5.20	25.27	43.35	206.00
20	MCU - 7	163.00	1.00	25.33	34.00	6.00	40.33	6.43	4.46	24.91	49.33	184.33
21	KH - 140	172.00	1.66	32.00	72.66	4.16	26.33	8.70	3.20	22.91	48.80	566.66
22	L - 769	144.33	2.00	24.00	65.33	3.52	35.00	6.40	3.46	25.84	47.90	229.66
23	L - 768	164.66	2.33	23.33	51.66	3.77	25.00	9.36	3.20	28.07	42.83	177.00
24	L - 864	161.66	1.66	21.66	35.66	4.82	22.33	12.33	3.60	28.90	44.73	175.00
25	RHH - 7553	165.66	1.66	23.00	71.66	3.63	28.33	10.76	4.40	26.22	46.23	256.00
26	Abhadita	142.00	1.33	23.66	47.66	4.42	40.00	8.60	5.63	28.03	48.20	205.00
27	ARB - 760	146.00	3.00	22.00	56.33	4.83	30.66	8.26	3.60	27.90	42.96	258.33
28	GJHV -392	153.66	2.00	24.33	36.00	6.32	34.33	8.30	4.36	29.66	46.00	201.66
29	GIHV- 53	183.33	1.66	25.66	66.00	5.77	26.00	12.20	4.40	27.55	46.30	371.66
30	LRK-5166	142.66	1.66	25.66	73.00	5.16	27.00	9.36	3.60	28.33	43.86	376.66
31	SCS- 101	169.33	2.66	27.00	47.33	5.50	28.00	11.60	4.56	24.55	49.63	243.33
32	RS -2141	154.33	2.33	31.66	70.33	4.09	41.00	5.70	4.10	25.95	47.73	283.00
33	GJHV- 99/307	192.00	2.00	24.00	73.66	4.52	20.66	13.36	3.26	25.93	45.03	275.33
34	TSH -9727	132.33	2.00	22.33	37.33	4.49	30.33	9.53	4.23	27.95	50.76	152.00

Contd…

Sl. No	Genotypes	Plant height (cm)	Monopodia/ plant	Sympodia/ plant	Bolls/ plant	Boll weight (g)	Ginning outturn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Uniformity ratio	Seed cotton yield/ plant (g)
35	CCH-18	191.00	2.33	22.00	62.00	6.14	37.33	7.23	4.33	24.85	47.16	387.33
36	MCU - 2	182.33	2.66	21.66	63.66	5.55	35.33	8.20	4.56	27.60	50.00	342.33
37	PKV Rajat	163.33	2.33	23.33	45.66	4.82	37.00	7.60	4.46	25.76	57.20	299.33
38	Surabhi	156.00	1.33	22.66	56.33	5.47	22.33	12.10	3.50	27.91	39.60	276.66
39	TCH - 1542	172.00	1.00	24.00	56.00	4.82	26.00	9.76	3.56	24.91	42.60	256.66
40	GMP - 5	115.00	2.66	21.00	46.33	3.44	29.66	7.63	3.33	28.45	47.03	242.33
41	HAG - 785	163.66	1.33	26.00	56.33	3.86	23.66	8.36	2.63	25.49	49.70	173.33
42	Khandwa	145.00	1.66	21.66	47.00	6.04	40.66	7.60	5.30	27.37	52.56	283.33
43	HLS - 271	154.66	1.33	22.00	52.33	4.36	32.33	9.20	4.50	26.25	50.66	241.66
44	ICMF - 230	135.66	1.66	22.33	36.00	4.18	29.66	10.60	4.56	27.15	49.90	152.00
45	RS - 2169	152.33	3.00	22.00	37.00	4.86	32.00	11.20	5.36	25.60	50.73	183.33
46	ICMF - 1542	174.00	2.66	25.33	74.33	3.46	35.33	7.46	4.20	27.99	47.60	193.33
47	CNH - 3003	136.00	2.33	22.00	77.66	4.67	28.00	9.43	3.70	25.48	44.90	224.33
48	ACS - 738	127.33	2.66	22.00	52.33	3.52	28.33	8.50	3.40	28.41	46.33	164.33
49	MCU - 12	194.66	2.66	24.33	83.33	3.44	37.00	7.60	4.56	27.83	45.53	225.00
50	NDLH - 1754	146.00	1.33	23.33	36.33	4.52	28.00	10.60	4.20	26.86	48.30	171.66
51	ARB - 784	161.66	2.33	22.33	44.00	4.76	31.00	12.76	5.76	28.59	46.96	205.00
52	SES - 21	164.00	1.00	25.33	37.00	4.45	30.33	10.40	4.60	23.09	48.66	148.33

Contd…

Sl. No	Genotypes	Plant height (cm)	Monopodia/ plant	Sympodia/ plant	Bolls/ plant	Boll weight (g)	Ginning outturn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Uniformity ratio	Seed cotton yield/ plant (g)
53	Krishna	162.00	1.33	31.00	34.00	5.82	25.33	7.56	2.60	25.03	50.03	212.00
54	BUSP - 13	163.00	1.66	25.00	45.66	4.76	32.00	9.20	4.26	25.91	45.70	226.66
55	ADB - 39	182.33	1.66	31.00	44.66	5.34	32.00	7.53	3.53	24.42	48.26	225.00
56	H - 1246	155.00	1.00	25.00	36.33	3.22	37.33	8.56	5.20	26.40	51.00	105.00
57	HD - 328	139.00	2.33	25.66	75.00	4.26	27.00	12.30	4.60	27.19	44.36	322.00
58	ARB - 2005	156.33	2.66	27.66	62.33	3.28	31.66	7.20	3.30	25.64	47.63	225.00
59	RCH - 1594	152.33	2.00	25.33	55.66	4.64	24.66	8.20	2.76	30.43	50.33	265.00
60	MCU - 9	116.00	1.33	24.66	66.00	3.45	33.66	8.63	4.56	27.95	48.13	252.00
	Mean	**150.72**	**2.01**	**24.22**	**56.23**	**4.40**	**31.66**	**9.18**	**4.26**	**26.52**	**47.12**	**240.77**
	C.V.	1.97	46.58	8.19	3.98	3.72	4.66	2.40	5.93	6.83	4.17	4.64
	S.E.	1.72	0.54	1.14	1.29	0.09	0.85	0.12	0.14	1.04	1.13	6.46
	C.D. 5%	4.82	1.51	3.21	3.61	0.26	2.38	0.35	0.40	2.93	3.18	18.10
	C.D. 1%	6.37	2.00	4.24	4.78	0.35	3.15	0.47	0.54	3.87	4.20	23.93

Table 10: **Mean, variability, heritability and genetic advance as per cent of mean for yield and yield components 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)	150.72	96.00	194.67	13.57	13.43	97.88	27.36
2	No. of monopodia/ plant	2.01	1.00	3.33	13.38	13.05	7.27	7.25
3	No. of sympodia / plant	24.22	17.67	32.33	13.48	10.71	63.05	17.51
4	No. of bolls/ plant	56.24	36.00	83.33	23.79	23.46	97.20	47.65
5	Boll weight (g)	4.40	2.77	6.32	19.47	19.11	96.34	38.64
6	Seed index (g)	9.19	5.70	13.37	21.07	20.93	98.69	42.84
7	Lint index (g)	4.27	2.60	6.47	20.81	19.94	91.87	39.37
8	Ginning out-turn (%)	31.67	20.66	41.00	16.98	16.34	92.45	32.36
9	2.5% span length (mm)	26.53	22.91	31.28	8.77	5.49	39.21	7.08
10	Uniformity ratio	47.13	37.53	57.20	7.55	6.29	69.44	10.80
11	Seed cotton yield/ plant (g)	240.78	105.00	566.66	31.31	30.96	97.79	63.07

Table 11: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients for yield and yield components in 60 genotypes of cotton (*Gossypium hirsutum* L.).

Sl. No	Character	Plant height (cm)	Mono-podia/ plant	Sympodia/ plant	Bolls/ plant	Boll weight (g)	Ginning outturn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Uniformity ratio	Seed cotton yield/ plant
1	Plant height (cm)	**1.00**	-0.03	0.25**	0.10	0.33**	-0.18*	0.10	-0.16*	-0.08	0.03	**0.251****
2	Monopodia/ plant	-0.13	**1.00**	-0.16*	0.19**	-0.08	0.11	-0.03	0.08	0.10	-0.04	**0.079**
3	Sympodia/ plant	0.31**	-0.50**	**1.00**	0.01	-0.06	-0.05	-0.15*	-0.22**	-0.09	0.06	**0.116**
4	Bolls/ plant	0.10	0.70**	0.02	**1.00**	-0.29**	0.03	-0.11	-0.11	-0.01	-0.34**	**0.509****
5	Boll weight (g)	0.34**	-0.39**	-0.06	-0.30**	**1.00**	-0.06	0.13	0.01	-0.10	0.13	**0.312****
6	Ginning outturn (%)	-0.19**	0.35**	-0.10	0.03	-0.06	**1.00**	-0.56**	0.58**	-0.01	0.16*	**-0.069**
7	Seed index (g)	0.11	-0.10	-0.19**	-0.11	0.14	-0.58**	**1.00**	0.28**	0.04	-0.09	**0.002**
8	Lint index (g)	-0.16*	0.28**	-0.30**	-0.11	0.02	0.58**	0.31**	**1.00**	0.05	0.15*	**-0.115**
9	2.5% span length (mm)	-0.13	0.46**	-0.21**	-0.02	-0.16*	-0.02	0.09	0.07	**1.00**	-0.21**	**-0.163***
10	Uniformity ratio	0.03	-0.11	0.03	-0.42**	0.16*	0.21**	-0.10	0.18*	-0.37**	**1.00**	**-0.044**
11	**Seed cotton yield/ plant (g)**	**0.26****	**0.22****	**0.14***	**0.52****	**0.32****	**-0.07**	**0.00**	**-0.12**	**-0.25****	**-0.05**	**1.00**

* and ** indicate significance at 5% and 1% level, respectively.

Table 13: Direct and indirect genotypic effects between yield and yield components in 60 genotypes of cotton (*Gossypium hirsutum* L.).

Sl. No	Character	Plant height (cm)	Monopodia / plant	Sympodia/ plant	Bolls/ plant	Boll weight (g)	Ginning outturn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Uniformity ratio
1	Plant height (cm)	**0.0916**	-0.0125	0.0292	0.0100	0.0316	-0.0180	0.0103	-0.0154	-0.0128	0.0035
2	Monopodia/ plant	0.0706	**-0.5183**	0.2593	-0.3657	0.2056	-0.1817	0.0540	-0.1503	-0.2394	0.0604
3	Sympodia/ plant	-0.0401	0.0628	**-0.1256**	-0.0031	0.0079	0.0129	0.0240	0.0381	0.0275	-0.0046
4	Bolls/ plant	0.1497	0.9690	0.0340	**1.3734**	-0.4219	0.0486	-0.1614	-0.1637	-0.0411	-0.5891
5	Boll weight (g)	0.2296	-0.2642	-0.0422	-0.2047	**0.6663**	-0.0446	0.0954	0.0137	-0.1071	0.1107
6	Ginning outturn (%)	0.9680	-1.7273	0.5055	-0.1743	0.3296	**-4.9289**	2.8684	-2.8986	0.1440	-1.0594
7	Seed index (g)	-0.4766	0.4395	0.8068	0.4958	-0.6039	2.4546	**-4.2178**	-1.3110	-0.3870	0.4563
8	Lint index (g)	-0.7240	1.2510	-1.3078	-0.5144	0.0887	2.5375	1.3412	**4.3150**	0.3307	0.8059
9	2.5% span length (mm)	-0.0141	0.0467	-0.0221	-0.0030	-0.0162	-0.0030	0.0093	0.0077	**0.1011**	-0.0377
10	Uniformity ratio	0.0077	-0.0237	0.0075	-0.0872	0.0338	0.0437	-0.0220	0.0380	-0.0758	**0.2033**
	Correlation coefficient with seed cotton yield/ plant	**0.2624****	**0.2230****	**0.1447***	**0.5268****	**0.3214****	**-0.0788**	**0.0015**	**-0.1265**	**-0.2599****	**-0.0507**

RESIDUAL EFFECT = 0.6102

* & ** = significant at 5% and 1% level

Table 12: Direct and indirect phenotypic effects between yield and yield components in 60 genotypes of cotton (*Gossypium hirsutum* L.).

Sl. No	Character	Plant height (cm)	Monopodia/ plant	Sympodia/ plant	Bolls/ plant	Boll weight (g)	Ginning outturn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Uniformity ratio
1	Plant height (cm)	**-0.0549**	0.0020	-0.0142	-0.0059	-0.0181	0.0101	-0.0060	0.0088	0.0046	-0.0020
2	Monopodia/ plant	-0.0009	**0.0248**	-0.0040	0.0049	-0.0020	0.0028	-0.0010	0.0021	0.0027	-0.0010
3	Sympodia/ plant	0.0367	-0.0229	**0.1420**	0.0024	-0.0097	-0.0073	-0.0223	-0.0324	-0.0129	0.0093
4	Bolls/ plant	0.0760	0.1391	0.0121	**0.7080**	-0.2088	0.0250	-0.0828	-0.0791	-0.0137	-0.2453
5	Boll weight (g)	0.1721	-0.0423	-0.0355	-0.1535	**0.5205**	-0.0356	0.0715	0.0103	-0.0521	0.0696
6	Ginning outturn (%)	0.0170	-0.0103	0.0047	-0.0033	0.0063	**-0.0923**	0.0518	-0.0536	0.0017	-0.0153
7	Seed index (g)	0.0002	-0.0001	-0.0003	-0.0002	0.0002	-0.0009	**0.0016**	0.0005	0.0001	-0.0001
8	Lint index (g)	-0.0021	0.0011	-0.0030	-0.0015	0.0003	0.0076	0.0038	**0.0131**	0.0007	0.0020
9	2.5% span length (mm)	0.0056	-0.0073	0.0061	0.0013	0.0067	0.0012	-0.0030	-0.0036	**-0.0672**	0.0143
10	Uniformity ratio	0.0045	-0.0051	0.0082	-0.0432	0.0167	0.0207	-0.0116	0.0191	-0.0266	**0.1248**
	Correlation coefficient with seed cotton yield/ plant	**0.2541****	**0.0791**	**0.1161**	**0.5090****	**0.3121****	**-0.0687**	**0.0022**	**-0.1147**	**-0.1628***	**-0.0437**

RESIDUAL EFFECT = 0.6800

* & ** = significant at 5% and 1% level

Table 14: Contribution of different characters towards genetic divergence in 60 genotypes of cotton.

Sl. No.	Character	Per cent contribution towards divergence	Times ranked 1st
1	Plant height (cm)	18.64	330
2	Number of monopodia/ plant	0.00	0
3	Number of sympodia/ plant	0.17	3
4	Number of bolls/ plant	9.44	167
5	Boll weight (g)	11.02	195
6	Ginning out-turn (%)	2.99	53
7	Seed index (g)	36.50	646
8	Lint index (g)	0.62	11
9	2.5% span length (mm)	0.00	0
10	Uniformity ratio	0.17	3
11	Seed cotton yield/ plant (g)	20.45	362

Table 15: Clustering of 60 cotton (*Gossypium hirsutum* L.) genotypes by Tocher's method.

Cluster No.	Number of genotypes	Name of the genotypes
I	13	ICMF-230, NDLH-1754, TSH-9727, CPD-787, RS-2169, SES-21, Abhadita, BUSP-13, HLS-271, ARB-9009, SCS-95, L-768, LK-861.
II	11	CCH-5104, HD-328, NDLH-1678, L-765, L-763, RHH-7553, Surabhi, TCH-1542, SCS-101, CNH-3003, LRK-5166.
III	21	SCS-51, L-769, ARB-2005, RAH-3, RS-2141, NA-1325, ARB-760, RCH-1594, ICMF-1452, HAG-785, NH-100, MCU-5, ACP-738, MCU-9, SRT-1, L-603, GMP-5, ARB-8906, PKV-Rajat, L-761, Khandwa.
IV	7	CCH-18, MCU-2, ADB-39, Krishna, GJHV-392, MCU-7, MCU-12.
V	1	CWROK-165.
VI	1	L-864.
VII	1	ARB-784.
VIII	1	H-1246.
IX	1	L-604.
X	3	GIHV-53, GJHV-99 / 307, KH-140.

Table 16: Average intra (Bold values) and inter cluster D^2 values of 10 clusters for 60 genotypes of cotton (*Gossypium hirsutum* L.).

Inter & Intra- cluster distances										
Clusters	**1 Cluster**	**2 Cluster**	**3 Cluster**	**4 Cluster**	**5 Cluster**	**6 Cluster**	**7 Cluster**	**8 Cluster**	**9 Cluster**	**10 Cluster**
1 Cluster	**61.130**	157.599	145.664	211.179	107.418	109.452	137.982	91.206	129.090	450.365
2 Cluster		**82.306**	221.993	254.295	216.804	165.346	146.748	323.816	258.136	224.989
3 Cluster			**95.272**	218.835	275.771	321.673	364.127	187.228	182.675	479.329
4 Cluster				**161.599**	420.093	290.809	338.489	278.522	362.338	409.855
5 Cluster					**0.000**	128.533	91.552	120.553	167.474	584.264
6 Cluster						**0.000**	37.302	190.458	258.602	411.508
7 Cluster							**0.000**	235.101	287.456	385.248
8 Cluster								**0.000**	198.794	702.395
9 Cluster									**0.000**	655.924
10 Cluster										**275.158**

Table -17: 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	VIII (91.206)	X (450.365)
II	VII (146.748)	VIII (323.816)
III	I (145.664)	X (479.329)
IV	I (211.179)	V (420.093)
V	VII (91.552)	X (584.264)
VI	VII (37.302)	X (411.508)
VII	V (91.552)	X (385.248)
VIII	I (91.206)	X (702.395)
IX	I (129.090)	X (655.924)
X	II (224.989)	VIII (702.395)

Table 18: Mean values of ten clusters (obtained by Tocher's method) estimated from 60 genotypes of cotton (*Gossypium hirsutum* L.) for 11 characters.

Cluster Means											
Clusters	**Plant height (cm)**	**Monopodia/ plant**	**Sympodia/ plant**	**Bolls/ plant**	**Boll weight (g)**	**Ginning outturn (%)**	**Seed index (g)**	**Lint index (g)**	**2.5% span length (mm)**	**Uniformity ratio**	**Seed cotton yield/ plant (g)**
1 Cluster	146.179	1.692	23.974	45.769	4.280	31.410	9.785	4.533	26.112	47.878	189.949
2 Cluster	153.364	2.030	23.667	65.061	4.738	28.030	11.112	4.406	26.084	45.485	290.242
3 Cluster	141.413	2.286	24.159	61.206	3.923	33.825	7.613	3.981	26.990	47.048	234.762
4 Cluster	175.571	1.952	25.667	51.095	5.517	34.524	7.552	4.062	26.331	48.048	253.952
5 Cluster	135.667	2.333	26.000	46.333	3.263	35.667	11.600	6.467	29.597	48.433	158.333
6 Cluster	161.667	1.667	21.667	35.667	4.823	22.333	12.333	3.600	28.907	44.733	175.000
7 Cluster	161.667	2.333	22.333	44.000	4.760	31.000	12.767	5.767	28.590	46.967	205.000
8 Cluster	155.000	1.000	25.000	36.333	3.223	37.333	8.567	5.200	26.403	51.000	105.000
9 Cluster	96.000	2.000	17.667	46.000	5.050	32.000	9.600	4.633	24.380	49.367	220.000
10 Cluster	182.444	1.778	27.222	70.778	4.817	24.333	11.422	3.622	25.466	46.711	404.556

Table 19: Eigen values, proportion of the total variability, cumulative per cent variability and component loading of different characters in cotton (*Gossypium hirsutum* L.).

	PC $_1$	**PC $_2$**	**PC $_3$**	**PC $_4$**
Eigen Value (Root)	**2059.432**	**1805.840**	**1022.742**	**480.227**
% Var. Exp.	**35.175**	**30.844**	**17.468**	**8.202**
Cum. Var. Exp.	**35.175**	**66.019**	**83.487**	**91.690**
Plant height	0.362	0.282	0.494	0.711
Monopodia / plant	-0.002	0.010	-0.021	0.009
Sympodia/ plant	-0.035	0.014	-0.008	0.001
Bolls/ plant	0.010	0.428	-0.504	0.231
Boll weight (g)	0.284	0.076	0.585	-0.477
Ginning outturn (%)	-0.174	0.001	0.113	-0.190
Seed index (g)	0.774	-0.340	-0.297	-0.057
Lint index (g)	0.281	-0.207	-0.165	-0.032
2.5% span length (mm)	0.094	-0.069	-0.069	-0.009
Uniformity ratio	-0.018	-0.076	0.086	-0.124
Seed cotton yield/ plant (g)	0.265	0.750	-0.136	-0.398

PC = Principal Component

Table 20: PCA scores of 60 genotypes of cotton (*Gossypium hirsutum* L.).

Sl. No.	Genotypes	PCA I	PCA II	PCA III
		X Vector	Y Vector	Z Vector
1	NA-1325	41.104	19.495	5.419
2	L-604	43.109	5.245	4.347
3	NDLH -1678	56.820	10.266	4.829
4	CWROK- 165	49.594	1.308	2.921
5	MCU - 5	43.669	11.991	2.939
6	L - 761	46.692	8.348	3.507
7	L - 765	56.056	11.894	5.129
8	L - 763	52.621	15.635	3.183
9	LK -861	44.812	9.929	4.265
10	L- 603	37.531	10.664	2.080
11	RAH- 3	39.850	15.820	7.901
12	SRT - 1	42.506	8.994	3.631
13	NH - 100	40.879	11.298	3.196
14	CCH - 5104	55.701	11.127	1.167
15	SCS - 95	46.256	10.844	5.462
16	ARB - 8906	39.205	14.803	4.952
17	SCS - 51	39.858	17.118	7.338
18	CPD - 787	48.813	2.532	5.056
19	ARB - 9009	44.041	9.125	6.292
20	MCU - 7	42.699	10.156	18.906
21	KH - 140	53.284	30.052	4.835
22	L - 769	38.831	15.717	6.602
23	L - 768	47.284	9.931	8.474
24	L - 864	54.819	3.845	10.001
25	RHH - 7553	52.426	13.567	3.257
26	Abhadita	44.835	8.058	8.695
27	ARB - 760	45.450	13.675	8.474
28	GJHV- 392	47.165	8.487	15.923
29	GIHV- 53	61.976	17.185	8.108

Contd..

Sl. No.	Genotypes	PCA I	PCA II	PCA III
		X Vector	Y Vector	Z Vector
30	LRK-5166	50.599	19.568	4.188
31	SCS- 101	56.397	8.789	10.655
32	RS -2141	40.134	19.489	8.375
33	GJHV- 99/307	62.156	14.296	5.079
34	SH -9727	44.759	3.747	8.991
35	CCH - 18	51.247	23.387	15.295
36	MCU - 2	51.519	19.772	12.195
37	PKV Rajat	45.935	14.781	12.745
38	Surabhi	56.630	11.145	6.881
39	TCH - 1542	51.639	13.855	9.817
40	GMP - 5	38.482	10.331	4.748
41	HAG - 785	44.900	11.938	9.128
42	Khandwa	45.793	12.804	12.985
43	HS - 271	47.760	11.229	8.430
44	ICMF - 230	47.242	2.353	7.831
45	RS - 2169	51.876	3.517	9.883
46	ICMF - 1542	44.381	15.555	7.190
47	CNH - 3003	47.145	13.357	2.914
48	ACS - 738	40.960	7.781	4.968
49	MCU - 12	47.506	19.072	7.474
50	NDLH - 1754	48.937	4.252	9.431
51	ARB - 784	57.096	3.999	7.692
52	SES - 21	49.913	4.548	11.533
53	Krishna	45.456	11.347	17.004
54	BUSP - 13	48.695	10.479	11.231
55	ADB - 39	47.328	13.936	16.454
56	H - 1246	42.621	3.442	10.286
57	HD - 328	55.368	13.135	-0.869
58	ARB - 2005	41.610	15.008	7.021
59	RCH - 1594	45.871	14.853	8.993
60	MCU - 9	42.090	11.603	0.723

Table 21: Clustering of 60 genotypes of cotton (*Gossypium hirsutum* L.) by Ward's minimum variance method.

Cluster No.	Number of Genotypes	Name of the Genotypes
I	7	NA 1325, RS 2141, ARB 8906, SCS-51, L-769, ARB-2005, RAH-3.
II	14	MCU-5, SCS-95, L-761, CNH-3003, LK-861, SRT-1, MCU-9, ARB-9009, Abhadita, L-604, NH-100, ACP-738, GMP-5, L-603.
III	8	CWROK-165, CPD-787, ICMF-230, NDLH-1754, TSH-9727, RS-2169, SES-21, H-1246.
IV	6	MCU-7, GJHV-392, Krishna, ADB-39, PKV Rajat, Khandwa.
V	9	L-768, HAG-785, ARB-760, RCH-1594, HLS-271, BUSP-13, TCH-1542, ICMF-1452, MCU-12.
VI	3	CCH-18, MCU-2, KH-140.
VII	9	NDLH-1678, L-765, RHH-7553, CCH-5104, HD-328, L-763, LRK-5166, GJHV-53, GJHV-99/307.
VIII	4	L-864, ARB-784, SCS-101, Surabhi.

Table 22: Intra (Bold values) -and inter-cluster squared Euclidian^2 distance between eight clusters formed by Ward's minimum variance method in 60 cotton (*Gossypium hirsutum* L.) genotypes

Euclidean² : Cluster Distances								
Clusters	**1 Cluster**	**2 Cluster**	**3 Cluster**	**4 Cluster**	**5 Cluster**	**6 Cluster**	**7 Cluster**	**8 Cluster**
1 Cluster	**131.78**	346.895	880.03	556.547	361.039	903.163	985.312	1209.205
2 Cluster		**202.055**	429.835	615.509	371.34	1291.112	767.442	771.988
3 Cluster			**162.241**	584.58	501.134	1671.909	806.818	396.225
4 Cluster				**193.039**	395.411	923.151	959.224	706.813
5 Cluster					**206.285**	784.706	561.042	557.508
6 Cluster						**498.419**	821.444	1241.931
7 Cluster							**269.426**	417.024
8 Cluster								**166.394**

Bold and diagonal values are intra - cluster distances

Table 23: Mean values of eight clusters (obtained by Ward's method) estimated from 60 genotypes of cotton (*Gossypium hirsutum* L.) for 11 characters.

Cluster Means											
Clusters	**Plant height (cm)**	**Monopodia/ plant**	**Sympodia/ plant**	**Bolls/ plant**	**Boll weight (g)**	**Ginning outturn (%)**	**Seed index (g)**	**Lint index (g)**	**2.5% span length (mm)**	**Uniformity ratio**	**Seed cotton yield/ plant (g)**
Cluster 1	143.762	2.238	25.429	66.571	3.928	35.952	6.481	3.733	25.639	46.095	258.000
Cluster 2	129.024	2.143	22.786	59.095	3.810	33.262	8.702	4.433	26.730	46.216	210.595
Cluster 3	144.167	1.708	24.833	38.542	4.109	31.625	10.475	4.925	26.656	49.357	154.333
Cluster 4	161.556	1.667	26.111	40.222	5.723	34.944	7.506	4.122	26.193	50.567	234.278
Cluster 5	165.000	2.000	24.148	59.074	4.217	29.630	8.604	3.700	27.199	46.437	224.111
Cluster 6	181.778	2.222	25.222	66.111	5.286	33.000	8.044	4.033	25.122	48.656	432.111
Cluster 7	158.778	2.074	23.815	68.667	4.659	27.852	11.656	4.533	26.395	46.104	315.407
Cluster 8	162.167	2.000	23.417	45.833	5.141	25.917	12.200	4.358	27.490	45.233	225.000

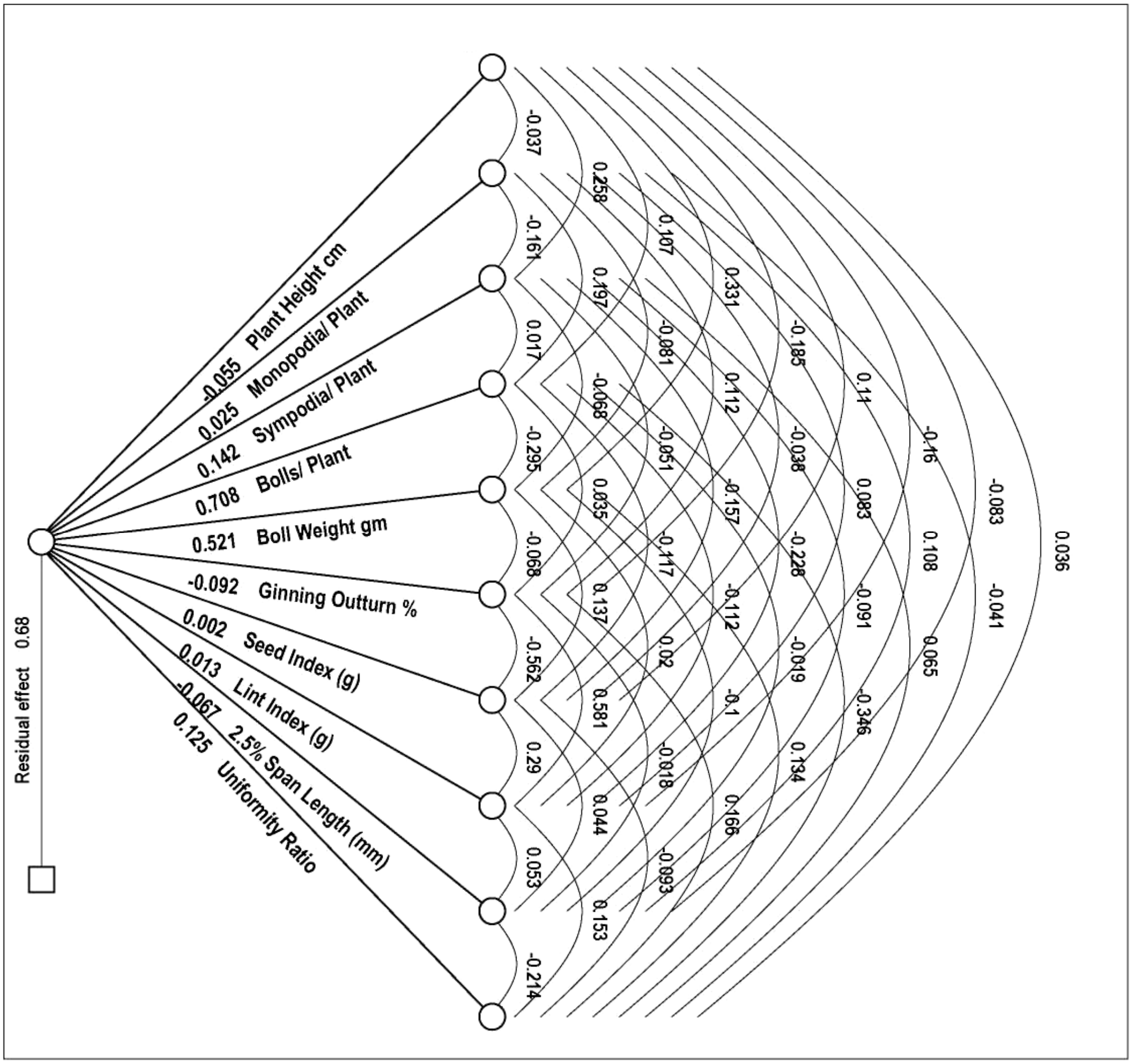

Fig. 1: Phenotypic path diagram showing cause and effect relationship of direct effect with seed cotton yield per plant in cotton (*Gossypium hirsutum* L.).

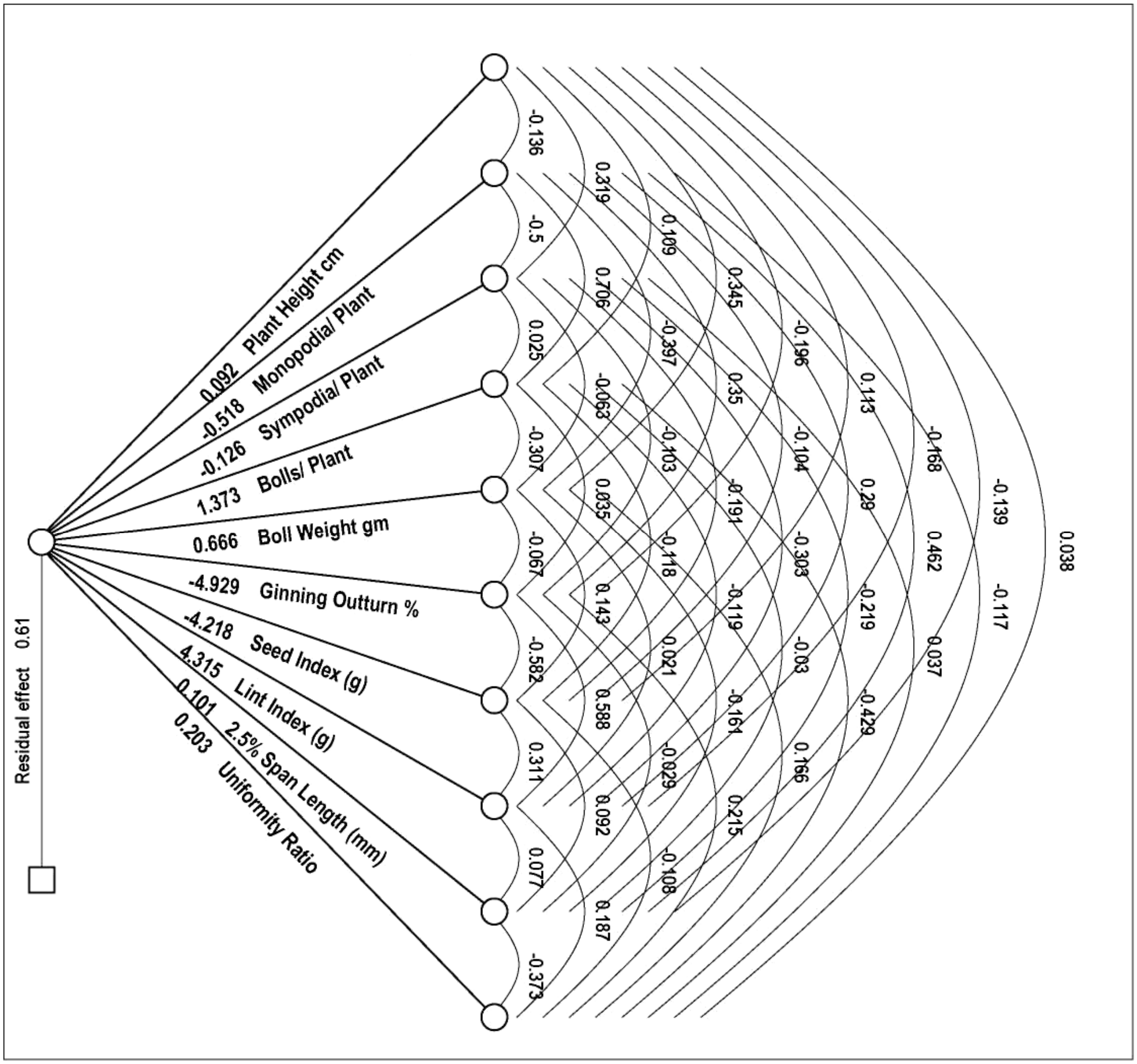

Fig. 2: **Genotypic path diagram showing cause and effect relationship of direct effect with seed cotton yield per plant in cotton (*Gossypium hirsutum* L.).**

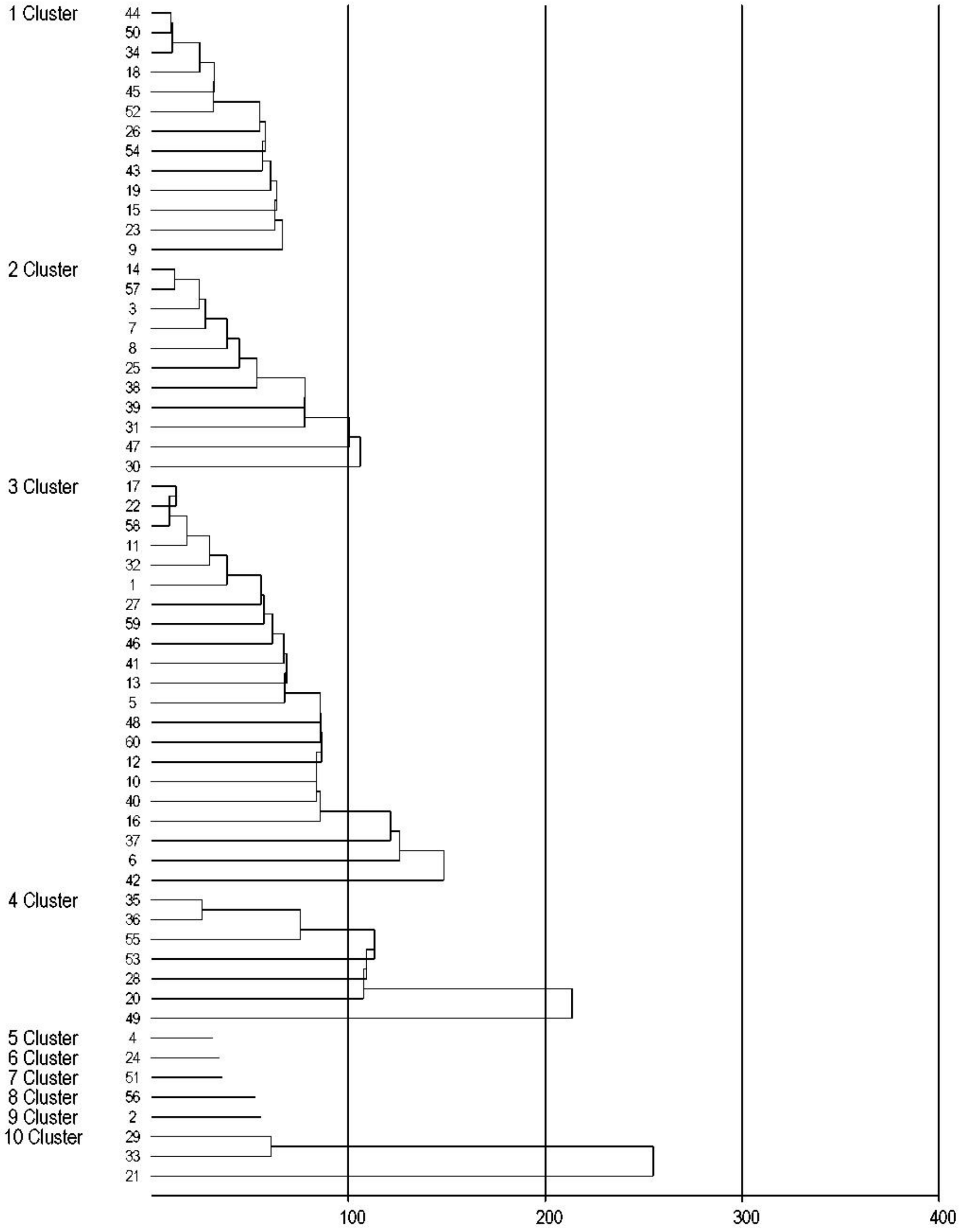

Fig. 3: Tocher's method dendrogram showing relationship 60 cotton (*Gossypium hirsutum* L.) genotypes in ten clusters.

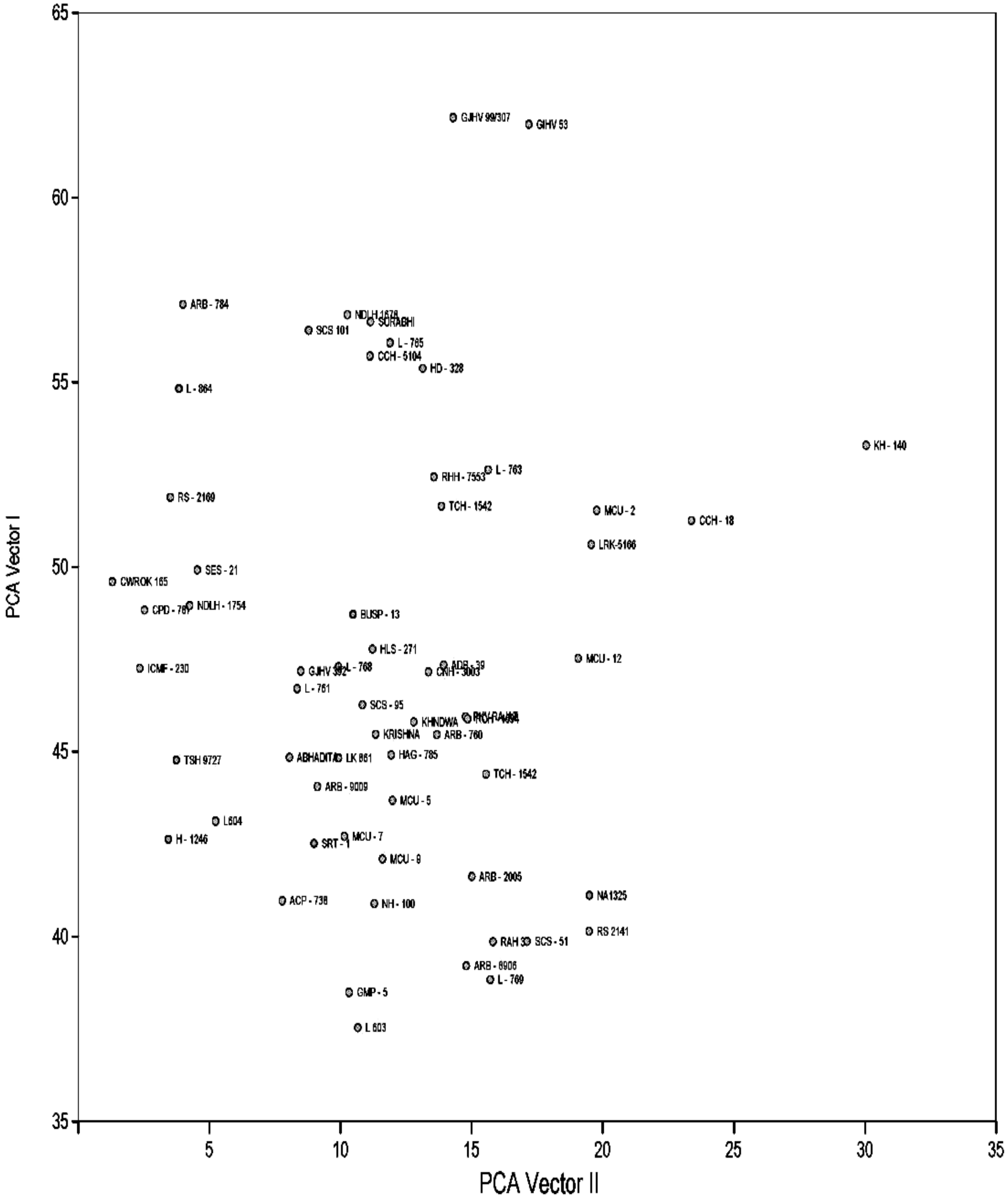

Fig. 4: **Two dimensional graph showing relative position of 60 cotton (*Gossypium hirsutum* L.) genotypes based on PCA scores.**

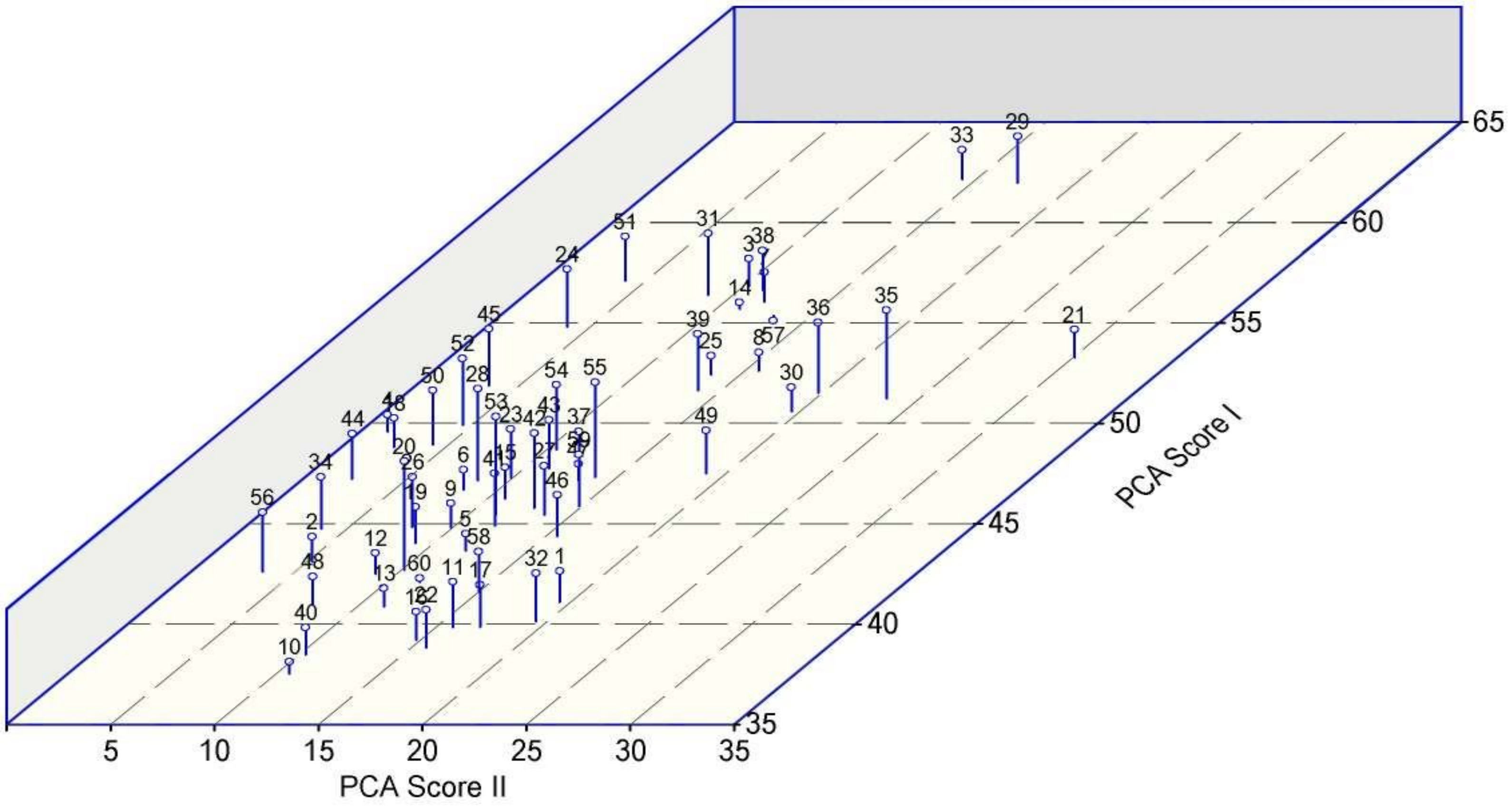

Fig. 5: Three dimensional graph showing relative position of 60 cotton (*Gossypium hirsutum* L.) genotypes based on PCA scores (Number of genotype as per the Table No. 6).

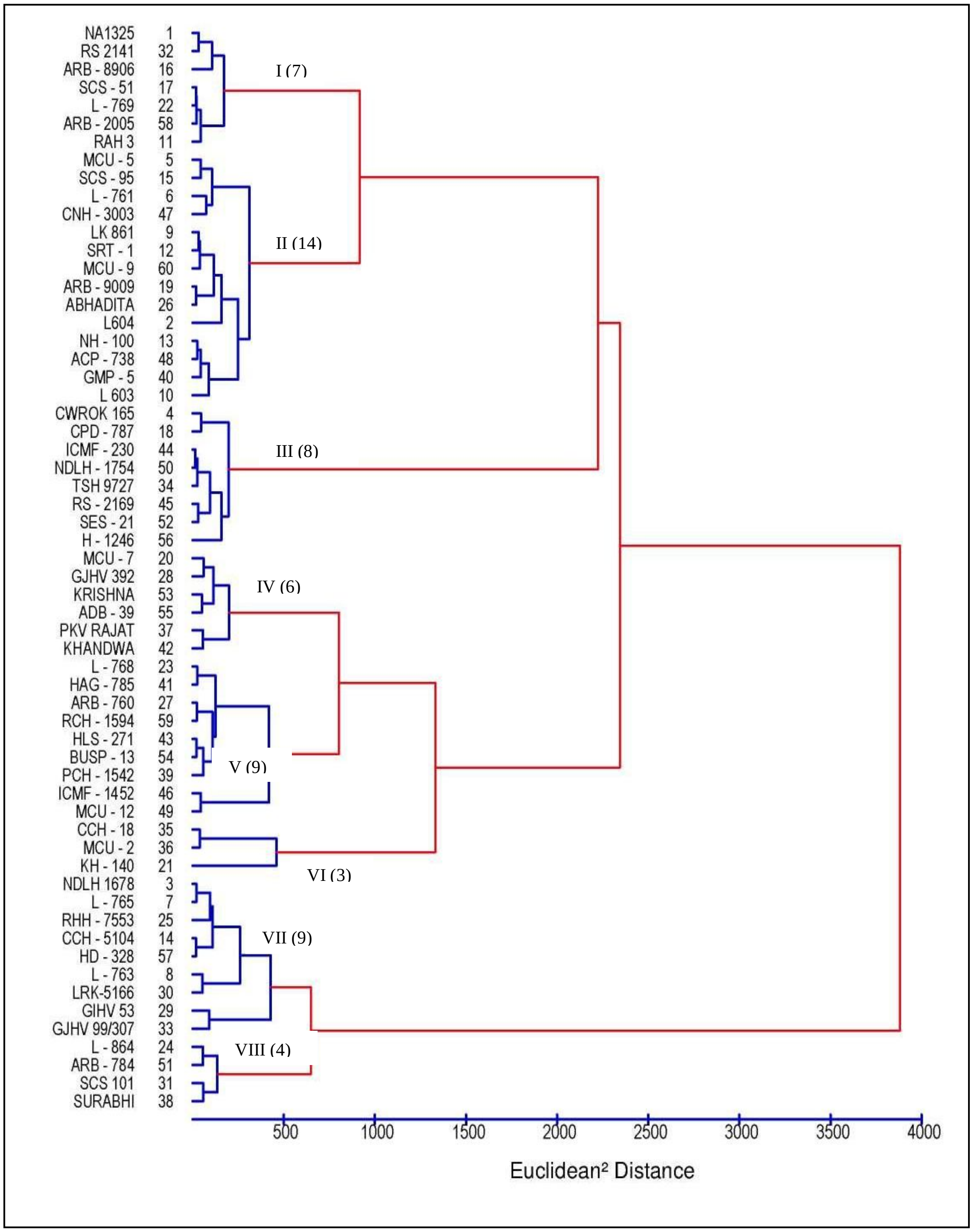

Fig. 6: Wards minimum variance dendrogram showing relationship of 60 upland cotton genotypes (*Gossypium hirsutum* L.) in 8 clusters.

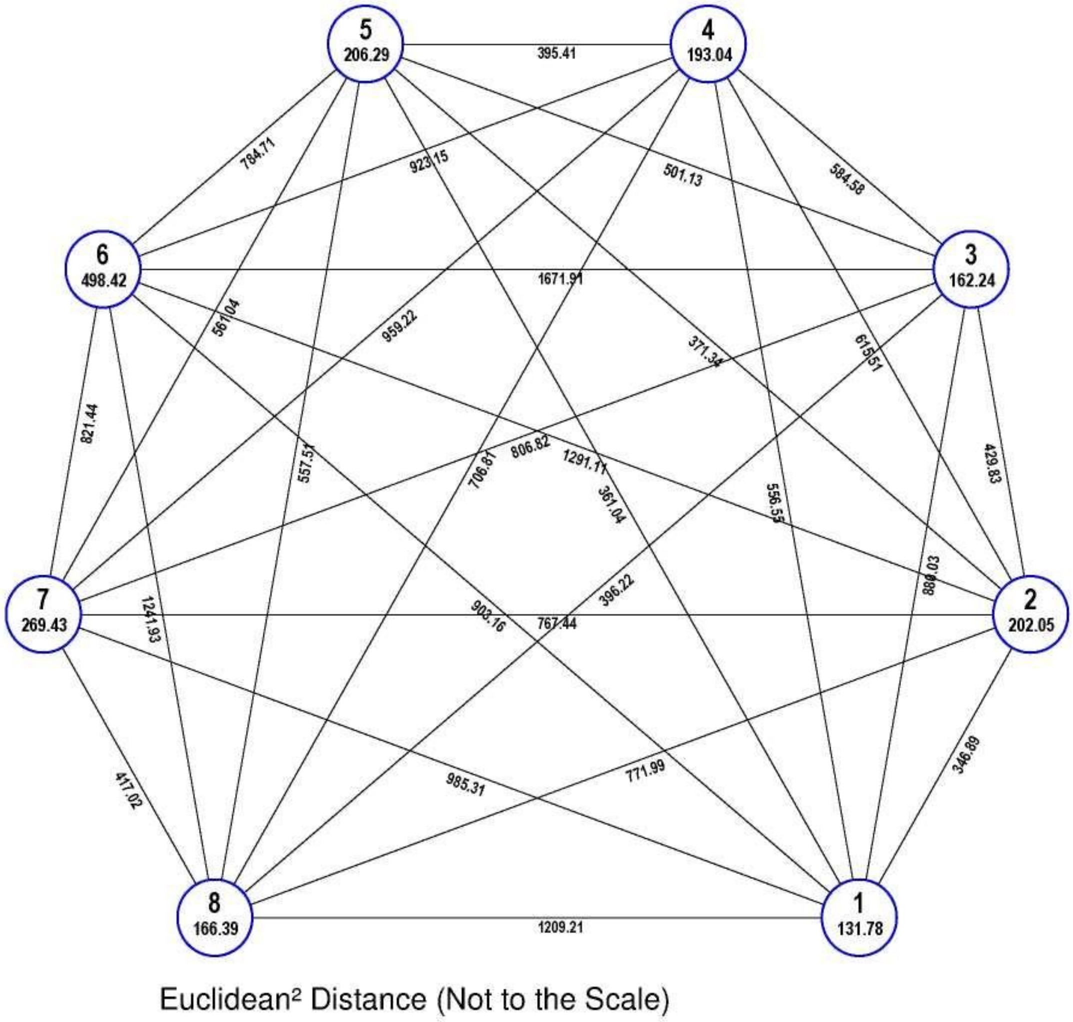

Fig. 7: Intra and inter-cluster distance of 60 cotton (*Gossypium hirsutum* L.) genotypes in nine clusters based on Euclidean^2 distance.

CHAPTER-V

DISCUSSION

The results obtained for 11 characters in 60 genotypes of cotton are discussed character – wise and presented here under the following headings.

5.1 Genetic variability

5.2 Character association

5.3 Path coefficient analysis

5.4 Genetic divergence

5.1 GENETIC VARIABILITY

The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wide range of variability helps in selecting a desired genotype. In addition to the genetic variability, knowledge on heritability and genetic advance helps the breeder to employ the suitable breeding strategy to achieve the objective rapidly.

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 out-of selection. The magnitude of heritable variability is the most important aspect of genetic contribution of the breeding material, which has close relationship on its response to selection.

Sixty genotypes of cotton (*Gossypium hirsutum* L.) collected across the country were evaluated in the present investigation representing a wide range of genotypes as evidenced by their significant differences among them in respect of all characters. Thus the data collected from the diverse material will yield reliable information. 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 PCV and GCV were moderate for plant height. These findings are in conformity with the results of Neelima *et al.* (2005), Tuteja *et al.* (2006), Kalpande *et al.* (2008) and Waqas Ahmed *et al.* (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 and therefore phenotypic selection would be effective in selecting the best genotypes for this character. Similar findings were reported by Neelam and Potdukhe (2002), Preetha and Raveendran (2007) and Sakthi *et al.* (2007).

5.1.2 Number of monopodia per plant

The PCV and GCV values were moderate for number of monopodia per plant. Similar findings were reported by Sivaprasad *et al.* (2004b), Karunakar Raju (2005), Tuteja *et al.* (2006), Gitte *et al.* (2007), Vijayalaxmi (2008) and Neelima *et al.* (2008). High heritability coupled with low genetic advance as per cent of mean was observed for this character indicating the predominance of non-additive gene action in governing the inheritance of this trait. These results are in agreement with the findings of Rao and Reddy (2001).

5.1.3. Number of sympodia per plant

The estimates of PCV and GCV were moderate for this trait. These findings are in conformity with the results of Kale *et al.* (2006), Tuteja *et al.*

(2006), Gitte *et al.* (2007) and Neelima *et al.* (2008). High heritability coupled with moderate genetic advance as per cent of mean was observed for this trait, indicating the role of additive gene action and therefore phenotypic selection would be effective in selecting the best genotypes for this character. Similar findings were reported by Verma *et al*. (2006), Gitte *et al*. (2007) and Sakthi *et al*. (2007).

5.1.4. Number of bolls per plant

The PCV and GCV values were high for number of bolls per plant. Similar findings were reported by Neelima *et al.* (2005), Prasad *et al*. (2005), Leela Pratap (2006) and Neelima *et al.* (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 and therefore phenotypic selection would be effective in selecting the best genotypes for this character. Similar findings were reported by Sivaprasad *et al.* (2004a), Leela Pratap (2006) and Vijayalaxmi (2008).

5.1.5. Boll weight (g)

The estimates of PCV and GCV were moderate for boll weight. These findings are in conformity with the results of Tuteja *et al.* (2006) and Waqas Ahmed *et al.* (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 and therefore phenotypic selection would be effective in selecting the best genotypes. Similar findings were reported by Verma *et al.* (2006), Sakthi *et al.* (2007) and Vijayalaxmi (2008).

5.1.6. Seed index (g)

The estimates of PCV and GCV were high for this trait. These findings are in agreement with the results of Gururajan and Sundar (2004) and Patnaik *et al*. (2004). High heritability coupled with high genetic advance as per cent of mean was observed for this trait, indicating the role of additive gene action. Similar findings were reported by Karunakar Raju (2005) and Vijayalaxmi (2008).

5.1.7. Lint index (g)

The estimates of PCV and GCV were high for lint index. Similar results were reported by Gururajan and Sundar (2004), Sivaprasad *et al*. (2004b) and Neelima *et al*. (2005). High heritability coupled with high genetic advance as per cent of mean was observed for this trait, indicating the role of additive gene action. These results are in agreement with Sambamurthy *et al*. (2006) and Vijayalaxmi (2008).

5.1.8. Ginning out-turn (%)

The estimates of PCV and GCV were moderate, as these results were in agreement with Patnaik *et al*. (2004), Neelima *et al*. (2005) and Tuteja *et al.* (2006). High heritability coupled with high genetic advance as per cent of mean was observed for this trait, indicating the role of additive gene action and therefore phenotypic selection would be effective in selecting the best genotypes for this character. Similar finding were reported by Gururajan and Sundar (2004) and Kale *et al*. (2006).

5.1.9. 2.5% span length (mm)

The estimates of PCV and GCV were low for this trait. These findings were in conformity with the results of Altaher and Singh (2003b), Neelima *et al*. (2005) and Tuteja *et al*. (2006). Moderate heritability coupled with low genetic advance as per cent of mean indicated the role of both additive and non-additive gene action. These results are in agreement with Tuteja *et al*. (2005a), Verma *et al*. (2006) and Vijayalaxmi (2008).

5.1.10 Uniformity ratio

The estimates of PCV and GCV were low for this trait. These findings were in conformity with the results of Karunakar Raju (2005), Leelapratap (2006), Neelima *et al*. (2008) and Vijayalaxmi (2008). High heritability coupled with moderate genetic advance as per cent of mean indicated the role of additive gene action and therefore phenotypic selection would be effective in selecting the best genotypes for this character.

5.1.11 Seed cotton yield per plant (g)

The estimates of PCV and GCV were high for this trait. Similar results were reported by Kaushik *et al.* (2003), Sivaprasad *et al.* (2004a) and Kale *et al*. (2006). High heritability coupled with high genetic advance as per cent of mean was observed for this trait, indicating the role of additive gene action and therefore phenotypic selection would be effective in selecting the best genotypes for this trait. Similar findings were reported by Sivaprasad *et al.* (2004a) and Kale *et al*. (2006).

In the present study, wide genetic variability was observed for number of monopodia per plant, number of bolls per plant, seed index, lint index and seed cotton yield per plant, where as it was moderate for plant height, number of sympodia per plant, boll weight and ginning out turn and low for remaining parameters. The characters *viz*., plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, seed index, lint index, ginning out-turn, uniformity ratio and seed cotton yield per plant recorded highest heritability where as it was moderate for 2.5% span length and low for number of monopodia per plant. Broad sense heritability includes dominance, epistasis as well as additive genetic variance and the estimates so obtained should be considered as maximum heritabilities (Paul, 1978). If the heritability is mainly due to additive gene action effects, then only it is associated with high genetic gain, where as, if the heritability is mainly due to non-additive effects, the genetic advance will be low in case of number of monopodia per plant and 2.5% span length. Characters with high heritability estimates together with high genetic gain can be improved through simple selection procedures, while, the improvement of traits having non-additive gene action needs cyclic hybridization and selection procedures.

5.2 CHARACTER ASSOCIATION

Seed cotton yield per plant is a complex and quantitatively inherited character. It is the resultant product of various component characters and is not under control of any single gene. Hence, improvement will be slow if the selection is based on yield alone, and effective improvement in yield is possible through component characters.

Yield component characters show association among themselves and also with yield. In the present study, correlation estimates were obtained for 11 characters in 60 genotypes of cotton and the results are discussed here under.

5.2.1. Plant height (cm)

Plant height showed positive significant association with number of sympodia per plant and boll weight at both genotypic and phenotypic levels. These results are in conformity with the reports of Verma *et al.* (2006), Leela Pratap *et al.* (2007) and Vijayalaxmi (2008) for number of sympodia per plant and Gnana Arul Samuel Rajan (1997) for boll weight. This trait showed negative significant association with ginning out-turn at both the levels. These results are in conformity with the reports of Sharad Batnagar (1995).

5.2.2. Number of monopodia per plant

Number of monopodia per plant showed positive significant association with number of bolls per plants at both genotypic and phenotypic levels. Similar results were reported by Kaushik *et al.* (2003), Leela Pratap *et al.* (2007) and Vijayalaxmi (2008).

The trait showed negative significant association with number of sympodia per plant at both the levels. Similar results were reported by Verma *et al.* (2006) and Vijayalaxmi (2008).

5.2.3. Number of sympodia per plant

Number of sympodia per plant showed negative significant correlation with seed index and lint index at both genotypic and phenotypic levels. These results are in agreement with the findings reported by Muraleedhar (2005).

5.2.4. Number of bolls per plant

Number of bolls per plant showed positive significant association with number of monopodia per plant and seed cotton yield per plant at both genotypic and phenotypic levels. Similar results were reported by Kaushik *et al.* (2003), Verma *et al.* (2006), Leela Pratap *et al.* (2007) and Vijayalaxmi (2008).

The trait showed negative significant association with boll weight and uniformity ratio at both the levels. These results are in agreement with the findings reported by Vijayalaxmi (2008).

5.2.5. Boll weight (g)

Boll weight showed positive significant association with seed cotton yield per plant at both genotypic and phenotypic levels. Similar results were reported by Karunakar Raju (2005), Sambamurthy *et al.* (2006) and Sakthi *et al.* (2007).

5.2.6. Seed index (g)

Seed index exhibited positive significant association with lint index at both genotypic and phenotypic levels. Similar results were reported by Karunakar Raju (2005), Neelima *et al.* (2005), Vijayalaxmi (2008) and Chenga Reddy *et al.* (2008).

This trait showed negative significant association with ginning out-turn at both the levels. Similar results were reported by Leela Pratap *et al.* (2007).

5.2.7. Lint index (g)

Lint index exhibited positive significant association with ginning out-turn and seed index at both genotypic and phenotypic levels. Similar results were reported by Muthu *et al.* (2004), Karunakar Raju (2005), Leela Pratap *et al.* (2007) and Vijaylaxmi (2008).

5.2.8. Ginning out-turn (%)

Ginning out-turn showed positive significant association with lint index and uniformity ratio at genotypic and phenotypic levels. Similar results were reported by Muthu *et al.* (2004) and Karunakar Raju (2005).

This trait exhibited negative significant association with seed index at both the levels. Similar results were reported by Leela Pratap *et al.* (2007).

5.2.9. 2.5% span length (mm)

2.5% span length showed negative significant association with uniformity ratio at both genotypic and phenotypic levels. Similar results were reported by Altaher and Singh (2003b), Karunakar Raju (2005), Leela Pratap *et al.* (2007) and Vijayalaxmi (2008).

5.2.10. Uniformity ratio

Uniformity ratio exhibited positive significant association with ginning out-turn at both genotypic and phenotypic levels. Similar results were reported by Muthu *et al.* (2004) and Karunakar Raju (2005).

5.2.11 Seed cotton yield per plant (g)

Seed cotton yield per plant showed significant positive association with plant height, number of bolls per plant and boll weight at both genotypic and phenotypic levels. Similar results were obtained by Muthu *et al.* (2004), Neelima *et al.* (2005), Tuteja *et al.* (2006), Verma *et al.* (2006), Sakthi *et al.* (2007) and Vijayalaxmi (2008).

This trait exhibited negative significant association with 2.5% span length at both the levels. Similar results were reported by Gururajan and Sundar (2004).

In the present investigation, the over all data on correlation revealed that the important yield attributes *i.e.*, plant height, number of bolls per plant and boll weight not only possessed positive and significant relationship with seed cotton yield per plant but also possessed positive and significant relationship among themselves and with several other important attributes. Therefore, tall plants with more number of weighty bolls can be included in the selection indices in choosing parental lines in any hybridization programme aimed at improvement of seed cotton yield per plant.

5.3 PATH COEFFICIENT ANALYSIS

Correlation between yield and particular yield component is the net result of direct effect of that component and indirect effects through various other yield components. The total correlation between yield and a component character may some times be misleading as it might be an over estimate or under estimate, because of its association with yield. Hence, direct selection based on correlated response sometimes may not be fruitful and also when many characters are affecting a given character, it is necessary to split the total correlation coefficients into direct and indirect effects of cause as devised by Wright (1921).

When the correlation coefficient and the direct effect of a causal factor are equal, it explains the true relationship between the factor and yield and hence, a direct selection for that factor will be effective. If the correlation coefficient is positive and direct effects are negative or negligible, the indirect effect seems to be the cause of correlation. In such situations the other factors influencing the trait have to be considered simultaneously. If the correlation coefficient is negative and direct effect is positive, a restricted simultaneous selection model is to be followed *i.e.*, restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of direct effects.

The results of path coefficient analysis in the present study for 11 characters with yield and the estimates of their direct and indirect contributions with yield are discussed here under.

5.3.1. Plant height (cm)

Plant height showed negative direct effect at phenotypic level and positive direct effect at genotypic level and positive correlation with seed cotton yield per plant at both phenotypic and genotypic levels. It had positive indirect effect through number of number of bolls per plant, boll weight and ginning out-turn at both the levels. Hence, the indirect effects seem to be the cause of positive correlation and the indirect causal factors are to be considered simultaneously for selection. Negative direct effects of this trait are in conformity with the reports of Karunakar Raju (2005), Verma *et al*. (2006) and Vijayalaxmi (2008).

5.3.2. Number of monopodia per plant

Number of monopodia per plant indicated positive direct effect at phenotypic level and negative direct effect at genotypic level and positive correlation with seed cotton yield per plant both at phenotypic and genotypic levels. It had positive indirect effect through number of bolls per plant and lint index. Hence, selection through these characters brings about improvement in seed cotton yield. These findings are in agreement with the reports of Kaushik *et al.* (2003), Altaher and Singh (2003a), Muthu *et al.* (2004) and Vijayalaxmi (2008).

5.3.3. Number of sympodia per plant

Number of sympodia per plant exhibited positive direct effect at phenotypic level and negative direct effect at genotypic level and positive correlation with seed cotton yield per plant both at phenotypic and genotypic levels. It had positive indirect effect through ginning out-turn at both the levels. The magnitude of the positive indirect effect is greater than negative indirect effects. Hence, selection through number of sympodia per plant may bring about improvement in yield. These are in agreement with the results of Neelima *et al.* (2005), Verma *et al.* (2006), Leela Pratap *et al.* (2007) and Vijayalaxmi (2008).

5.3.4. Number of bolls per plant

This trait exhibited positive direct effect and positive correlation with seed cotton yield per plant both at phenotypic and genotypic levels. It had positive indirect effect through number of monopodia per plant, number of sympodia per plant and 2.5% span length at phenotypic level. Hence, selection through number of bolls per plant may bring about improvement in yield. These are in conformity with the results of Karunakar Raju (2005), Verma *et al*. (2006), Leela Pratap *et al*. (2007) and Vijayalaxmi (2008).

5.3.5. Boll weight (g)

Boll weight showed positive direct effect and positive correlation with seed cotton yield per plant at phenotypic and genotypic levels. It had positive indirect effect through ginning out-turn, seed index, lint index, 2.5% span length and uniformity ratio at phenotypic level. Hence, greater emphasis should be given to boll weight in selection for improvement of yield. These results were in agreement with the findings of Gururajan and Sundar (2004), Karunakar Raju (2005) and Vijayalaxmi (2008).

5.3.6. Ginning out-turn (%)

Ginning out-turn exhibited negative direct effect and negative correlation with seed cotton yield per plant at both phenotypic and genotypic levels. Hence, both values were negative it is better to drop the selection based on this character. Positive indirect effects were recorded for lint index at both the levels. Similar results were obtained by Gururajan and Sundar (2004), Karunakar Raju (2005) and Vijayalaxmi (2008).

5.3.7. Seed index (g)

Seed index exhibited positive direct effect at phenotypic level and negative direct effect at genotypic level and positive correlation with seed cotton yield per plant at phenotypic and genotypic levels. It had positive indirect effect through ginning out-turn and lint index at both the levels. Hence, selection through seed index may bring about improvement in yield. Similar results were obtained by Siva Prasad (2003), Samba murthy *et al.* (2006) and Vijayalaxmi (2008).

5.3.8. Lint index (g)

Lint index showed positive direct effect and negative correlation with seed cotton yield per plant at phenotypic and genotypic levels. It has positive indirect effect through plant height, number of monopodia per plant, boll weight, seed index and uniformity ratio at phenotypic level. Hence, restricted selection for these characters is to be practiced to mitigate the undesirable effects. These results are in agreement with the results of Sivaprasad (2003), Muthu *et al.* (2004) and Leela Pratap *et al.* (2007).

5.3.9. 2.5% span length (mm)

2.5% span length showed negative direct effect at phenotypic level and positive direct effect at genotypic level and negative correlation with seed cotton yield per plant at both phenotypic and genotypic levels. Since both values were negative at phenotypic level, it is better to drop the selection based on this character. Positive indirect effects were recorded through the characters *viz.*, ginning out-turn and lint index at both the levels. Similar results were obtained by Sivaprasad (2003), Gururajan and Sundar (2004), Verma *et al.* (2006) and Vijayalaxmi (2008).

5.3.10 Uniformity ratio

Uniformity ratio exhibited positive direct effect and negative correlation with seed cotton yield per plant at both phenotypic and genotypic levels. It had negative indirect effect through number of bolls per plant and ginning out-turn while, positive indirect effect through boll weight and lint index. Hence, restricted selection for this character is to be practiced to mitigate the undesirable effects. These results are in conformity with the finding of Sivaprasad (2003), Karunakar Raju (2005), Sambamurthy *et al*. (2006) and Vijayalaxmi (2008).

In the present study, the residual effect both at phenotypic and genotypic levels is high. This clearly shows the importance of inclusion of some more characters like lint yield per plant and quality parameters *etc*. for clear partition of the direct and indirect effects among the yield components and seed yield.

The path analysis indicated that number of number of bolls per plant, boll weight, lint index and uniformity ratio had direct positive effects on seed cotton yield per plant both at phenotypic and genotypic levels.

The present study revealed that breeding programmes aimed at improvement of seed cotton yield major emphasis should be laid out on selection process with more number of heavy weight bolls per plant.

5.4 GENETIC DIVERGENCE

In hybridization programmes genotypes obtained from different geographic and ecological regions are being utilized with the assumption of their natural diversity and expected desirable improvement in their progenies. It is a difficult task for the plant breeder to select most suitable and genetically diverse parents for successful hybridization programme unless provided with the information regarding genetic divergence in the material.

The populations from the heterogeneous environment could be expected to accumulate more genetic variability as compared to populations present in a similar ecological region. In hybridization programmes, diversity of parents was very much understood, because the crosses between the genotypes with maximum genetic divergence would be responsible for obtaining desirable improvement as they are likely to yield desirable recombinants in the progenies. Generally, phenotypic or genotypic diversity could be considered as a measure of genetic diversity. However, this is an inferential criterion and may not be used for discrimination among populations occupying ecological marginal habitats (Arunachalam and Ram,1967).

The multivariate analysis using Mahalanobis' D^2 statistic provides an useful statistical method for measuring the amount of genetic diversity in a given population in respect of characters considered together. Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discrimination between populations.

In the present study the data collected on 11characters from 60 genotypes of cotton were subjected to multivariate analyses using Mahalanobis' D^2 statistic, principal component and cluster analyses.

5.4.1. Mahalanobis D^2 analysis

In the present investigation, 60genotypes of cotton were considered for the assessment of nature of genetic diversity through Mahalanobis D^2 analysis. Based on D^2 values for all the pairs of genotypes, 60 genotypes were grouped into 10 clusters which indicate that there was considerable genetic diversity in the material studied.

The knowledge on characters influencing divergence is an important aspect to a breeder. Character wise rank has shown that no single character lonely had a greater contribution to total genetic divergence. Nevertheless, relatively maximum contribution was by seed index, seed cotton yield per plant, plant height, boll weight and number of bolls per plant. Similar results were reported by Sambamurthy *et al.* (1995), Kiran *et al.* (2004), Vijayalaxmi (2008) and Gopinath *et al.* (2009).

The largest cluster was cluster 3 comprising 21 genotypes followed by cluster 1 with 13 genotypes, cluster 2 with 11 genotypes, cluster 4 with 7 genotypes and cluster 10 with 3 genotypes. Clusters 5,6,7,8 and 9 were solitary. 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. Similar results were reported by Kowsalya and Raveendran (1996), Altaher and Singh (2003a), Karunakar Raju *et al.* (2005) and Satish *et al.* (2009).

The intra- and inter-cluster distances revealed that inter-cluster distance values were greater than intra-cluster distance values. Cluster 10 had maximum intra-cluster distance followed by cluster 4, cluster 3, cluster 2 and cluster 1. Five clusters (Clusters 5, 6, 7, 8 and 9) which were solitary had no intra-cluster distances. The high intra-cluster distance in cluster 10 indicates the presence of wide genetic diversity among the genotypes present within this cluster. It was suggested to attempt crosses among the genotypes with in cluster 10 (GIHV-53, GJHV-99 / 307 and KH-140) and 4 (CCH-18, MCU-2, ADB-39, Krishna, GJHV-392, MCU-7 and MCU-12) in all possible combinations. Similar results were obtained by Kalsy and Garg (1995) and Sambamurthy *et al.* (1995).

Genotypes grouped into 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). In the present study, inter-cluster distances were worked out considering 11 characters and these distances ranged from 37.302 (between cluster 6 and 7) to 702.395 (between cluster 8 and 10).

The inter-cluster distance was maximum between clusters 8 (H-1246) and 10 (GIHV-53, GJHV-99 / 307 and KH-140) followed by clusters 9 (L-604) and 10 (GIHV-53, GJHV-99 / 307 and KH-140); clusters 5 (CWROK-165) and 10 (GIHV-53, GJHV-99 / 307 and KH-140) and clusters 3 (SCS-51, L-769, ARB-2005, RAH-3, RS-2141, NA-1325, ARB-760, RCH-1594, ICMF-1452, HAG-785, NH-100, MCU-5, ACP-738, MCU-9, SRT-1, L-603, GMP-5, ARB-8906, PKV-Rajat, L-761 and Khandwa) and 10 (GIHV-53, GJHV-99 / 307 and KH-140). 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.

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 four 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 four principal components with eigen value more than one contributed to 91.69 per cent of the variability among 60genotypes evaluated for 11traits. 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.

First principal component (PC_1) described maximum variability. The characters *viz.*, seed index, plant height, boll weight, lint index and seed cotton yield per plant had a greater positive loading on first principal component (PC_1).

The second principal component (PC_2) accounted for 30.84 per cent of total variability. Positive loading values were observed among seed cotton yield per plant, number of bolls per plant and plant height while, seed index showed negative loading value.

Third principal component (PC_3) contributed 17.46 per cent to the total variability. Boll weight and plant height loaded positively whereas, number of bolls per plant and seed index were negatively loaded.

The fourth principal component (PC_4) described 8.20 per cent contribution towards the total variability. Plant height loaded positively where as other remaining characters were negatively loaded.

The PCA scores for 60 cotton genotypes were plotted on graph to get the 2D and 3D scattered diagram. These graphs showed wide divergence between the genotypes. The genotypes 21 (MCU-7), 33 (GJHV-99/307), 50 (NDLH-1754), 4 (CWROK-165), 29 (GIHV -53), 10 (L-603) and 49 (MCU-12) scattered widely and can be utilized the breeding prorammes for the production of heterotic hybrids.

5.4.3. 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. Sixty genotypes were grouped into 8 clusters and distribution of various genotypes into various clusters were random indicating the absence of relationship between geographical diversity and genetic diversity. Among all the clusters, cluster 2 was the largest one containing 14 genotypes followed by clusters 5 and 7 with 9 genotypes, cluster 3 with 8 genotypes, cluster 1 with 7 genotypes, cluster 4 with 6 genotypes, cluster 8 with 4 genotypes and cluster 6 with 3 genotypes.

Of the eight clusters formed, maximum intra-cluster Euclidean^2 distance was recorded by cluster 6 (498.41) (CCH-18, MCU-2 and KH-140) followed by cluster 7 (269.42) (NDLH-1678, L-765, RHH-7553, CCH-5104, HD-328, L-763, LRK-5166, GJHV-53 and GJHV-99/307) and cluster 5 (206.28) (L-768, HAG-785, ARB-760, RCH-1594, HLS-271, BUSP-13, TCH-1542, ICMF-1452, MCU-12).

The maximum inter-cluster distance was observed between clusters 3 (CWROK-165, CPD-787, ICMF-230, NDLH-1754, TSH-9727, RS-2169, SES-21 and H-1246) and 6 (CCH-18, MCU-2 and KH-140) (1671.909) followed by clusters 2 (MCU-5, SCS-95, L-761, CNH-3003, LK-861, SRT-1, MCU-9, ARB-9009, Abhadita, L-604, NH-100, ACP-738, GMP-5 and L-603) and 6 (CCH-18, MCU-2 and KH-140) (1291.112) and clusters 6 (CCH-18, MCU-2 and KH-140) and 8 (L-864, ARB-784, SCS-101 and Surabhi) (1241.931). 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 cluster analysis based on PCA scores were compared with the results of the PCA on a visual aid in desecrating clusters in the 2D and 3D scattered diagrams. The genotypes falling in same cluster were presented closer to each other in scattered diagram.

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

All the eight clusters recorded high mean value for seed cotton yield per plant followed by plant height and low mean value for number of monopodia per plant followed by lint index.

5.4.4. Comparative study of D^2 analysis, Principal component analysis and 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 11 attributes. In D^2 analysis, seed index followed by seed cotton yield per plant and plant height contributed maximum genetic divergence. While in PCA the characters *viz*., seed index in PC_1, seed cotton yield per plant in PC_1 and PC_2 and plant height in PC_1, PC_2, PC_3 and PC_4 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, PC_3, and PC_4.

D^2 analysis grouped the 60 cotton genotypes into 10 clusters where as PCA grouped them into 8 clusters. In D^2 analysis, Cluster 3 is the largest with 21 genotypes followed by cluster 1 (13 genotypes), cluster 2 (11 genotypes) and cluster 4 (7 genotypes) where as in PCA, cluster 2 is the largest comprising of 14 genotypes followed by cluster 5 and 7 (9 genotypes) and cluster 3 (8 genotypes).

The pattern of distribution of genotypes into different clusters was at random. Further more the two clustering methods grouped the genotypes differently and clustering pattern for genotypes was not same. There was no solitary cluster in Ward's minimum variance method, where as in case of D^2 analysis cluster 5,6,7,8 and Cluster 9 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 group within a cluster, so relative position of the genotypes within the clusters can be done 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.

CONCLUSIONS

The following conclusions were drawn from the results and discussion on various aspects of the present study.

The material chosen represented wide range of variability as evidenced by the significant differences among them in respect of all the characters studied. Thus the data collected from the above diverse material had yielded the following valid conclusions.

- It was observed that the values of phenotypic coefficient variation were higher than genotypic coefficient variation for all the traits, suggesting that the observed variations were not only due to genotypes but also due to influence of environment. Number of monopodia per plant, number of bolls per plant, seed index, lint index and seed cotton yield per plant have high and plant height, number of sympodia per plant, boll weight and ginning out-turn have moderate genotypic and phenotypic coefficients of variation.

- High and significant positive association of plant height, number of bolls per plant and boll weight with seed cotton yield per plant was observed from correlation studies.
- The path analysis indicated number of bolls per plant, boll weight, lint index and uniformity ratio exerted direct positive effects on seed cotton yield per plant.
- The results of multivariable analysis revealed that the distribution of 60 cotton genotypes into 10 clusters in case of D^2 analysis and into eight clusters in case of cluster analysis was at random indicating that the genetic diversity and geographical diversity were not related.
- By Mahalanobis D^2 statistic, it could be inferred that seed index, seed cotton yield per plant, plant height, boll weight and number of bolls per plant contributed maximum towards genetic divergence. Based on the intra-and inter-cluster distances among the groups, suggestions were made to attempt crosses after confirming their general combining ability between cluster 8 (H-1246) and cluster 10 (GIHV-53, GJHV-99 / 307 and KH-140) followed by cluster 9 (L-604) and cluster 10 (GIHV-53, GJHV-99 / 307 and KH-140) to obtain better and desirable segregants.

- Principal component analysis identified four principal components (PC_s), which contributed 91.69 per cent of cumulative variance. The population with high PC_1 values were characterized by Seed index and Plant height where as, population with high PC_2 values were characterized by seed cotton yield per plant and number of bolls per plant. In PC_3 characters like boll weight and plant height showed maximum weightage.

- Agglomerative cluster analysis revealed that wide genetic distance exists between cluster 3 (CWROK-165, CPD-787, ICMF-230, NDLH-1754, TSH-9727, RS-2169, SES-21 and H-1246) and cluster 6 (CCH-18, MCU-2 and KH-140) followed by cluster 2 (MCU-5, SCS-95, L-761, CNH-3003, LK-861, SRT-1, MCU-9, ARB-9009, Abhadita, L-604, NH-100, ACP-738, GMP-5 and L-603) and cluster 6 (CCH-18, MCU-2 and KH-140). Therefore during hybridization programme selection of parents from these clusters will produce superior segregants.

- It may be concluded that selection would be effective in cotton plant for more number of high weighing bolls per plant for developing high yielding cotton varieties in future plant breeding programmes.

CHAPTER - VI

SUMMARY

The present investigation was carried out during *kharif*, 2007 at Regional Agricultural Research Station, Lam Farm, Guntur with 60 genotypes of upland 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 11characters *viz.*, plant height (cm), number of monopodia per plant, number of sympodia per plant, seed index (g), number of bolls per plant, boll weight (g), lint index (g), ginning out-turn (%), 2.5% span length (mm), uniformity ratio and seed cotton yield per plant (g).

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the data generated from the above diverse material will yield reliable information. The genotypic coefficients of variation for all the characters studied were lesser than phenotypic coefficients of variation indicating the masking effects of the environment. The characters *viz.*, number of monopodia per plant, number of bolls per plant, seed index, lint index and seed cotton yield per plant indicated high variability where as plant height, number of sympodia per plant, boll weight and ginning out-turn showed moderate variability. High heritability coupled with high genetic advance was noted in the case of plant height, number of bolls per plant, boll weight, seed index, lint index, ginning out-turn and seed cotton yield per plant. This indicates the predominance of additive

gene action and direct selection for these traits may effective in improving these traits. High heritability coupled with moderate genetic advance was observed in case of number of sympodia per plant and uniformity ratio revealing the role of additive and non-additive gene action. 2.5% span length showed moderate heritability and low genetic advance indicating the operation of non-additive gene action. It might be exploited through heterosis breeding, cyclic hybridization, biparental mating and diallel selective mating system.

The correlation studies indicated that plant height, number of bolls per plant and boll weight had significant positive association with seed cotton yield per plant. The path analysis indicated that number of bolls per plant, boll weight, , lint index and uniformity ratio exerted direct positive effects on seed cotton yield per plant.

The results of multivariate analysis revealed that the distribution of 60 cotton genotypes into 10 clusters in case of D^2 analysis and into 8 clusters in case of principal component analysis was at random indicating that the genetic diversity and geographical diversity were not related.

On the basis of D^2 analysis, the maximum intra-cluster distance was observed in cluster 10 (275.16) and minimum intra-cluster distance was observed in cluster 5,6,7,8 and 9 (0.00). While on the basis of cluster analysis maximum intra-cluster distance was observed in cluster 6 (498.41) and minimum intra-cluster distance was observed in cluster 3 (162.241).

By Mahalanobis' D^2 statistic, it could be inferred that the seed index contributed maximum towards genetic divergence followed by seed cotton yield per plant, plant height, boll weight, number of bolls per plant, ginning out-turn, lint index, number of sympodia per plant and uniformity ratio. Based on the intra and inter-cluster distances among groups, suggestions were made to attempt crosses after confirming their general combining ability between clusters 8 (H-1246) and cluster 10 (GIHV-53, GJHV-99 / 307 and KH-140) followed by cluster 9 (L-604) and cluster 10 (GIHV-53, GJHV-99 / 307 and KH-140) to obtain better and desirable segregants.

In the principal component method, first 4 principal components altogether explained 91.69% of the variability. The population with high PC_1 values were characterized by seed index and plant height where as, population with high PC_2 values were characterized by seed cotton yield per plant and number of bolls per plant. In PC_3 characters like boll weight and plant height showed maximum weightage.

Agglomerative cluster analysis revealed that wide genetic distance exists between cluster 3 (CWROK-165, CPD-787, ICMF-230, NDLH-1754, TSH-9727, RS-2169, SES-21 and H-1246) and cluster 6 (CCH-18, MCU-2 and KH-140) followed by cluster 2 (MCU-5, SCS-95, L-761, CNH-3003, LK-861, SRT-1, MCU-9, ARB-9009, Abhadita, L-604, NH-100, ACP-738, GMP-5 and L-603) and cluster 6 (CCH-18, MCU-2 and KH-140). Therefore during hybridization programme selection of parents from these clusters will produce superior segregants.

LITERATURE CITED

Ahuja S L and Tuteja O P 2000 Variability and association analysis for chemical components imparting resistance to (*Gossypium hirsutum* L.) cotton. Journal of Cotton Research and Development 14 (1): 19-22.

Allard R W 1960 Principles of Plant Breeding. John Wiley and Sons Inc., New York pp:145-147

Altaher A F and Singh R P 2003a Genetic diversity studies in upland cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 28(3): 158-163.

Altaher A F and Singh R P 2003 b Yield component analysis in upland cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 28(3): 151-157.

Amudha K, Raveendran T S and Krishnadoss D 1997 Genetic diversity in coloured linted cotton varieties. Madras Agricultural Journal 84 (6): 334-337.

*Anderberg M R 1993 Cluster Analysis for Application. Academic Press, New York.

Arunachalam V and Ram J 1967 Geographical diversity in relation to genetic divergence in cultivated sorghum. Indian Journal of Genetics and Plant Breeding 27: 369-380.

*Banfield C F 1978 Principal Component Analysis for Genstat. Journal of Statistics and Computer Simulations 6: 211-222.

Basha M 1997 Genetic analysis of yield and yield components of intraspecific hybrid cotton (*Gossypium hirsutum* L.). Ph.D. thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Brown J S 1991 Principal component and cluster analysis of cotton cultivars variability across the U.S. cotton belt. Crop Science 31: 915-922.

*Burton G W 1952 Quantitative inheritance in grasses. Proceedings of the 6th International Grass Congress pp. 277-283.

Chengareddy V and Neelima S 2008 Genetic parameters of yield and fibre quality traits in American cotton (*Gossypium hirsutum* L.). Indian Journal of Agricultural Research 42(1): 67-70.

Cochran G W and Cox M G 1950 Experimental Designs. John Wiley and Sons, New York pp. 45-67.

Dedaniya A D and Pethani K V 1994 Genetic variability, correlation and path analysis in desi cotton (*Gossypium arboreum* L.). Indian Journal of Genetics 54 (3): 229-234.

Deshpande L A and Baig K S 2003 Combining ability analysis for yield, economic and morphological traits in American cotton (*Gossypium hirsutum* L.). Journal of Research ANGRAU 31 (3): 28-34.

Dewey D R and Lu K H 1959 A correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal 51 (9): 515-518.

Dhanda S S, Tyagi A P and Jatasra D S 1984 Character association among quantitative and quality attributes of upland cotton. Indian Journal of Agricultural Sciences 54: 24-29.

Ehrenberg A S C 1985 Data Reduction Analysis and Interpreting Statistical Data. John Wiley and Sons Inc, New York: 24(1): 54-56.

Eswar G 2008 Genetic divergence in cotton (*Gossypium hirsutum* L.) M.Sc. (Ag.) thesis, Acharya N.G. Ranga Agricultural University, Rajendra Nagar, Hyderabad.

Everitt B S 1974 Cluster Analysis. John Wiley and Sons Inc., New York pp. 1-117.

Falconer D S 1964 An Introduction to Quantitative Genetics. Second Edition, Oliver and Boyd, Edinburgh pp. 312-324.

Fisher R A and Yates F 1963 Statistical Tables for Biological, Agricultural and Medical Research. Oliver and Boyd, London pp. 46-63.

Ganapathy S 2001 Heterosis and combining ability for oil content and other economic traits in cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Tamil Nadu Agricultural University, Coimbatore.

Ganapathy K N, Sreedhar Y and Gunasekaran M 2006 Character association and component analysis for yield and fibre quality traits in upland cotton (*Gossypium hirsutum* L.). Crop Research 32(2): 225-229.

Gopinath M, Rajamani S, Naik R K and Rao C M 2009 Genetic divergence for lint characters for upland cotton (*Gossypium hirstum* L.) Journal of Cotton Research and Development 23(1): 46-48.

Girase V S and Mehetre S S 2002 Variability, heritability and genetic advance studies in cotton (*Gossypium hirsutum* L.). Journal of Cotton Research and Development 16 (1): 81-82.

Gitte V K, Misal M B, Kalpande H V and Deshmukh J D 2007 Genetic variabtility studies in F_2 populations of upland cotton (*Gossypium hirsutum* L.) Journal of Cotton Research and Development 21(1): 27-28.

Gnana Arul Samuel Rajan 1997 Studies on heterosis and combining ability in cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Tamil Nadu Agricultural University, Coimbatore.

Gururajan K N 2000 Yield component analysis in Egyptian cotton (*Gossyium barbadense* L.). Journal of the Indian Society for Cotton Improvement 25 (1): 17-22.

Gururajan K N and Manickam 2002 Genetic divergence in Egyptian cotton (*Gossypium barbadense* L.) Journal of the Indian Society for Cotton Improvement 27(2): 77-83.

Gururajan K N and Sundar S 2004 Yield component analysis in American cotton. Paper presented in International symposium on "Strategies for Sustainable Cotton Production – A Global Vision" held at University of Agricultural Sciences, Dharwad, 23rd – 25th November, 2004.

*Hanson C H, Robinson H F and Comstock R E 1956 Biometrical studies of yield in segregating populations of Korean Lespedza. Agronomy Journal 48(6): 268-272.

*Jackson J E 1991 A User's Guide to Principal Components . John Wiely and Sons, New York.

Jain P P and Yadav I S 2001 Studies on genetic divergence in American cotton (*Gossypium hirsutum* L.). Journal of Cotton Research and Development 15(1): 81-83.

Johnson H W, Robinson H F and Comstock R E 1955 Estimates of genetic and environmental variability in soybean. Agronomy Journal 47 : 314-318.

Kale U R, Kalpande S, Annapurve S N and Gite V K 2007 Yield components analysis in American cotton (*Gossypium hirsutum* L.). Madras Agricultural Journal 94(7-12): 156-161.

Kale U V, Kalpande H V, Gunjkar A S and Gite V K 2006 Variability heritability and genetic advance studies in cotton. Journal of Maharashtra Agricultural Universities 31(3): 389-390.

Kalpande H V, Mukewar A M and Kalpande V V 2008 Combining ability analysis in upland cotton (*Gossypium hirsutum* L.). Journal of Cotton Research and Development 22(1): 10-13.

Kalsy H S and Garg H R 1995 Genetic divergence and heterosis in American cotton. Crop Improvement 22(2): 232-236

Karunakar Raju G B 2005 Character association and genetic divergence in upland cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Karunakar Raju G B, Chenga Reddy V and Panduranga Rao C 2005 Multivariate analysis of genetic diversity in upland cotton. The Andhra Agricultural Journal 52(1&2): 66-74.

Kaushik S K, Kapoor C J and Koli N R 2003 Association and path analysis in American cotton (*Gossypium hirsutum* L.). Journal of Cotton Research and Development 17 (1): 24-26.

Kiran L S, Narisi Reddy A and Neelima S 2004 Studies on genetic divergence in American cotton (*Gossypium hirsutum* L.). Paper presented in “National Symposium on Changing World Order – Cotton Research, Development and Policy in context”, held at Acharya N G Ranga Agricultural University, Rajendranagar, Hyderabad. 10th – 12th August 2004.

Kowsalya R and Raveendran T S 1996 Correlation and path coefficient analysis in cotton. Madras Agricultural Journal 83 (11): 705-707.

Krishnarao K V and Mary T N 1990 Variability correlation and path analysis of yield and fibre traits in upland cotton. Madras Agricultural Journal 77: 146-151.

Kumar P R, Raveendran T S and Krishnan V 2000 Genetic diversity and association studies for fibre characters in cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 14(1): 111-118.

Kumari S R and Chamundeswari N 2005 Studies on genetic variability heritability and genetic advance in cotton (*Gossypium hirstum* L.). Research on Crops 6(1): 98-99.

Ladole M Y and Meshram L D 2000 Correlation and path coefficient analysis in naturally coloured cotton (*Gossypium hirsutum* L.). Journal of Cotton Research and Development 14 (1): 89-92.

Laxman S and Ganesh M 2003 Combining ability for yield components and fibre characters in cotton (*Gossypium hirsutum* L.). Journal of Research, ANGRAU 31 (4): 19-23.

Leela Pratap K 2006 Combining ability and heterosis in cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Leela Pratap K , Chenga Reddy V , Rama Kumar P V and Srinivasa Rao V 2007 Correlation and path coefficient analyses for yield and yield component traits in cotton (*Gossypium hirsutum* L.). The Andhra Agricultural Journal 54 (1&2): 31-35.

Legendre L and Legendre P 1984 Ecologia numerique press de Iuniversite de Quebee . Vol : 1-2.

*Lush J L 1940 Intra-sire correlation on regression of off spring on dams as a method of estimating heritability of characters. Proceedings of American Society for Animal Production 33: 392-401.

*Mahalanobis P C 1928 A statistical study at Chinese head measurement. Journal of Asiatic Society of Bengal 25: 301-307.

Mandloi K C, Holkar S, Julka R and Kotu G K 2003 Character association studies in colour cotton. Journal of the Indian Society for Cotton Improvement 28 (1): 45-47.

Meena R A, Mishra M N and Dani R G 2001 Genetic variability and correlation for seed-quality parameters of upland cotton (*Gossypium hirstutum* L.). Indian Journal of Agricultural Sciences 71(6): 417-420.

Ministry of Textile, Government of India 2008-09 www.indiastat.com

Muraleedhar S A 2005 Genetic divergence in tetraploid cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Muraleedhar S A, Murthy J S V S, Rama Kumar P V and Srinivasa Rao V 2005 Mahalanobis' D^2 and principal component analysis of genetic diversity in tetraploid cotton. The Andhra Agricultural Journal 52 (1&2): 99-104.

Murthy J S V S 1997 Analysis of character association and component analysis in American cotton. Annals of Agricultural Research 18(4): 573-576.

Muthu R, Kandasamy G and Jayaramachandran N 2004 Correlation and path coefficient analysis for yield and fibre quality traits in cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 29 (1): 17-20.

Muthuswamy A, Vivekanandan P and Jayaramachandran M 2003 Combining ability and gene action for fibre characters in upland cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 28 (2): 127-131

Muthuswamy A and Vivekanandan P 2004 Correlation studies on seed yield and yield components in hirsutum cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 29 (1): 7-9.

Naphade P S, Khardes R P, Potdukhe N R and Meshram L D 2004 Heterosis and combining ability for quality attributes in inter varietal crosses of diploid cotton. Paper presented in International Symposium on "Strategies for Sustainable Cotton Production – A Global Vision" held at University of Agricultural Sciences, Dharwad, 23rd-25th November, 2004.

Narisireddy A and Ratnakumari S 2004 Genetic components of variation of physiological attributes for drought screening of genotypes in American cotton (*Gossypium hirsutum* L.). Annals of Agricultural Research, New Delhi 25 (3): 412-414.

Neelam G D and Potdukhe N R 2002 Studies on variability and correlations in upland cotton for yield and its components. Journal of the Indian Society for Cotton Improvement 27 (3): 148-152.

Neelima S 2002 Heterosis and combining ability analysis for yield and yield components in cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G.Ranga Agricultural University, Rajendranagar, Hyderabad.

Neelima S, Chenga Reddy V and Narisireddy A 2005 Association and path analysis in American cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 30 (1): 53-58.

Neelima S, Chenga Reddy V and Narisireddy A 2008 Genetic parameters of yield and fibre quality traits in American cotton (*Gossypium hirsutum* L.). Indian Journal of Agricultural Research 42 (1): 67-70.

Pankaj Rathore, Garg H R, Dharminder Pathak and Makwana M C 2004 Association among seed cotton yield and fibre quality traits in American cotton. Crop Improvement 31 (1): 107-112.

Panse V G and Sukhatme P V 1957 Genetics of quantitative characters in relation to Plant breeding. Indian Journal of Genetics and Plant Breeding 17: 318-328.

Panse V G and Sukhatme P V 1978 Statistical Methods for Agricultural Workers. Second Edition, Indian Council of Agricultural Research, New Delhi: pp 103-108.

Paramasivan P and Udayasoorian C 1989 Association analysis for yield components of summer irrigated cotton. Madras Agricultural Journal 76: 230-232.

Patil F B, Shinde Y M and Thombre M V 1991 Heterosis in multiple environments for yield components and its relation with genetic divergence in cotton. Indian Journal of Genetics and Plant Breeding 51 (1): 118-124.

Patnaik R K, Sial P, Patil S A, Khadi B M and Patil S S 2004 Heterosis for fibre quality parameters in intra-hirsutum crosses of cotton (*Gossypium hirsutum* L.). Paper presented in International symposium on “Strategies for Sustainable Cotton Production – A Global Vision” held at University of Agricultural Sciences, Dharwad, 23rd-25th November, 2004.

Paul N K 1978 Genetic architecture of yield and components of yield in mustard (*Brassica juncea* L.). Theoretical and Applied Genetics 53: 233-237.

Pradeep T and Sumalini K 2005 Studies on performance and pattern of genetic variability for plant type and productive traits in multiple crosses of cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 30 (1): 59-66.

Preetha S and Raveendran T S 2007 Genetic variability and association analysis in three different morphological groups of cotton (*Gossypium hirstum* L.). Asian Journal of Plant Sciences 6(1): 122-128.

Pushpam R, Raveendran T S, Devasena N and Ravikesavan R 2004 Studies on genetic diversity in upland cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton improvement 29 (2): 154-162.

*Rao C R 1952 Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York pp. 236-272.

Rao G N and Reddy M S S 2001 Studies on heritability and variability for yield and its components in hirsutum cotton. Journal of Cotton Research and Development 15 (1): 84-86.

Rao G N, Reddy M S S and Shanti P 2001 Correlation and path analysis of seed cotton yield and its components in cotton. Journal of Cotton Research and Development 15 (1): 81-83.

Ravikumar 2004 Genetic divergence studies in introgressed material of upland cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Reddy A N 2001 Heterosis, combining ability and stability analysis of hybrids for yield and yield components in cotton (*Gossypium hirsutum* L.). Ph.D. thesis. Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Sakthi A R, Kumar M and Ravikesavan R 2007 Variability and association analysis using morphological and quality traits in cotton (*Gossypium hirsutum* L.). Journal of Cotton Research and Development 21(2): 148-152.

*Samanc B and Ozkaynak E 2000 Determination of some agronomic traits of cotton (*Gossypium hirsutum* L.) cultivars and lines under antalya conditions. Ziraat Fakultesi Dergisi, Akdemiz Universitesi 13 (2): 113-122.

Sambamurthy J S V, Gopinath M and Mukundan S 1994 Association of characters and path coefficient analysis in upland cotton (*Gossypium hirstum* L.). Madras Agricultural Journal 81: 308-311.

Sambamurthy J S V, Reddy D M and Reddy K H G 1995 Genetic variability correlation and path analysis in cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 20(2): 133-138.

Sambamurthy J S V, Chamundeswari N and Udayasree P 2006 Assessment of genetic variability and relationship of yield attributes in introgressed lines of American cotton. The Andhra Agricultural Journal 53 (3&4): 129-132.

Sangeetha K 1998 Character association of quality traits on yield and yield components in cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Satish Y, Jain P P and Chhabra B S 2009 Studies on genetic diversity in upland cotton (*Gossypium hirsutum* L.). Journal of Cotton Research and Development 23(1): 18-22.

Sharad Bhatnagar 1995 Correlation studies of yield, yield contributing and qualitative characteristics of segregating and stable materials of cotton. Haryana Agricultural University 25: 187-193.

Singh R K and Chaudhary B D 1977 Biometrical Methods in quantitative Genetic Analysis. Kalyani Publishers, New Delhi pp. 215-218.

Singh T H and Gill S S 1984 Genetic diversity in upland cotton under different environments. Indian Journal of Genetics and Plant Breeding 44(3): 506-513.

Sivaprasad U 2003 Heterosis and combining ability studies for yield and yield components in cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Sivaprasad U, Chenga Reddy V and Narisireddy A 2004a A combining ability studies for yield and yield components in American cotton. Paper presented in International symposium on “Strategies for Sustainable Cotton Production – A Global Vision” held at University of Agricultural Sciences, Dharwad 23rd – 25th November, 2004.

Sivaprasad U, Chenga Reddy V and Narisireddy A 2004 b Studies on genetic variability in American cotton (*Gossypium hirsutum* L.). Paper presented in International Symposium on “Strategies for Sustainable Cotton Production – A Global Vision” held at University of Agricultural Sciences, Dharwad, 23rd-25th November, 2004.

Sivasubramanian S and Menon M 1973 Heterosis and inbreeding depression in rice. Madras Agricultural Journal 60: 1139-1149.

*Sorenson T A 1948 A method of establishing groups of equal amplitude in plant sociology based on similarity of species content and its application to analysis of the vegetation on Danish Commons. Biologiske Skrifter 5: 1-34.

*Sneath P H A and Sokal R R 1973 Numerical taxonomy. W.H. Freeman and Company, Sanfransisco.

Sumathi P and Nadarajan N 1995 Character association and component analysis in upland cotton. Madras Agricultural Journal 82 (4): 225-228.

Sumathi P and Nadarajan N 1996 Genetic variability in cotton. Journal of Indian Society for Cotton Improvement 21: 33-36.

Swarup and Chaugle B S 1962 Studies on genetic variability in sorghum; phenotypic variation and heritable component in some quantitative characters contributing towards yield. Indian Journal of Genetics and Plant Breeding 22: 31-36.

Tuteja O P, Puneet Luthra and Sunil Kumar 2003 Combining ability analysis in upland cotton (*Gossypium hirsutum* L.) for yield and its components. Indian Journal of Agricultural Sciences 73 (12): 671-675

*Tuteja O P, Gopalkrishnan and Sunil Kumar N 2004 Studies on heterosis for oil content and its related traits in intra-hirsutum hybrids based on CMS system. National Journal of Plant Improvement 6(2): 112-114.

Tuteja O P, Sunil Kumar, Hamid Hasan and Mahendar Singh 2005a Heterosis and interrelationship between seed-cotton yield and quantitative characters in upland cotton (*Gossypium hirsutum* L.). Indian Journal of Agricultural Sciences 75 (3): 169-171

Tuteja O P, Sunil Kumar and Mahendar Singh 2006 Selection parameters and yield enhancement of upland cotton (*Gossypium hirsutum* L.) under irrigated ecosystem of North India. Indian Journal of Agricultural Sciences 76(2): 77-80.

Tuteja O P, Sunil Kumar, Mahendar Singh and Hamid Hasan 2005b Heterosis in GMS based intra-hirsutum hybrids (*Gossypium hirsutum* L.) for fibre quality characters. Journal of the Indian Society for Cotton Improvement 30(1): 47-52.

Tyagi A P 1994 Association of yield components and fibre traits and their functions in upland cotton (*Gossypium hirsutum* L.). Indian Journal of Agricultural Research 28 (3): 159-165.

Verma S K, Tuteja O P, Koli N R, Jal Singh and Monga D 2006 Assessment of genetic variability nature and magnitude of character association in cytotype genotypes of upland cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 31 (3): 129-133.

Vijayalaxmi G 2008 Genetic divergence in cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Waqas Ahmed, Khan N U, Khalil M R, Aisha Praveen, Umm-e-Aiman Muhammed, Saeed Samiullah and Shah S A 2008 Genetic variability and correlation analysis in upland cotton (*Gossypium hirsutum* L.) Sarhad Journal of Agriculture 24(4): 573-580.

*Wright S 1921 Correlation and causation. Journal of Agricultural Research 20: 557-585.

* **Original not seen**

The literature is cited according to thesis guidelines prescribed by Acharya NG Ranga Agricultural University, Rajendra Nagar, Hyderabad – 500 030